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Best Local Similarity: Query Match:	LI 18 ADD39309 standard; protein; 248 AA. Human secreted/transmembrane protein US200309694-A1.	PD ZZ-mAY-ZOUS. PA (GETH) GENENTECH I Best Local Similarity: Querry Match:	Out 1/ Human secreted/transmembrane protein PR US2003092061-Al.		LI 18 ADD40263 standard; protein; 248 AA. Human secreted/transmembrane protein PRO1303 US2003082627-A1.	PD 01-MAY-2003. PA (GETH) GENENTECH I Best Local Similarity: Query Match:	KESULI 19 ID ADES0484 standard; protein; 248 AA. DE Human secreted/transmembrane protein		ur 20 ADE20096 standard; protein; 2 Human secreted/transmembrane US2003092883-Al.	PD 15-MAY-2003. PA (GETH) GENENTECH I Best Local Similarity:	ADESOU07 standard; protein; 248 AA. Human secreted/transmembrane protein US2003082626-A1.	PD 01-MAY-2003. PA (GETH) GENENTECH 1 Best Local Similarity: Query Match:	or 22 ADE21565 standard; protein; 2 Human secreted/transmembrane US2003082628-Al.		0 standard; ecreted/tra: 04053-A1.	30-OCT-2003. (GETH) GENENTECH I Local Similarity:	rESOLI 248 AA. ID APF55883 standard; protein; 248 AA. DE Human secreted/transmembrane protein PN US2003204064-A1. PD 30-OCT-2003.	ETH) GE cal Simi
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RESULT 34 ID ADH04513 standard; protein; 2 DE Human secreted/transmembrane bn 1152004005655-31	tein; 248 AA mbrane prote	248 AA. protein PRO1303.	
3 t		Mismatches: Indels:	00
KESULI 33 ID ADHG1514 standard; protein; 3 DE Human secreted/transmembrane PN US2004014110-A1.	tein; 248 AA. mbrane protein	in PRO1303.	
, t		Mismatches: Indels:	00
30LT 36 ADN10927 standard; Human kallikrein 12 WO2004029285-A2.	protein; 248 AA 2, marker of end	AA. endocrine cancer.	
PD 08-MEN-2004. PA (MOUN) MOUNT SINAI HO Best Local Similarity: 100 Query Match: 66.	HOSPITAL. 100.00% 66.51%	Mismatches: Indels:	00
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PD IS-APK-2004. PA (GETH) GENENTECH INC. 3est Local Similarity: 100 20ery Match: 66.	INC. 100.00% 66.51%	Mismatches: Indels:	
ADT94373 standard; Human PRO1303 prote AU2003259607-A1.	protein; 248 AA. in.		
ጀ ።	INC. 100.00% 66.51%	Mismatches: Indels:	•
39 \B21303 standard; \man KLK-L5 prote: \200053776-\2.	protein; 254 AA in #3.		
14-SEP-2000. (MOUN) MOUNT SINAI st Local Similarity: 8	HOSPITAL. 85.19% 66.43%	Mismatches: Indels:	0 43
6 standard; allikrein 12	protein; 254 AA 2, marker of end	AA. endocrine cancer.	
08-APR-2004 (MOUN) MOUNT SINAI St Local Similarity: 8 ery Match: 6	. HOSPITAL. 85.19% 66.43%	Mismatches: Indels:	0 43
SULT 41 ADP56174 standard; Human PRO protein s	protein; 254 AA sequence SEQ ID	 NO:2150.	
PD 13-MAY-2004. PD 13-MAY-2004. Best GETH) GENENITECH INC. Best Local Similarity: 85.19% Ouery Match: 66.43%		Mismatches: Indels:	0 43
AAO29516 standard; Human kallikrein-li WO33394475-A2.	protein; 248 AA ke protein 5 (1	AA. (18817) .	
PD IS-MAX-2003. PA (MILL-) MILLENNIUM PHARM BEST Local Similarity: 99.60 Query Match: 66.17 RESULT 43	INC.	Mismatches: Indels:	

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AAY03220 standard; protein; 260 AA.
Amino acid seguence of human tumour antigen derived gene-14 protein.
WO9909138-A1.
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RESULT 49
ID AAB44300 standard; protein; 260 AA.
DE Human PRO322 (UNQ283) protein sequence SEQ ID NO:395.
PN W0200053756-A2.
PD 14-SEP-2000.
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Human secreted protein from cDNA clone HKAFV61.
WO9940183-A1.
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DE Human neuropsin protein.
DE J2131318461-A.
DP 24-NOV-1999.
PA (SHIO/) SHYOZAKA S.
PA (IGAKU SEIBUTSUGAKU KENKYUSHO KK.
Best Local Similarity: 48.08*
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DB Human PRO322 polypeptide sequence.

PN W0200140466-A2.

PD 07-UNY-2001.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.08$ Miss Overy Watch:

RESULT 52
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ID AAB21322 standard; protein; 260 AA.

DE Human neuropsin.
PN WO200053776-A2.
PD 14-SEP-2000.
PD (MOUNT SINAI HOSPITAL.

Best Local Similarity: 48.08% M

Query Match: 30.61% I
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Human PRO322 protein sequence.
WO9946281-32.
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     AAB21301 standard; protein; 184 AA.
Human KLK-L5 protein #1.
WO200053776-A2.
ID AAB21301 standard; protein; 184
DE Human KLK-L5 protein #1.
PN W020063776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 100.00$
Query Match: 49.32$
RESULT 44
ID AAY28642 standard; protein; 162
DE Human secreted protein from cDNA W05940183-A1.
PD 12-AUG-1999.
PA (HUMA-) HUWAN GENOME SCI INC.
Best Local Similarity: 64.11$
Query Match: 39.25$
                                                                                                                                                                                                                                                                                           ID AAY32852 Standard, F.-.
DB Human serine protease protein
PN JP1122765-A.
PD 24-AUG-1999.
PA (SUNR ) SUNYORY LTD.
Best Local Similarity: 48.08*
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DE Amino acid sequence of human
PN W09909138-A1.
PD 25-FEB-1999.
PA (UYAR-) UNIV ARKANSAS.
Best Local Similarity: 48.08%
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RESULT 51
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in PRO322, SEQ ID NO:127.	Mismatches: 96 Indels: 13	364.	Mismatches: 96 . Indels: 13	ID NO:72.	Mismatches: 96 Indels: 13		Mismatches: 96 Indels: 13	PRO322 SEQ ID NO: 72.							Mismacches: 96 Indels: 13	. 612.		Mismatches: 96 Indels: 13	
AABS3087 standard; protein; 260 AA. Human anglogenesis-associated protein PRO322, SEQ ID NO:127 WO200053753-A2.	PD 14-SEP-2000. PA (GETH) GENENTECH INC. Best Local Similarity: 48.08% Query Match: 30.61%	KESULT 53 KESULT 53 KESULT 53 KESULT 53 KESULT 53 KESULT 52 KESULT 60 KESULT 50 KESULT	Est Local Similarity: 48.08% Query Match: 30.61% RESHIF 54	ABB64852 standard; protein; 260 AA. Human PR0322 protein sequence SEQ ID NO:72 WO200200690-A2.	PD 03-JAN-2002. PA (GETH) GENENTECH INC. Best Local Similarity: 48.08% Query Match: 30.61%	AAU81959 standard; protein; 260 AA Human PRO322.	PN W0200109327-A2. PD 08-FEB-2001. PA (GETH) GENENTECH INC. GETL LOCAL Similarity: 48.08\$ Query Match: 30.61\$	RESULT 56 ID ABB95458 standard; protein; 260 AA. DE Human angiogenesis related protein PRO322	WOZUUZUSZ84-AZ. 31-JAN-2002. (GETH) GENENTECH INC.	(BAKE/) BAKER K P. (FERR/) FERRARA N. (GERR/) GERRER H	/) GODOWSKI /) GURNEY A	ccs	PAN J.	 (WOOD/) WOOD W:I.	Best Local Similarity: 48.08% Query Match: 30.61%	ADI17076 standard; protein; 260 AA Human NOVX protein homologue SeqID	ı İ	PA (CURA-) CURAGEN CORP. Best Local Similarity: 48.08% Query Match: 30.61%	RESULT 58 ID AB017813 standard, protein, 260 AA.

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uman secreted and transmembrane protein PRO322.
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Human secreted/transmembrane protein PRO322.
US2003004102-A1.
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OV11h protein SEQ ID NO:62.
29424-A2.
                                                                                      7 standard; protein; 260 AA.
RO polypeptide #198.
04311-Al.
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RO polypeptide #198.
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PD 02-JAN-2003. PA (GETH) GENENTECH : Best Local Similarity: Query Match: RESULT 69	DE Human secreted/transmembrane, PN US2003032155-A1.	PD 13-FEB-2003. PA (GETH) GENENTECH : Best Local Similarity: Query Match:	ID ADA45915 standard; protein; DE Novel human secreted and tra	PN USZUSZZZB-A1. PD 30-JAN-2003. PA (GETH) GENENTECH : Best Local Similarity: Query Match:	standard, O polypept 3212-A1. 003. GENENTECH	Query Match: RESULT 72 ID ADA18996 standard;	4517-A1. 003. GENENTECH	RESULT 73 ID ADA61619 standard; protein;	-40005	RESULT 74 ID ADB19404 standard; DE Novel himan secrets	8796-A1. 003. GENENTECH	RESULT 75 ID ADB27945 standard; protein; DE Human PRO polypeptide #198. PN US2003082704-Al. PN 01-MAX-2003	PA (GETH) GENENTECH 1 Best Local Similarity: Query Match:	KESULI (ADA86424 standard; protein; DE Novel human secreted and tr. PN US2000082711-Al.	GOS. GENENTECH milarity:	KESULI''' ID ADBIS988 standard; protein; DE Human PRO polypeptide #198. PN US2003087350-A1. PD 08-MAY-2003.

Mismatches: 96		Mismatches: 96 Indels: 13	260 AA.	Mismatches: 96 Indels: 13	260 AA.	Mismatches: 96 Indels: 13	protein; 260 AA. ed and transmembrane protein PRO322	Mismatches: 96 Indels: 13	260 AA.	Mismatches: 96 Indels: 13	260 AA.	Mismatches: 96 Indels: 13	n; 260 AA. transmembrane protein PRO322.	Mismatches: 96 Indels: 13	260 AA.	Mismatches: 96 Indele: 13	ndard; protein; 260 AA. secreted and transmembrane protein PRO322
INC.	30.61% protein; de #198.	INC. 48.08% 30.61%	protein; de #198.	INC. 48.08% 30.61%	protein; de #198.	INC. 48.08% 30.61%	protein;	INC. 48.08% 30.61%	protein; de #198.	INC. 48.08% 30.61%	protein; de #198.	INC. 48.08% 30.61%	protein;	INC. 48.08% 30.61%	rotein; e #198.	INC. 48.08% 30.61%	protein; Sed and tra
(GETH) GENENTECH	Query Match: RESULT 78 ID ADA47774 standard; DB Human PRO polypepti PN US2003077315-All	17-APR-2003. (GETH) GENENTECH st Local Similarity: ery Match:	ADA67569 standard; Auman PRO polypept 152003068795-A1.	(GETH) GENENTECH st Local Similarity: ery Match:	ADB30576 standard; Human PRO polypept US2003068794-Al.	PA (GETH) GENENTECH : Best Local Similarity: Query Match:	ADA85872 standard; Novel human secret US2003082693-A1.	PD 01-MAI-2003. PA (GETH) GENENTECH : Best Local Similarity: Query Match:	02 0A97084 standard; uman PRO polypept S2003082705-A1.	3. NENTECH larity:	A79388 standard; man PRO polypept :2003082763-A1.	(GETH) GENERTECH st Local Similarity: ery Match:	ADA87527 standard, Novel human secret US2003087345-A1.	# ··	4 4 8 8	-MAY-2003. ETH) GENENTECH cal Similarity: atch:	resold & Abasis standard; TD Abasis standard; DE Novel human secrete PN US2003082694-Al.

Query Match: RESULT 96 ID ADA74522 stan	DE Human PRO pol PN US2003068798- PD 10-APR-2003.	st Local S: ery Match: SULT 97	Human PRC US2003077 24-APR-20	GETH) GETH) G st Local Sin sry Match:	ID ADA82279 Stan DE Human PRO pol PN US2003082701-	# 7 7 15	ID ADA75242 stan DE Human PRO pol PN 'US2003073216-	# # 5	DE Novel human EPN US2003082695-	PD 01-MAY-2003. PA (GETH) GENER Pest Local Similar Query Match:	RESULT 101 ID ADA84768 star	DE Novel human E PN US2003082708- PD 01-MAY-2007 PA (GETH) GENER	st Local S: ery Match: SULT 102	1D ADE30024 BCAR 1D ADE30024 BCAR DE Human PRO pol PN US2003073214-1 PD 17-APR-2003.	# # E	ID ADA80552 star DE Human PRO POI PN US2003082761- PD 01-Max-2003. PA (GRTH) GENDS.	st Local Si ery Match: SULT 104	DE Human PRO po. PN US2003082703- PN US2003082703- PN 01-MAY-2003-	st Local Sery Match:
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Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA. nsmembrane protein	Mismatches: Indels:	JT 89 ADB18845 standard; protein; 260 AA. Novel human secreted and transmembrane protein PRO322	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA. nsmembrane protein	Mismatches:		260 AA.	Mismatches: Indels:	n; 260 AA. transmembrane protein PRO322	Mismatches: Indels:	T 94 ABO19701 standard; protein; 260 AA. ANOLI human secreted and transmembrane protein US2003056240-A1.	Mismatches: Indels:	260 AA. e polypeptide PRO322	Mismatches:
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Best Local Similarity: Query Match: PRSHT R7	DE Human PRO polypeptide #198. PN US2003087351-A1.	# 2	RESULT 88 ID ADA24934 standard; protein; DE Novel human secreted and tra	ភី អ៊ី	RESULT 89 ID ADB18845 standard; DE Novel human secrete	PN US2003073211-A1. PD 17-APR-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48. Query Match: 30.	SULT 90 ADA94060 standard, Human PRO polypepti	PN US2003077722-A1. PD 24-APR-2003. PA (GETH) GENENTECH I Best Local Similarity: Query Match:	RESULT 91 ID ADB19956 standard; protein; DE Novel human secreted and tra	PN US2003082691-A1. PD 01-MAY-2003. PA (GETH) GENENTECH I Best Local Similarity:	Query Match:	ID ADB13268 standard, protein, DE Human PRO polypeptide #198. PN US203082710-A1.	벁뱮	Ĕ	PD 06-MAR-2003. PA (GETH) GENENTECH I Best Local Similarity: Query Match:	RESULT 94 ID ABO19701 standard; DE Novel human secrete PN US2003050240-A1.	Ξ	5 standard; ecreted/tran 55216-A1.	PD 20-MAR-2003. PA (GETH) GENENTECH 1 Best Local Similarity:

Query M		30.61%	Indels:	13
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PD PA Best Quer		INC. 48.08% 30.61%	Mismatches: Indels:	96
NE DE S	D1 37 ADB24755 standard; protein; 3 Human PRO polypeptide SEQ ID US2003077713-A1.	protein; 260 ide SEQ ID NO	. AA. . 396.	
PD 2 PA Best I		INC. 48.08% 30.61%	Mismatches: Indels:	96 13
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atch: 142 B73901 standard; protein; 2003 Standard; protein; MAR-2003. ETH) GENENTECH INC. cal Similarity: 48.08\$ atch: 143 B86751 standard; protein; wan PRO polypeptide #60. 2003082687-A1. 2003082687-A1. ETH) GENENTECH INC. cal Similarity: 48.08\$ atch: 2003082687-A1. 2003082697-A1. 2003082697-A1. ETH) GENENTECH INC. cal Similarity: 48.08\$ atch: MAY-2003. ETH) GENENTECH INC. cal Similarity: 48.08\$ atch: AND polypeptide #60. MAY-2003. ETH) GENENTECH INC. cal Similarity: 48.08\$ atch: MAY-2003. ETH) GENENTECH INC. cal Similarity: 48.08\$ atch: AND polypeptide #60. AND polypeptide SEQ ID AND po	Indels: 260 AA.	Mismatches: Indels:	260 AA. nsmembrane protein	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA. nsmembrane protein	Mismatches: Indels:	3 B		39	Äi		C	260 AA. NO 396.
atch: 142 142 2003045462-A1. 2003045462-A1. 2003045462-A1. 2013. ETH CENENTECH 2013 B47144 Standard; 847144 Standard; 847144 Standard; 847144 Standard; 847144 Standard; 8487751 Standard; 8487751 Standard; 8487751 Standard; 84970303032548-A1. 8787-2003.	30.61% protein; ide #60.	INC. 48.08% 30.61%	protein; ed and tra	INC. 48.08%	protein; ide #198.	INC. 48.08% 30.61%	protein; ide #60.	INC. 48.08% 30.61%	protein; ed and tra	INC. 48.08\$	protein;	INC. 48.08%	sv.614 protein; ide SEQ II	INC. 48.08% 30.61%	protein; ide SEQ II	INC. 48.08% 30.61%	protein; ide SEQ II
HAD AS GRANT AS GRANT BOOK HAD BOOK BOOK BOOK BOOK BOOK BOOK BOOK BOO	Query Match: RESULT 142 ID ADB71901 standard; DE Human PRO polypept: PN US2003045462-A1.	06-MAR-2003. (GETH) GENENTECH : Local Similarity: Match:	r 143 ADB47144 standard; Novel human secret	US2003082687-A1. 01-MAY-2003. (GETH) GENENTECH Local Similarity: MAFCH.	I 144 ADB86751 standard; Human PRO polypept: JS2003082697-A1.	PD 01-MAY-2003. PA (GETH) GENENTECH: Best Local Similarity: Query Match:	RESULT 145 ID ADB76617 standard; DE Human PRO polypept: PN US2003083248-A1.	PD 01-MAY-2003. PA (GETH) GENENTECH : Best Local Similarity: Query Match:	L 146 ADB77356 standard; Novel human secret:	PD 0520050505.T. PD 01-MAY-2003. PA (GETH) GENENTECH :	r 147 ADB34513 standard; Juman PRO polypept:	PD 24-APR-2003 PD 24-APR-2003 PA (GETH) GENENTECH : Best Local Similarity:	Query maccn: RESULT 148 ID ADB35617 standard; DE Human PRO polypept:	PD 24-APR-2003. PA (GETH) GENENTECH : Best Local Similarity: Ouery Match:	r 149 ADB33961 standard; Human PRO polypept: JS2003077716-A1.	PD 24-APR-2003. PA (GETH) GENENTECH Best Local Similarity: Query Match:	ADB35065 standard; Human PRO polypept: US2003077718-Al.

	96 13	PRO322.	96 13		96 13		96 13		96 13		96 13		96 13		96 13		96 13
0 AA. O 396.	Mismatches: Indels:	0 AA. membrane protein	Mismatches: Indels:	60 AA. protein, PRO322.	Mismatches: Indels:	260 AA. protein, PRO322.	Mismatches: Indels:	260 AA. protein, PRO322.	Mismatches: Indels:	260 AA. protein, PRO322.	Mismatches: Indels:	60 AA. protein, PRO322.	Mismatches: Indels:	260 AA. protein, PRO322.	Mismatches: Indels:	60 AA. protein, PRO322.	Mismatches: Indels:
rd; protein; 260 eptide SEQ ID NO	CH INC. Y: 48.08% 30.61%	rd; ret	CH INC. y: 48.08% 30.61%	protein; 2 nsmembrane	CH INC. Y: 48.08% 30.61%	rd; protein; 260 transmembrane pr	CH INC. y: 48.08% 30.61%	767 standard; protein; 260 secreted/transmembrane pr 3054405-A1.	CH INC. Y: 48.08% 30.61%	rd; protein; 260 transmembrane pr	CH INC. y: 48.08% 30.61%		Y: 48.088 30.618		CH INC. Y: 48.08\$ 30.61\$	rd; protein; 260 transmembrane pr	CH INC. y: 48.08% 30.61%
RESULT 1515 DD ADB36169 standard; protein; 2 DE Human PRO polypeptide SEQ ID NUSSO03077720-A1.	GETH) (GETH) Local S	152)B46564 sta)vel human)2003082692	01-MAY-2003. (GETH) GENENTECH Local Similarity: // Match:	LT 153 ADC44043 standard; Human secreted/trai 202003054986-A1.	GETH) GENENTECH Local Similarity: Y Match: LT 154	ADC61803 standard; protein; 26 Human secreted/transmembrane p US2003049684-A1.	13-MAK-2003. (GETH) GENENTECH Local Similarity: MAtch:	200	PD 20-MAR-2003. PA (GETH) GENENTECH Best Local Similarity: DECTY 156	ADC66867 standard; protein; 26 Human secreted/transmembrane p US2003060406-A1.	27-MAR-2003. (GETH) GENENTECH Local Similarity: Y Match:	Arc68991 standard; protein; Human secreted/transmembrane US2003064407-A1.	(GETH) GENENTECH Local Similarity: Y Match:		(GETH) GENENTECH Local Similarity: Y Match:	ADC68116 standard; protein; 26 Human secreted/transmembrane p US2003069178-A1.	10-APR-2003. (GETH) GENENTECH Local Similarity: Y Match:
RESU ID PN	PA PA Best J Query	RESULT ID AL DE NG	PD (PA Best I Query	PN US	5 6 5		PD 13 PA (G Best Lo Query M	PER	70 00 7	ñ	m 0) (7	S S S S S S	PA ((2	0 0 0		PD 1 PA (Best L Query

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	96 13		96 13		96 13		96 13	PRO322.	96 13	PRO322.	96 13	PRO322.	96 13	Seg ID396.	96 13	Seq ID396.	96 13
260 AA. e protein, PRO322.	Mismatches: Indels:	60 AA. protein, PRO322.	Mismatches: Indels:	260 AA. : protein, PRO322.	Mismatches: Indels:	260 AA. : protein, PRO322.	Mismatches: Indels:	in, 260 AA transmembrane protein PRO322	Mismatches: Indels:	in; 260 AA. transmembrane protein	Mismatches: Indels:	n; 260 AA. transmembrane protein PRO322	Mismatches: Indels:	.n; 260 AA. transmembrane protein	Mismatches: Indels:	otein; 260 AA. and transmembrane protein	Mismatches: Indels:
protein; S smembrane	INC. 48.08% 30.61%	protein; smembrane	INC. 48.08% 30.61%	protein; smembrane	INC. 48.08% 30.61%	protein; smembrane	INC. 48.08% 30.61%	protein;	INC. 48.08% 30.61%	protein; d and tra	INC. 48.08% 30.61%	indard; protein; secreted and tra 5-A1.	INC. 48.08% 30.61%	indard; protein; 260 AA secreted and transmemb:	INC. 48.08% 30.61%	indard; protein; 260 AA. secreted and transmembr	INC. 48.08% 30.61%
ID ADC41436 standard; protein; 260 AA. DB Human secreted/transmembrane protein, NB US2003072745-A1. PD 17-APR-2003.	PA (GETH) GENENTECH II Best Local Similarity: Query Match:	KESULT 161 ID ADC67491 standard; protein; 260 AA. DE Human secreted/transmembrane protein, by US2003031313-A1.	PD I/-AFK-2003. PA (GETH) GENENTECH I. Best Local Similarity: Query Match:	RESULT 162 D ADC62427 standard; protein; 260 AA. DE Human secreted/transmembrane protein, PW US2003073624-A1.	7, 7,	standard; creted/tran 4998-Al.	ig at	RESULT 164 ID ADC50437 standard; protein; DE Novel human secreted and tra PN US2003092106-A1.	PD IS-MAI-2003. PA (GETH) GENENTECH I Best Local Similarity: Query Match:	RESULT 165 ID ADC71984 standard; protein; DE Novel human secreted and tr; PN US2003092107-A1.	PD 15-MAY-2003. PA (GETH) GENENTECH I Best Local Similarity: Query Match:	RESULT 166 ID ADC59963 standard; DE Novel human secrete PN US2003092105-A1.	15-MAY-2003. (GETH) GENE st Local Simila	0 sta uman 87365	PD 08-MAY-2003. PA (GETH) GENENTECH INC. BEST LOCAL SIMILARITY: 48. QUERY MATCH: 30.	SULT 168 ADC57324 sta Novel human US200308736	08-MAY-2003. (GETH) GENENTECH 1 st Local Similarity: sry Match:

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DB ADC58547 standard; protein; 260 AA.

DB Novel human secreted and transmembrane protein Seq ID396.

BN US2003087346-A1.

DD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 48 08% Indels: 13

Ouery Macch: 13
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Novel human secreted and transmembrane protein Seq ID396.
US2003087359-A1.
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DE Novel human secreted and transmembrane protein Seq ID396.

PN US2003087360-A1.

PD 08-MAY-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 48.08% Mismatches: 96

QUERY MACCh: 13
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DE Novel human secreted and transmembrane protein Seq ID396.

PN 10220030697363-A1.

PD 08-MAY-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 48.08%

Mismatches: 96
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Novel human secreted and transmembrane protein Seq 1D396.
US2003087364-A1.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087367-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08% Mismatches: 96
20ery Match: 30.61% Indels: 13
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Novel human secreted and transmembrane protein PRO322.
US2003092104-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC90213 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
                                                                                                                                              Novel human secreted and transmembrane protein PRO322. US2003087361-A1.
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Human PRO polypeptide #198.
US2003087362-A1.
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PA (GETH) GENENTECH INC.
Best Local Similarity: 48.08%
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PA (GETH ) GENENTECH INC.
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PAR (GETH ) GENENTECH INC.

Best Local Similarity: 48.08%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%
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ADC55977 standard;
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RESULT 175
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ESULT 170
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96 13	96 13	96 133	96 13	PRO322.	96 13	PRO322.	96 13		96 13		96 13	36.	96 13	
Mismatches: Indels: 260 AA.	Mismatches: Indele:	260 AA. Mismatches: Indels:	260 AA. Mismatches: Indels:	in; 260 AA. transmembrane protein	Mismatches: Indels:	n; 260 AA. transmembrane protein	Mismatches: Indels:	: 260 AA. SEQ ID NO:2.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA. : PRO polypeptide #3	Mismatches: Indels:	260 AA.
	ide #198. INC. 48.08% 30.61%			protein; ed and tra	INC. 48.08% 30.61%	indard; protein; secreted and tra	INC. 48.08% 30.61%	protein; protein S	I HOSPITAL 48.08% 30.61%		INC. 48.08% 30.61%	protein; nsmembrane	INC. 48.08% 30.61%	
FN 02200308738-A1. PD 08-MAY-2003. PA (GETH) GENENTECH) Best Local Similarity: Query Match: RESULT 179 ID ADC69632 standard;	DE Human PRO polypeptide #198. PN US2003194770-Al. PD 16-OCT-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.08% Query Match: 30.61%	ID ADC48521 standard, protein, DE Human PRO polypeptide #198. DE 1003194773-A1. PD 16-OCT-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.08% RESULY 181.	0 standard; RO polypept 94776-A1. 2003. GENENTECH imilarity:	ADD04625 standard; protein; Novel human secreted and tra US2003087354-Al.	PA (GETH) GENENTECH 1 Best Local Similarity: Query Match:	sta man 2103	PD 15-MAY-2003. PA (GETH) GENENTECH 1 Best Local Similarity: Ouery Match:	standard; llikrein 8 5404-Al.	PA (MOUN) MOUNT SINAI HOSPITAL Best Local Similarity: 48.08% Moery Match: 30.61%	ADD11088 standard; protein; Human PRO polypeptide #198. US2003194774-A1. 16-OCT-2003.	ENTECH arity:	ULI 186 MDD10361 standard; protein; 260 AA. Human secreted/transmembrane PRO polypeptide US2003105011-AI.	N-2003:) GENENTECH Similarity: h:	KESULI 18/ ID ADC47969 standard; protein; DE Human PRO polypeptide #198.

96 13	PRO322.	96 13	. 92	96 13		96 13	PRO322.	96		96 13		96 13	PRO322.	96 13	. 91	96 13	protein.
Mismatches: Indel8:	AA. Abrane protein	Mismatches: Indels:	AA. polypeptide #3	Mismatches: Indels:	AA.	Mismatches: Indels:	260 AA. ansmembrane protein	Mismatches: Indels:	AA.	Mismatches: Indels:	AA.	Mismatches: Indels:	260 AA. ansmembrane protein	Mismatches: Indels:	AA. polypeptide #36	Mismatches: Indels:	AA. e-14 (TADG-14)
INC. 48.08% 30.61%	; protein; 260 AA. ted and transmembrane	INC. 48.08 30.61	; protein; 260 P ansmembrane PRO	INC. 48.08% 30.61%	protein; 260 ide #198.	INC. 48.08% 30.61%	; protein; 260 f ted and transmen	INC. 48.08% 30.61%	; protein; 260 ß tide #198.	INC. 48.08% 30.61%	; protein; 260 Å tide #198.	INC. 48.08% 30.61%	protein; ed and tr	INC. 48.08% 30.61%	protein; 260 nsmembrane PRO	INC. 48.08% 30.61%	protein; 260 en derived gen
16-OCT-2003. (GETH) GENENTECH Local Similarity: Match:	029 standard human secre	08-MAY-2003. (GETH) GENENTECH Local Similarity: MATCH:	189 DD11321 standard Iman secreted/tr 12003105013-A1.	05-JUN-2003. (GETH) GENENTECH Local Similarity: Match:	8 standard RO polypep 94775-A1.	ETH Scal	191 0041211 standard vvel human secre 12003203438-A1.	30-OCI-2003. (GETH) GENENTECH Local Similarity: Match:	132 D52350 standard man PRO polypep [2003194769-A1.	ETH) GE cal Simi latch:	D53090 standard man PRO polypep 2003194792-A1.	18-001-2003. (GETH) GENENTECH Local Similarity: Y Match:	D53642 standard wel human secre	30-OCT-2003. (GETH) GENENTECH Local Similarity: Match:	D37114 standard man secreted/tr 2003105012-A1.	GETH) GENENTECH Local Similarity: Match:	W00074 standard W00074 standard 2002037581-A1. -MAR-2002.
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nismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA. nsmembrane protein	Mismatches: Indels:	260 AA. : protein, PRO322.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	37 standard; protein; 260 AA. human secreted and transmembrane protein PRO322 1194765-A1.
30.61%	d, protein; ptide #198.	H INC. : 48.08% 30.61%	d, protein; ptide #198.	H INC. : 48.08% 30.61%	d; protein; ptide #198.	H INC. : 48.08% 30.61%	d, protein; sted and tra	1 INC. 48.08% 30.61%	1; protein; ransmembrane	1 INC. : 48.08% 30.61%	1, protein; ptide #198.	1 INC. : 48.08% 30.61%	1, protein; ptide #198.	1 INC. : 48.08% 30.61%	l; protein; ptide #198.	1 INC. : 48.08% 30.61%	l, protein; sted and tra
Query Match: RESULT 197	ADD51798 standard; protein; Human PRO polypeptide #198. US2003194779-A1.	FD 19-CCI-2003. Best GETH) GENENTECH Query Match:	ADD02597 standard; protein; Human PRO polypeptide #198. US2003203431-A1.	PA (GETH) GENENTECH Best Local Similarity: Query Match:	ADD02031 standard; protein; Human PRO polypeptide #198. US2003203433-A1.	PA (GETH) GENENTECH Best Local Similarity: Query Match:	ADD54213 standard; protein; Novel human secreted and tra US2003203432-A1.	PD 30-OC1-2003. PA (GETH) GENENTECH Best Local Similarity: Query Match:	ADE4929 standard; protein; 260 AA. Human secreted/transmembrane protein, US2003096744-A1.	PD 22-MAY-2003. PA (GETH) GENENTECH Best Local Similarity: Query Match:	DE Human PRO polypeptic PN US2003199030-A1.	PA (GETH) GENENTECH Best Local Similarity: Query Match: RESULT 203	ADD91426 standard; 1 Human PRO polypepti US2003199055-A1.	PA (GETH) GENENTECH Best Local Similarity: Query Match:	ADE04040 standard; Human PRO polypept: US2003199057-Al. 23-OCT-2003.	PA (GETH) GENENTECH Best Local Similarity: Query Match:	ADE32337 standard; Novel human secret US2003194765-A1.

96	96 13	96 13	96 13	96 13	96 13	96 13	96 13	96 13 PRO322.
Mismatches: . Indels: 50 AA.	Mismatches: Indels: 50 AA.	Mismatches: Indels: :60 AA. protein, PRO322.	Mismatches: Indels: 560 AA. protein, PRO322.	Mismatches: Indels: 60 AA. protein, PRO322.	Mismatches: Indels: 0 AA.	Mismatches: Indels: 50 AA.	Mismatches: Indels: :0 AA.	Mismatches: Indels: 260 AA. ansmembrane protein Mismatches:
st Local Similarity: ery Match: SULT 206 ADE22269 standard; Human PRO polypept US2003199056-A1.	Sert	NC. 48.08\$ 30.61\$ protein; 2	INC. 48.08% 30.61% protein; in	30-OCT-2003. (GETH) GENENTECH INC. (GETH) GENENTECH INC. st Local Similarity: 48.08% BY Match: 30.61% SULT 210 ADD73212 standard; protein; 2 Human secreted/transmembrane	26.2	PD 16-OCT-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.08% Query Match: RESULT 212 RESULT 212 B ADE17846 standard; protein; 260 DE Human PRO polypeptide #198.	Sarat	INC. 48.08\$ 30.61\$; protein; ted and tr INC. 48.08\$

9 standard RO polypepi 03429-Al. 2003.	PA (GETH) GENENTECH INC. Best Local Similarity: 48.08\$ Mismatches: 96 Query Match: 30.61\$ Indels: 13 RESULT 225	ID ADE32889 standard; protein; 260 AA. DE Novel human secreted and transmembrane protein PRO322. PN US2003194766-A1. PD 16-OCT-2003.	PA (GETH) GENENTECH INC. Best Local Similarity: 48.08% Mismatches: 96 Query Match: 30.61% Indels: 13 RESILT 226	581 standard; PRO polypept 3199032-A1. T-2003.	(GEIR) CEMENIECH INC. ST. Match: SULT 227	1D ADE1/21 Standard; protein; 260 AA. DE Human secreted/transmembrane protein, PRO322. PN US-003203433-A1. PD 30-OCT-2003.	(GETH) GENENTECH INC. It Local Similarity: 48.08% STY Match: 30.61% SULT 228	ID ADD80597 standard; protein; 260 AA. DE Human PRO polypeptide #198. PN US2003207418-A1. DD 06-MOV-2009	(GETH) GENENTECH INC. st Local Similarity: 48.08* sry Match: 30.61*	ID ADD89625 standard; protein; 260 AA. DE Human PRO polypeptide #198. PN 422003199028-A1. PD 23-OCT-2003	(GETH) GENERATECH INC. st Local Similarity: 48.08% sry Match: 30.61%	polypepi polypepi 31-A1. 33.	ID ID ID	; process; section tide #198.	st Local Similarity: 48.08% ery Match: 30.61% SULT 232	1D ADE9283/ Standard; protein; 260 AA. DE Human PRO polypeptide #198. PN US2003194777-A1. PD 16-077-2003.	(GEIR) st Local Si ery Match: SULT 233
13 PRO322.	96 13		96 13		96 13		96 13		96 13		96 13		96 13		96 13	:	96 13
ls: protein	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA. : protein, PRO322.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA.	Mismatches: Indels:
ζ. Έ	PD 16-OCT-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.08% Query Match: 30.61%	5 standard; protein; RO polypeptide #198. 07417-A1.	و بر	2 standard; protein; RO polypeptide #198. 94768-A1.	PA (GETH) GENERATECH INC. Best Local Similarity: 48.08* Query Match: 30.61*	KESULI 416 ID ADD72570 standard; protein; 260 AA. DE Human secreted/transmembrane protein, PRO322 PN US2003194781-A1.	PD 16-OCT-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.084 Query Match: 30.618	standard; protein; O polypeptide #198. 9025-1	PD 23-0CT-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.08% Query Match: 30.61%	50 standard; protein; PRO polypeptide #198. 199026-Al	PD 23-0CT-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.08% Query Match: 30.61%	6 standard; protein; RO polypeptide #198. 99033-A1.	# K	standard; protein; O polypeptide #198. 9059-A1.	ال الم	1 2821 standard; protein; n PRO polypeptide #198. 03199064-Al.	PD (SETH) GENENTECH INC. Best Local Similarity: 48.08% Query Match: 30.61%

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	INC. 48.08% 30.61%	indard; protein; secreted and trai	INC. 48.08% 30.61%	andard; protein; secreted and train-	INC. 48.08% 30.61%	otein; #198.	INC. 48.08% 30.61%	protein; ide #198.	INC. 48.08% 30.61%	protein; nsmembrane	INC. 48.08% 30.61%	protein; nsmembrane	INC. 48.08% 30.61%	protein;	INC. 48.08% 30.61%	indard; protein; secreted and tri L-Al.	INC. 48.08% 30.61%
Human secreted/tran US2003195333-A1.	PD 16-001-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.08% Query Match: 30.61%	6 Bta	. # ;	sta man	003. SENENTECH	2 standard; RO polypept: 07370-A1.	3. NENTECH larity:	RESULT 237 ID ADG80586 standard; protein; DE Human PRO polypeptide #198. PN US2003207373-Al.	PD 06-NOV-2003. PA (GETH) GENENTECH 1 Best Local Similarity: Query Match:	JT 238 ADG52992 standard; protein; 260 AA. Human secreted/transmembrane protein, nc2003316561-A1.		RESULT 239 DD ADG60312 standard, protein; 5 DB Human secreted/transmembrane PN US2003206915-A1.	06-NOV-2003. (GETH) GENENTECH Local Similarity:	RESULT 240 ID ADG80034 standard; protein; DE Human PRO polypeptide #198. PN US2003207372-A1.	PD 06-NOV-2003. PA (GETH) GENENTECH BEST Local Similarity: Query Match:	. 23 ¤ €	-NOV-2003. BTH) GENENTECH cal Similarity: atch:
	PA PA Best]	KESOL ID DE	PD PA PA Ouery	KESUL TO DE DE	감상	RESUL ID DE DE	PD PA Best Query	RESUI ID DE PN	PD PA Best Query	RESUI ID DE	PD PA Best Query	RESUI ID DE PN	PD PA Best	RESUL DE DE	PD PA Best Quer	RESU ID DE PN	PD U6 PA (G Best Lo Ouery M

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ADN39182 standard; protein; 260 AA.
Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:500.
WQ2003042661-A2.
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RESULT 247
ID ADM82576 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087355-A1.
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Novel human secreted and transmembrane protein PRO322.
US2003087385-A1.
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DE Novel human secreted and transmembrane protein PR0322.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Locard Similarity: 48.08% Mismatches: 96 Query Match: 30.61% Indels: 13
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PA (GETH ) GENENTECH INC.
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PA (GETH) GENENTECH INC.
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INC. 48.08% 30.61%	protein; 260) nsmembrane PRO	INC. 48.08% 30.61%	protein; 260 ide #198.	INC. 48.08% 30.61%	protein; 260 ide #198.	INC. 48.08% 30.61%	protein; 260 ide #198.	INC. 48.08% 30.61%	protein; 260 ide #198.	INC. 48.08% 30.61%	protein; 260 ide #198.	ጃ 44 W OL1	uc #156 48.08% 30.61% protein de #198	INC. 48.08% 30.61% protein; 260 nsmembrane prc	
05-JUN-2003. (GETH) GENENTECH 1 Local Similarity: Match:	322 standard; secreted/tra 3100497-Al. Y-2003.	TH) GENENTECH 1 al Similarity: ch:		TH) GENENTECH I	s standard; RO polypept 92110-A1.	GENENTECH imilarity:	568 standard; PRO polypept 3092111-A1.	GENENTECH imilarity:	3 standard; RO polypept 03439-A1.	03. ENENTECH ilarity:	standard; polypept 062-A1.	GENENTECH imilarity: 8 standard;	94-A1. 3. NENTECH larity: tandard; polypept 54-A1.	2003. GENENTECH imilarity: 0 standard; ecreted/tra	JUL-2003.
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PA (ASHK/) PA (BAKE/) PA (BATE/) PA (EDTS/) PA (FILV/) PA (FORG/) PA (GAOW/) PA (GAOW/) PA (GADW/)	(WOOD) Bt Local ery Match	RESULT 270 ID ADF6147 DE Human 8 PN US20031 PD 16-OCT- PA (GETH) Best Local S	Cuery Macch: RESULT 271 ID ADF40162 DE Human se PN US00319 PN 23-OCT-2	2000	ID ADF459 DE Human BN US2003 PD 16-OCT PA (GETH	Best Local S Query Match: RESULT 273 ID ADE9472 DE Human P PN US20031		PD 23-OCT- PA (GETH) Best Local S Guery Match: RESULT 275 ID ADE9527 DE Human P PN US20031
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Mismatches: Indels: AA.	Mismatches: Indels: AA. otein, PRO322.	Mismatche Indels: AA. otein, PRO32	Mismatches: Indels: AA. otein, PRO322.	Mismatches: Indels: AA. otein, PRO322.	Mismatches: Indels: AA.	Mismatches: Indels: AA.	Mismatches: Indels:) AA. cotein, PRO322.	Mismatches: Indels: 260 AA. ansmembrane protein
INC. 48.08% 30.61% ; protein; 260 tide #198.	NC. 48.08% 30.61% protein; 260	INC. 48.08* 30.61* ; protein; 260	INC. 48.08% 30.61% ; protein; 260 ansmembrane pr	INC. 48.08% 30.61% ; protein; 260 ansmembrane pr	INC. 48.08\$ 30.61\$, protein; 260 ride #198.	INC. 48.08% 30.61% ; protein; 260 ; protein; 260	1 INC. 48.08 30.61\$ 1; protein; 260	INC. 48.08% 30.61% ; protein; ted and tr.
23-OCT-2003. (GETH) GENENTECH II. Local Similarity: 'Y March: LT 276 ADE93389 standard; IHuman PRO Polypeptil	23-OCT-2003. (GETH) GENENTECH Local Similarity: Match: Match: ADP24354 standard ADP24354 standard	Al. TECH ity: ity: dard	03. ENENTECH ilarity: standard sreted/tr 402-A1.	TECF ity: darc	1200319478 1-OCT-2003 1-OCT-2003 1-OCT-2003 1-OCT-2003 1-OCT-2003 1-OCT-2003	(GETH) GENENTECH Local Similarity: Match: 17 282 ADF27180 standard; Human secreted/tra	(GETH) GENERITECH Local Similarity: // Match: LT 283 LT 283 Human secreted/tra US2003199437-A1.	
PD 23-OCT-PA (GETH) Best Local S Query Match: RESULT 276 ID ADE9338 DE HUMAN P PN US20031	Sert	SUS t	PD 23-0CT-20 PA (GETH) G Best Local Sim Query Match: RESULT 279 ID ADP23730 DE HUMAN SEC	SELT.	PN US PD 16 PA (G PA (G Duery Lo Query Lo RESULT ID AL PN US	a tr	# £ £	PD 23 PA (C Best LC Query LC RESULT ID AN PN US PN US PD 23

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(GETH) GENENTECH Local Similarity:	KESULT 285 ID ADB90566 standard; protein; DE Human PRO polypeptide #198. PN US2003199063-A1. PD 23-OCT-2003.	(GETH) GENENTECH] Local Similarity: Y Match:	DE Human secreted/transmembrane protein, US2003199435-AL.		RESULI 260 AA. ID ADP33089 standard; protein; 260 AA. DE Human secreted/transmembrane protein, 18 US2003211091-A1.	(GETH) GENENTECH : Local Similarity: Y Match:	DE Human secreted/transmembrane protein, 1860 AA. WIS2003211092-AI.	13-NOV-2003. (GETH) GENENTECH Local Similarity: Match:	kESULT 289 ID ADF26556 standard; DE Human secreted/tran	US2003199674-A1. 23-OCT-2003. (GETH) GENENTECH Local Similarity:	JT 290 ADF34345 standard; protein; 260 AA. Human secreted/transmembrane protein, US2003194410-A1.	Ε÷	APF4582 standard; protein; 260 AA. Human secreted/transmembrane protein, US2003195344-A1.	16-OCT-2003. (GETH) GENENTECH 1 Local Similarity: " Match:	ID ADESIJ3 standard; protein; 260 AA. DE Novel human secreted and transmembrane N US2003199058-A1.	PD 23-OCT-2003. PA (GETH) GENENTECH I Best Local Similarity: Overy Match:	ADG02312 standard; protein; 2. Human PRO polypeptide #198. US2003207352-A1. 06-NOV-2003. (GETH) GENENTECH INC.
PA Best Query	RESUL ID DE PN	PA Best Query	SER	PA PA Query	ID DE CE	PA Best Query	ID DE C	PA PA Best Query		PN PD PA Best Query	RESUL ID DE PN	PD PA Best Query		PD PA Best Query	10 E	PD PA Best Query	DE DE PN

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ŞΣ	SULT 294 ADG22098 standard; Novel human secret US2003207360-A1.	PD 05-NOV-2003. PA (GETH) GENENTECH Query Match: PESTIT 295	255 man PRO polypept 22003207376-A1. 5-NOV-2003. 9ETH) GENENTECH coal Similarity:	6 8074 standard; n PRO polypept 03207422-A1. OV-2003. H) GENENTECH I Similarity: Ch:	297 (2422) standard; vel human secret 2003207426-A1. -NOV-2003. ETH) GENENTECH cal similarity:	REGULT 298 ID ADF98645 standard; DE Human PRO polypepti PN US2003208055-A1. PD 06-NOV-2003. PA (GETH) GENENTECH I Best Local Similarity:	G03476 standard; man PRO polypept 2003207351-A1. -NOV-2003. ETH) GENENTECH cal Similarity: datch: 799197 standard;	DE Human PRO polypepti PN US2003207353-A1. PD 06-NOV-2003. PA (GETH) GENENTECH I Best Local Similarity: Query Match: RESULT 301 ID ADG16782 standard; DE Human PRO polypepti PN US2003207359-A1.	PD 06-NOV-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.08* Query Match: 30.61* RESULT 302 ID ADG05241 standard; protein; DE Human PRO polypeptide #198. PN US2003207375-A1. PD 06-NOV-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.08*

RESULT 312

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	30.61	protein; 260 .de #198.	INC. 48.08% 30.61%	protein; 260 .de #198.	INC. 48.08% 30.61%	indard; protein; 260 secreted and transme	INC. 48.08% 30.61%	protein; 260 ide #198.	INC. 48.08% 30.61%	protein; 260 ide #198.	INC. 48.08% 30.61%	protein; 260 ide #198.	INC. 48.08% 30.61%	ndard; protein; 260 AA. secreted and transmembrane	INC. 48.08% 30.61%	protein; 260 ide #198.	INC. 48.08% 30.61%	indard; protein; 26(secreted and transf	INC. 48.08% 30.61%
	Query Match: RESULT 303	ADG19508 standard; protein; Human PRO polypeptide #198. 082003207425-A1.	PD 06-7003. PA (GETH) GENENTECH I Best Local Similarity: Query Match:	ADG13345 standard; protein; Human PRO polypeptide #198. US2003207357-A1.	PD 06-NOV-2003. PA (GETH) GENENTECH I Best Local Similarity: Ouery Match:	Bta man	V-2003.) GENENTECH Similarity: h:	RESULT 306 ID ADG15572 standard, protein, DE Human PRO polypeptide #198. PN US2003219885-A1.	PA (GETH) GENENTECH] Best Local Similarity: Query Match:	US200320731-A1.	PD 08-NOV-2003. PA (GETH) GENENTECH 1 Best Local Similarity: Query Match:	RESULT 308 DE ADG06155 standard; protein; DE Human PRO polypeptide #198. PN US2003207374-Al.	PD 06-NOV-2003. PA (GETH) GENENTECH 1 Best Local Similarity: Query Match:	RESOLI 303 ID ADG23739 standard; DE Novel human secrett	/383-A1. 003. GENENTECH milarity:	8 standard; RO polypept 07423-A1.	PD 06-NOV-2003. PA (GETH) GENENTECH: Best Local Similarity: Ouery Match:	9 sta uman	田 ::

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ID AD057481 standard; protein; 260 AA.

BE Novel human secreted and transmembrane protein PR0322.

PN 06-NOV-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 48.08$ Mismatches: 96

Query Match:

DA AD056929 standard; protein; 260 AA.

DE Novel human secreted and transmembrane protein PR0322.

PN US300320734-A1.

PA (GETH) GENENTECH INC.

Best Local Similarity: 48.08$ Mismatches: 96

Best Local Similarity: 76.14
ID ADG07226 standard; protein; 260 AA.

DE Novel human secreted and transmembrane protein PR0322.

PN US2003207350-A1.

PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.08$ Mismatches: 96

Query Match: 30.61$ Indels: 13
                                                                                                                                                                              ID ADG07778 standard; protein; 260 AA.

DE Novel human serreted and transmembrane protein PR0322.

PN US200320736-A1.

PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.

A8.08* Mismatches: 96

Query Match: 30.61* Indels: 13

RESULT 314
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RESULT 320

ID ADG55825 standard; protein; 260 AA.

DE Novel human secreted and transmembrane protein PRO322.

PN US2003207365-A1.
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Novel human secreted and transmembrane protein PRO322.
US2003207390-A1.
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30.61$ Indels: 13
RESULT 316
ID ADG$2041 standard; protein; 260 AA.
En Novel human secreted and transmembrane protein PRO322.
PN US2003207428-A1.
PD 06-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                       ID ADG55273 standard; protein; 260 AA.

BE Novel human secreted and transmembrane protein PRO322.

BE Novel human secreted and transmembrane protein PRO322.

PD 16-0CT-2003.

PD 6-0CT-2003.

PD 6-0CT-2003.

PD 6-0CT-2003.

Best Local Similarity: 48.08*

Mismatches: 96

Query Match: Indels: 13
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ADG07778 standard; protein; 260 AA.
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DE Novel human secreted and trip
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%
Query Match:
RESULT 321
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DE Human PRO polypeptide #198.
PN US200320738-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08*
Query Match:
RESULT 318
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PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08%
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PA (GETH) GENENTECH INC.

Best Local Similarity: 48.08%
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RESULT 315
ID ADG60937
DE Novel hum
PN US2003207
PD 06-NOV-20
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RESULT 317
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RESULT 313
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PD 2 PA (Best L	OUENT OUENT RESULT ID A	DE PN PN PN PD	Best Coulons of the C	0 09 0		DE PN BD	Best L Query RESULT ID A	DE POR	Best L Query RESULT ID A	DE PN	PA (Best L Query RESULT ID A	DE DE PN PD PA	Query RESULT		PA (Best L Query RESULT	A G G G G G G G G G G G G G G G G G G G	PA (Best L Query RESULT TR TT	
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numero de la constanta de la c	Mismatches: Indels:	11 344 ADG70951 standard; protein; 260 AA. Novel human secreted and transmembrane protein NSOA330A30A30-A1	Mismatches: Indels:	in; 260 AA. transmembrane protein	Mismatches: Indels:	in; 260 AA. transmembrane protein	Mismatches: Indels:	in; 260 AA. transmembrane protein PRO322	Mismatches: Indels:	260 AA. : protein, PRO322.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	n 342 ADH12019 standard, protein, 260 AA. WS2003207419-A1.	Mismatches: Indels:	
	INC. 48.08% 30.61%	protein; ed and tra	INC. 48.08% 30.61%	protein; ed and tra	INC. 48.08% 30.61%	undard; protein; secreted and tra 5-A1.	INC. 48.08% 30.61%	protein; ed and tra	INC. 48.08% 30.61%	protein; nsmembrane	INC. 48.08% 30.61%		48.08% 30.61%	protein; ide #198.	INC. 48.08% 30.61%	protein; ed and tra	INC. 48.08% 30.61%	•
NOVEL AUMAA SECFECT US2003207368-A1. 06-NOV-2003	(GETH) GENENTECH) Local Similarity: Match:	RESOLT 322 ID ADG70951 standard; DE Novel human secreté PN 11S2003207420-21	PD 06-NOV-2003. PA (GETH) GENENTECH 1 Best Local Similarity: Query Match: RESULT 323	ADG58033 standard; protein; ADG58033 standard; protein; US2003207363-A1.	PD 06-NOV-2003. PA (GETH) GENENTECH 1 Best Local Similarity: Query Match:	RESULT 324 ID ADG53617 standard; DE Novel human secrete PN US2003207415-A1.	x	1 342) ADG71503 standard; protein; Novel human secreted and tr. JS2003207421-Al.	s. WENTECH Larity:	T 326 ADG50568 standard; Human secreted/tra	PN US2003207803-A1. PD 06-NOV-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.08% Mism Query Match: 30.61% Inde	KESULT 327 ID ADG81690 standard; protein; DE Human PRO polypeptide #198. PN US2003207055-A1.	Best Local Similarity: Query Match:	A. 3.25 A. 3.25 Human PRO polypeptide #198. US2003077723-A1.	PD 24-APK-2003. GETH) GENENTECH INC. Best Local Similarity: 48.08* Query Match: 30.61*	KESULI 329 ID ADH12019 standard; DE Novel human secrete PN US2003207419-A1,	PD 06-NOV-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.08% Query Match: 30.61%	RESULT 330

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ADG5241 standard; protein; 260 AA.
ADG5241 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207414-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
Local Similarity: 48.08$ Mismatches: 96
                                                                                                                                                                                                                                                                                                                                                       AD554169 standard; protein; 260 AA.
AD554169 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PR0322.
US2003207416-A1.
06-NOV-2003.
(GFTH ) GENENTECH INC.
Local Similarity: 48.08* Mismatches: 96
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ADH12643 standard; protein; 260 AA.
ADH12643 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207378-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
Local Similarity: 48.08* Mismatches: 96
T. March: Indels: 13
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ADGA148man seareted and transmembrane protein PRO322.
US2003207429-A1.
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ADGSJANT standard; protein; 260 AA.
NOVEL human secreted and transmembrane protein PRO322.
US2003207366-A1.
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Indels:
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ADG51816 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003215908-A1.
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Indels:
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ADG49320 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
20-NOV-2003.
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ADG4666 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003216560-A1.
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ADGB1138 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003194793-Al.
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20-NOV-2003.
(GETH ) GENENTECH INC.
* Local Similarity: 48.08*
US2003215905-A1.
20-NOV-2003.
(GETH ) GENENTECH INC.
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(GETH) GENENTECH INC.
Local Similarity: 48.08%
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(GETH ) GENENTECH INC.
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Mismatches: Indels:	60 AA. Mismatches: Indels:	n; 260 AA. transmembrane protein Mismatches: Indels:	n; 260 AA. transmembrane protein Mismatches: Indels:	260 AA. protein, PRO322. Mismatches: Indels:	60 AA. Mismatches: Indels:	260 AA. : protein, PRO322. Mismatches: Indels:	260 AA. : protein, PRO322. Mismatches: Indels:	260 AA. Mismatches: Indels: 260 AA.
TH INC. 48.08%	protein; 2 de #198. NC. 88.08%	d; protei eted and H INC. : 48.08%	d; protei eted and H INC. : 48.08%	protein; insmembrane INC.	rd, protein, 2	; protein; ansmembrane INC. 48.08%	protein; nsmembrane INC. 48.08%	; protein; tide #198. INC. 48.08 30.61% ; protein;
Aat Ca	34 JH2 JH2 JH2 JH2 JH2 JH2 JH2 JH4 JH4	T 341 ADG54721 standard; Novel human secrete US2003207367-A1. 06-NOV-2003. (GETH) GENENTECH : Local Similarity: Match:	LT 342 ADG59761 standard; Novel human secret US2003207369-A1. 06-NOV-2003. (GETH) GENENTECH LOCAL SIMILARITY: V MACCH:	2 standa ecreted/ 05312-A1 2004. GENENTE	RESULT 344 ID ADH43505 standard, 1 E Human PRO polypeptic DE HUMAN PRO POLYPEPTIC PN US200324984-A1. PD 04-DEC-2003. PA (GETH) GENENTECH ID Best Local Similarity: Ouery Match:	6 stande ecreted/ 05657-A1 2004. GENENTI	346 NDG62 NUMBD IS200 IS200 NB-JA (GETH	r 347 MIBLES stand MIBLES stand MIBLES 1-19 MIBLES 1-1
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DE Human neurotrimin homologue related protein sequence SEQ ID NO:395.

DE Human neurotrimin homologue related protein sequence SEQ ID NO:395.

PN EP1386931-A1.

PD 04-FEB-2004.

PA (GETH) GENENIECH INC.

Best Local Similarity: 48.08$ Mismatches: 96

Query Match:

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Novel human secreted and transmembrane protein PRO322.
US2004039164-A1.
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ID ADI14731 standard; protein; 260 AA.
ID ADI14731 standard; protein; 260 AA.
ID Novel human secreted and transmembrane protein PR0322.
DE Novel human secreted and transmembrane protein PR0322.
PD US200320733-A1.
PD GETH ) GENENTECH INC.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08$
Indels: 13
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Novel human secreted and transmembrane protein PRO322. US2004009547-A1.
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Novel human secreted and transmembrane protein PRO322
US2003207349-A1.
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NOVEL human secreted and transmembrane protein PR0322.

DE Novel human secreted and transmembrane protein PR0322.

PN USC003207382-A1.

PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.

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Abovel human secreted and transmembrane protein PRO322.
US2004009548-A1.
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RESULT 355
ID AD137154 standard; protein; 260 AA.
ID Human TADG-14 protein.
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UTAR-) UNIV ARKANSAS.
BAST LOCAL Similarity: 48.08$ Missinalarity:
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Human PRO polypeptide #198.
US2004038333-A1.
GE-FBB-2004.
(GETH ) GENENTECH INC.
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.
Best Local Similarity: 48.08%
Query Match:
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PD 06-NOV-2003.

PA (GETH ) GENEWIECH INC.

Best Local Similarity: 48.08%
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PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.08*
Query Match:
RESULT 351
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(GETH) GENENTECH INC.
Local Similarity: 48.08%
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PD GETH ) GENENTECH INC.
Best Local Similarity: 48.08%
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RESULT 356
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RESULT 354
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RESULT 353
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RESULT 350
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RESULT 352
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Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA.	Mismatches: Indels:	260 AA. : protein, PRO322.	Mismatches: Indels:	260 AA. protein, PRO322.	Mismatches: Indels:	60 A.A	Mismatches: Indels:	260 AA.					
48.08% 30.61%		INC. 48.08% 30.61%		INC. 48.08% 30.61%		INC. 48.08% 30.61%	protein; ; nsmembrane	INC. 48.08% 30.61%	protein; ; nsmembrane	INC. 48.08% 30.61%	protein; ; ide #198.	INC. 48.08% 30.61%	rotein;			ž: .0	 	
Local Similarity: Match: T 388	AX S2850 standard; protein; Human PRO polypeptide #36. US2004043927-A1.	PD 04-MAR-2004. PA (GETH) GENENTECH 1 Best Local Similarity: Query Match:	M. 2005624 standard; protein; Human PRO polypeptide #198. US2004038335-A1.	PD 26-FEB-2004. PA (GETH) GENENTECH : Best Local Similarity: Ouery Match:	KESULT 360 ID ADM2760 standard; protein; DE Human PRO polypeptide #198. PN US2004048333-A1.	PD 11-MAR-2004. PA (GETH) GENENTECH : Best Local Similarity: Query Match:	. 361 DM17394 standard; Tuman secreted/tra	PN USZ00404833Z-A1. PD 11-MAR-2004. PA (GETH) GENENTECH INC. Best Local Similarity: 48.08% Query Match:	. 362 DL07228 standard; uman secreted/tra	PN US2004063921-Al. PD 01-APR-2004. PA (GETH) GENENTECH INC. BEST Local Similarity: 48.08% Misma' OMESY MATCH: Indel	DM42484 standard; uman PRO polypept:	424-A1. 04. ENENTECH ilarity:	RESULT 364 ID ADN62866 standard; pi DE Human NOVIIh. PN US2004038223-A1.	6-FEB-2004. SMIT/) SMITHSON G. MILL/) MILLET I.	(FEIM) FEIMAN J. A. (KEKU/) KEKUDA R. (JUJJ/) JU J. (LILL/) LI L.	GUO X. PATTURAJAN SPYTEK K A) BLLERMAN K	
Best Lo Query M	ID A	PD (PA (Best LQuery	ID DE PN CI H	بري يري	KESULT ID A DE H DN U	PD 1 PA (Best L Query	RESULT ID A	PN U PD 1 PA (Best L Query	RESULT ID A	PN U	RESULT ID A	PN D PD 2 PA (Best L	RESULT ID A OE H			E A A A	,,,,,	

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ADR72883 standard; protein; 260 AA.
Human ovarian cancer-related tumour marker kallikrein 8 (hK8) protein.
WO2004075713-A2.
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RESULT 370

ID AAW87703 standard; protein; 260 AA.

DE A human serine protease designated HGBAB90.

PN EP887414-A2.

PD 30-DEC-1998.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

Pest Local Similarity: 48.25% Mismatches:

Query Match:

RESULT 371
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Indels:
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DE Antipsoriatic protein sequence #302.

PN W02004028479-A2.

PN W02004028479-A2.

PN W62004028479-A2.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.08% Misme Query Match: 30.61% Index RESULT 366

ID ADM28346 standard; protein; 260 AA.

PN USCO04077064-A1.

PD 22-ARR-2004.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.08% Misme Query Match: 30.61% Index Misme Query Match: 30.61% Index Misme Query Match: 30.61% Index Index Misme Query Match: 30.61% Index Index Index Misme Query Match: 30.61% Index Index Index Index Index Misme Query Match: 30.61% Index Ind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE Human ovarian cancer-related tum
PN W02004075713-A2.
PD 10-SEP-2004.
PA (MOUN ) MOUNT SINAI HOSPITAL.
Best Local Similarity: 48.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID AB21311 standard, protein, 27
DE Human neuropsin.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 48.25%
(MILL/) MILLER C E.
(RAST/) RASTELLI L.
(STON/) STONE D J.
(PENA/) PENA C E A.
(SHEN/) SHENOY S G.
(SHEN/) SHENOY S G.
(SHEN/) SHENOY S G.
(SHEN/) ROTHENBERG M E.
(LEAC/) LEACH M D.
(RESE/) AERE M L.
(BERG/) BERCHS C.
(DIPI/) DIPIPPO V A.
(EISE/) BISEN A.
(GANG/) GANGOLLI E A.
(RIEG/) RIEGER D K.
(RIEG/) RIEGER D K.
(RIEG/) RIEGER D K.
(RIEG/) SPADERNA S K.
(LOCAI SIMILATIY: 48.08*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
RESULT 365
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RESULT 381		PA (UYAR-) Best Local Si Query Match: RESULT 382 ID ADI37155	DE Mouse ne PN US200319 PD 23-OCT-2	# 2.5	DE Human TL PN W0200053 PD 14-SEP-2	# 2.2	DE Human PR PN WO200012 PD 09-MAR-2 PA (GETH)	ery Sur	DE Protein PN W200078 PD 28-DEC-2 PA (GETH)	Best Local Si Query Match: RESULT 386	1D ANOLIZAZA DE Human PR PN WO200140 PD 07-JUN-2	st Sury		ery Sur	DE Human PR PN W0200208 PD 31-JAN-2	PA (GETH) Best Local Si Query Match: RESULT TO ABGG 1816	DE Prostate PN WO200230 PD 18-APR-2 PA (EOSB-)	Best Local Si Query Match: RESULT 390
			249.								production.				SEQ ID NO:533.			
Indels: 13	ence .	Mismatches: 90 Indels: 2	gene 2 clone HWJAE49	Mismatches: 90 Indels: 2	s AA. SEQ ID NO:2464.	Mismatches: 90 Indels: 2	.10.	Mismatches: 93 Indels: 7	:	Mismatches: 97 Indels: 13	antibody	HO KK. Mismatches: 93 Indels: 5	1	Mismatches: 93 Indels: 5	sequence	JURIDICAL PERSON. Mismatches: 93 Indels: 5	b. (D 609.	Mismatches: 93 Indels: 5
30.42%	standard; protein; 305 AA ine protease protein sequ 5-A.	50.85* 30.35*	protein; 306 AA tein encoded by	ME SCI INC. 50.85% 30.35%		ME SCI INC. 50.85% 30.35%	protein; 260 AA. comologue SeqID 610)RP. 47.04% 30.28%	protein; 260 AA M-7.	A7.69% 30.23%	; protein; 260 AA. neuropsin; used for	SUTSUGAKU KENKYUSHO KK. 48.99% Mismat 30.13% Indels	; protein; 260 AA rotein.	3. 48.99% 30.13%	; protein; 260 AP ondition related	N SCHOOL JURIDICE 48.99% 30.13%	; protein; 260 Az in homologue Segl	CORP. 7: 48.99% 30.13%
Query Match:	9 er	PD 24-AUG-1999. PA (SUNR) SUNTORY LTD Best Local Similarity: Opery Match:	AAB37985 standard; protein; 306 AA. Human secreted protein encoded by gene WG900065471-Aa.	PD 21-SEP-2000. PA (HUMA-) HUMAN GENOME Best Local Similarity: 50 Query Match: 30	T 374 ABP41332 standard; protein; 31: Human ovarian antigen HCOQP78, WO200200677-A1.	PD 03-JAN-2002. PA (HUMA-) HUMAN GENOME Best Local Similarity: 50 Query Match: 30	KESULI 3.7074 standard; protein; DE Rat NOVX protein homologue. PN WO200266649-A2.	PA (CURA-) CURAGEN CORP Best Local Similarity: 4 Query Match: 3	T 3/6 AAY06438 standard, protein; Human protease HUPM-7. WO9936550-A2.	PA (INCY-) INCYTE PHARM INC Best Local Similarity: 47.69 Query Match: 30.23	694 standard recombinant 45700-A.	PD 24-SEP-1996. A (IGAK-) IGAKU SEIBUTSUGAKU Best Local Similarity: 48.99% Query Match: 30.13%	.f. 378 AAW1293 standard; protein; Mouse neuropsin protein. JP08311099-A.	PD 26-NOV-1996. PA (SHIO/) SHIOZAKA S BEST LOCAL Similarity: Querry Match:	n 3/9 BB57219 standard, protein, 260 AA. Mouse ischaemic condition related protein WO200188188-A2.	PD 22-NOV-2001. PA (UXNI-) UNIV NIHON Best Local Similarity:	1, 38D 17073 standard; protein; 260 AA. ADI17073 standard; protein homologue SeqID WO20068649-A2.	AGEN
Query	RESULT ID A DE PN	PD PA Best I Query	DE D	ائع تا	RESULT 374 ID ABP41 DE Human	ř,ř.	KESULT 3/5 ID ADII7 DE Rat No PN WO200	PA Best] Query	KESOLT 376 ID AAY06 DE Human PN W0993	ř,ř	RESULT 377 ID AAW10 DE Human	i i	ğ	FD 26-NO PA (SHIO Best Local Query Matc	ID DE DIE SOL	PD 22-NO PA (UYNI Best Local Query Matc	PN BI	PA Best Query

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O standard; protein; 250 AA.
RO1279 (UNQ649) amino acid sequence SEQ ID NO:170.
2708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 standard; protein; 250 AA.
secreted protein encoded by gene 179 SEQ ID NO:427.
52891-A2.
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cate cancer-associated protein #17.
230266-A2.
PR-2002.
B-) EOS BIOTECHNOLOGY INC.
Mismatch
i Similarity: 48.19% Mismatch
ch:
29.94% Indels:
                                                                                                                                                                                                                                                                                                                                                                                           139 standard; protein; 250 AA.
in of the invention #51.
079951-A1.
C-2000.
) GENENTECH INC.
51 GENENTECH 29.94* Ind.
                                                                                              155 standard; protein; 260 AA.
neuropsin.
3199010-A1.
T-2003.
-) UNIV ARKANSAS.
Similarity: 48.99$ Mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 standard; protein; 250 AA. PRO1279 polypeptide sequence. 10466-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 standard; protein; 250 AA.
PRO protein, Seq ID No 186.
08288-A2.
                                                                                                                                                                                   is standard; protein; 250 AA.
LSP.
1 standard; protein; 260 AA.
europsin protein.
13-B1.
                                 2003.
) UNIV ARKANSAS MEDICAL SCI.
Similarity: 48.99$
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-) HUMAN GENOME SCI INC.
Similarity: 48 19%
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) MOUNT SINAI HOSPITAL.
Similarity: 48 19%
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) GENENTECH INC.
Similarity: 48.19%
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) GENENTECH INC.
Similarity: 48.19%
29.94%
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N-2002.
() GENENTECH INC.
L Similarity: 48.19%
29.94%
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83

89

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ABU92140 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003088063-A1.
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Novel human secreted and transmembrane protein PRO1279, 200-07AN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABUG7098 standard; protein; 250 AA.
Human secreted/transmembrane, PRO, protein SEQ ID 506.
W22003032155-A1.
13-FBB-2003.
                                                                                                                   Novel secreted and transmembrane protein PRO1279. US2003017563-A1.
                                                                                                                                                                                                                                       Human secreted/transmembrane protein (PRO) #253.
US2003136179-A1.
20-FEB-2003.
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                                                                                                     protein; 250 AA.
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Human PRO polypeptide #253.
US2003073212-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA61729 standard; protein; 250 AA.
                                                                                                                                                                                                                             ABO25093 standard; protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABJ72320 standard; protein; 250 AA.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19*
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(GETH ) GENENTECH INC.
Local Similarity: 48.19%
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Onerv Match: 29.94%
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Best Local Similarity: 48.19%
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PA (GETH) GENENTECH INC.
Best Local Similarity: 48.
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Best Local Similarity: 48.
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Best Local Similarity: 48.
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PA (GETH) GENENTECH INC.
Best Local Similarity: 48.
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.
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US2003050448-A1.
                                                                                                      ABU59903 standard;
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US2003049816-A1.
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RESULT 402
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RESULT 405
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RESULT
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                                                                                                                                ABB95526 standard; protein; 250 AA.
Human angiogenesis related protein PRO1279 SEQ ID NO: 208.
WO200208284-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABOL/868 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US20030313156-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID ABO33797 standard; protein; 250 AA.

DB Novel human secreted and transmembrane protein PRO1279.

PD 06-MAR-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.19% Mismatches: 89
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         ABB84920 standard; protein; 250 AA.
Human PRO1279 protein sequence SEQ ID NO:208.
WO200200690-A2.
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Lung cancer-associated polypeptide #332.
W2020286443-A2.
31-0CT-2002.
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US2003004311-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU80831 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003036635-A1.
20-PEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU66822 standard; protein; 250 AA.
Human PRO polypeptide #253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EOSB-) EOS BIOTECHNOLOGY INC.
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Local Similarity: 48.19%
/ Match: 29.94%
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(GETH ) GENENTECH INC.
E Local Similarity: 48.1
ry Match: 29.9
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GURNEY A L.
HILLAN K J.
MARSTERS S A.
PAN J.
PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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Best Local Similarity: 48.
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8 8	PRO1279.	80 rv		8 S	PRO1279.	8 S		8 S		8 S		8 S	PRO1279.	81 93		8 S	
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ETH) GENI cal Simila latch:	15) B19514 Bta Wel human	soes/se-A1. R-2003.) GENENTECH Similarity: h:	ADB28055 standard; Human PRO polypept:	FN USZUOVSZOWATI. DO 01-MAY-2003. PA (GETH) GENENTECH INC. BEST LOCAL Similarity: 48.19* Query Match:	4 standard uman secre	Y-2003.) GENENTECH Similarity: h:	KESULI 4110 ID ADB16098 standard; protein; DE Human PRO polypeptide #253. PN US2003087350-A1.	PA (GETH) GENENTECH : Best Local Similarity: Query Match:	RESULT 411 ID ADA47884 standard; protein; DE Human PRO polypeptide #253. DN 1522003015-21	PD 17-APR-2003. PA (GETH) GENENTECH Best Local Similarity: Query Match:	RESULT 412 ID ABO44736 standard; protein; 250 A DE Novel human secreted protein #179 PN US2003065160-A1.	PA (HUMA-) HUMAN GENOME Best Local Similarity: 46 Query Match: 28	RESULT 413 LD ABO33632 standard; protein; DE Novel human secreted and tre	PD 17-AFK-2003. PA (GETH) GENENTECH Best Local Similarity: Querry Match:	JA 414 MAG7679 standard; protein; Human PRO polypeptide #253. US2003068795-A1.	PD 10-AFR-2003. PA (GETH) GENENTECH Best Local Similarity: Querry Match:	ul 415 ADB30686 standard; protein; Human PRO polypeptide #253. US2003068794-Al.
PA (G Best Lo Query M RESILL	0100	PN USZOU PD DSZOU PD 10-AP PA (GETH Best Local Query Matc	DE DE SOL	PD PD PA Best I Query	RESUL:	ary at	5	PA PA Best J Query	RESUL ID DE	r i	RESUL ID DE PN	PA Best Query	RESUL ID DE PN	PA PA Best Query	DE DE	PA PA Best Query	TESOF DE PN

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DE AD91931 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.

PN US2003082694-A1.

PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.19% Mismatches: 89

Query Match: 29.94% Indels: 5
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PN US2003073211-A1.

PD 17-APR-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.19% Mismatches: 89

Query Match: 59.94% Indels: 5
                                                                ID ADAS5982 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.

PN US2003082693-A1.

PD 01-MAY-2003.

Best Local Similarity: 48.19$ Mismatches: 89

Query Match: 29.94$ Indels: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA87637 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003087345-A1.
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Indels:
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ID ADA97194 standard; protein; 250 AA.

ID ADA97194 standard; protein; 250 AA.

DE Human PRO polypeptide #253.

PN US200302705-A1.

PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.19% Miss
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ID ADB16839 standard; protein; 250 AA.
ID ADB16839 standard; protein; 250 AA.
DE Human Copolypeptide #253.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mis
                                                                                                                                                                                                                                                                                                                                                    ADA79498 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082763-A1.
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Human PRO polypeptide #253.
US2003077722-A1.
24-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                   DE Human PRO POLYPEPTIGE #253.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19%
RESULT 419
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19%
Query Match: 29.94%
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PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19
Query Match:
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RESULT 421
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RESULT 422
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RESULT 423
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RESULT 424
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RESULT 416
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RESULT 417
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RESULT 418
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Mismatches: Indels:

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Indels:

83

Mismatches: Indels: 8 2

Mismatches: Indels: 83

Mismatches: Indels: 83

Mismatches: Indels: 89

Mismatches: Indels: 83

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Mismatches: Indels: 89

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μ̈́β	Human PF US200307 17-APR-2	gr g	DE Human PRO polypeptide #253. PN US2003082761-A1. PD 01-MAY-2003. PA (GETH) GRENDTECH INC.	វិជីជី	DE Human PRO polypeptide #253. PN US2003082703-A1. PD 01-MAY-2003.	# KE	DE ALMATIZE SCANGALLY, PLOCELLY, DE HUMAN PRO POLYPEPTIGE #253. PN US2003073210-A1. PD 17-APR-2003. PA GEFF) GENENTECH INC.	# ÇE	1D ADS2945 Standard, procedur, 250 DE Human PRO polypeptide SEQ ID NO PN US2003077715-A1. PD 24-APR-2003.	m m in	DE Human PRO polypeptide #253. PN US2003077721-A1. PD 24-APR-2003. O (Gerru) GENEWERT INC	m m m	DE Human PRO polypeptide #253. PN US2003092147-A1. PD 15-MAY-2003.		DE Human PRO polypeptide #253. PN US2003096886-A1. PD .22-MAY-2003. PA (GETH) GENENTECH INC.	Sign	1D ABJ/2448 BEARGARG, PROCEIN; DE Human PRO1279 protein. PN US2003027988-A1. PD 06-FEB-2003. PA (GETH) GENENTECH INC.	st Local Si ery Match:
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. 68	PRO1279.	889 5		89 5	PRO1279.			89 5		89 5		89 5		89 5	PRO1279.	89 5	PRO1279.	68
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48.19% 29.94%	andard; protein; 250 AA. secreted and transmembrane)1-A1.	:003. GENENTECH INC. milarity: 48.19% 29.94%	14.26 ADB13378 standard; protein; 250 Human PRO polypeptide #253. US2003082710-A1. 01.PMY-2003.	(GEIR) GENENIECH INC. Local Similarity: 48.19% Match: 29.94%	ABO43401 standard; protein; 250 Novel human secreted and transme to 250 May 152003044945-A1.	GETH) GENEVTECH INC. Local Similarity: 48.19% Match:	1.428 ADA74632 standard; protein; 250 Human PRO polypeptide #253. US2003068798-Al.	(GETH) GENENTECH INC. Local Similarity: 48.19% Amcch: 29.94%	ADB24865 standard; protein; 250 Human PRO polypeptide SEQ ID NO 1922033077713-Al.	2003.) GENENTECH INC. Similarity: 48.19%	ADAB2189 standard; protein; 250 Human PRO polypeptide #253.	(GETH) GENEVIECH INC. Local Similarity: 48.19% March: 29.94%	; protein; 250 cide #253.	GELH CEMENTECH INC. LOCAL SIMILARITY: 48.19% MATCh: 29.94% T 432	ADA85430 standard; protein; 250 Novel human secreted and transme US2003082695-A1.	GENENTECH INC. milarity: 48.19% 29.94%	TT 433 ADA84878 standard; protein; 250 Novel human secreted and transme VIS2003082708-Al.) GENENTECH INC. Similarity: 48.19%

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RESULT 443 ID ADA61166 standard, DE Homo sapiens. PN US2003049817-A1. PD 13-MAR-2003. PA (GETH) GENEWTECH) Best Local Similarity: Query Match:	RESULT 444 1D ADB24313 standard; protein; DE Human PRO Polypeptide SEQ II PN US2003077714-A1. PD 24-APR-2003. PA (GETH) GENENTECH INC. PA (GETH) SIMILIATILY: 48.19\$	RESULT 445 ID ADA96642 standard; pro BE Human PRO polypeptide PN US2003082690-A1. PD 01-MAY-2003. PA (GETH) GRNENTECH INC. Best Local Similarity: 488 Query Match: 299	RESULT 446 ID ADAB1214 standard; DE Human PRO polypepti: PN US2003082702-A1. PD 01-MAY-2003. PA (GETH) GENENTECH II Best Local Similarity: Query March:	RESULT 447 ID ADA96090 standard; protein, DE Human PRO polypeptide #253. BN US2003082759-A1. PD 01-MAY-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.19% Query Match:	RESULT 448 ID ADB26399 standard, prol DE Human PRO polypeptide : PN US2003082760-A1. PD 01-MAY-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.	st 276 276 003 GEN	RESULT 450 ID ABO34343 standard; protein; 250 AA. ID B. Human secreted/transmembrane polypeptide PN US2003044934-A1. PD 06-MAR-2003. BA (GETH) GENENTECH INC. Best Local Similarity: 48.19\$ Opery Match: Indels	ESOUL #31 ID ADA7763 standard; DE Human PRO polypepti PN US2003068797-A1. PD 10-APR-2003. PA (GETH) GENENTECH I Best Local Similarity: Query Match:
RESULT ID AN DE HO PN UW PD 1.0 PA (G Best LA	RESULT ID A DE PN PD PD PA Beat I	RESULT ID 1 DE PN 1 PD 0 PA 0	RESULTION ID A POR COMMENT OF THE PROPERTY OF	RESULT ID F DE H PN (PD (PA (RESULT ID P DE P PN U PD O PA (RESULTY ID A DE N PN (PD (PA (Best I	RESULTIDE DE POR LE PO CO PA CO CO PA CO	ID P DE F DE F PN U PD 1 PA (Best I Query

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PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19$ Mismatches: 89
Query Match:
LOCAL Similarity: 48.19$ Indels: 5
RESULT 455
ID ADAB8189 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003082700-A1.
PN US2003082700-A1.
PN USZ003082700-A1.
PN USZ003082700-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19$ Mismatches: 89
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Novel human secreted and transmembrane protein PRO1279.
US2003054516-A1.
                                                                                                                                          ADA87086 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082709-A1.
01-MAY-2003.
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DE Human protein from novel secreted protein gene 179.

PN US625174-B1.

PD 25-FEB-2003.

PA (HUMA-) HUMAN GENOME SCI INC.

Best Local Similarity: 48.19% Mismatches: 89

Query Match: 5
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Indels:
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Indels:
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RESULT 454
ID ABO44485 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003044641-A1.
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Indels:
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RESULT 458
ID ADB29159 standard, protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENEWIECH INC.
Best Local Similarity: 48.198 Miss
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Human PRO polypeptide #253.
US2003059909-A1.
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RESULT 461
ID ABO33509 standard; protein; 250 AA.
ADB18403 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003077710-A1.
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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
BEST LOCAL SIMILARITY: 48.19$
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PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19$
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PD GETH ) GENENTECH INC.
Best Local Similarity: 48.19%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19%
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                PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19%
RESULT 45.
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RESULT
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RESULT
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Beet Local Similarity Query Match: RESULT 471 ID ADB15546 standar DE Human PRO POLYP PN US2003087352-A1.	PD 08-MAY-2003. PA (GETH) GENENTEC	Query Match: RESULT 472 ID ADB83676 standax DE Novel human sect	PN USZUDJUJSEL4-AL. PD 17-APR-2003. PA (GETH) GENENTEC Best Local Similarity Query Match:	RESULT 473 ID ADB80782 standar DE Novel human secr	ي پړ	RESULT 474 ID ADB73323 standar DE Novel human secr	PN US2003096968-A1. PD 22-MAY-2003. PA (GETH) GENENTEC	Query Match: RESULT 475 TD ADRIATOR standar	DE Novel human secr PN US2003082766-Al. PD 01-MAY-2003.	PA (GETH) GENENTE Best Local Similarity Query Match: RESULT 476	1D ADB'8405 standar DE Novel human sect PN US20030288-A1. PD 15-WAY-2003. PA (GETH) GENENTEC	H A	DE NOVEL human examples DE NOVEL human examples PN US2003087347-Al. PD 08-MAY-2003. PA (GETH) GENEWIEC	Best Local Similarity Query Match: RESULT 478	DE NOVEL human escaration of the Novel human escaration of the Novel human escaration of the Novel human escaration of the Novel human escar	st Local S: ery Match: SULT 479	Human PRC US2003073 17-APR-20
8 9 9	PRO1279.	89 5		89 5		89 5	PRO1279.	, ,	amino acid sequence.	89 5		89 5		89 5		89 S	RO1279.
Mismatches: 89 Indels: 5	AA. mbrane protein	Mismatches: Indels:	250 AA.	Mismatches: Indels:	250 AA.	Mismatches: Indels:	ADB22436 standard; protein; 250 AA. Novel human secreted and transmembrane protein P. W2203087344-A1.	Mismatches: Indels:	ABJ72150 standard; protein; 250 AA. Human membrane bound receptor/protein PRO1279 am US2003065147-A1.	Mismatches: Indels:	250 AA.	Mismatches: Indels:	250 AA.	Mismatches: Indels:	250 AA. D NO 506.	Mismatches: Indels:	7.17) ADA92483 standard; protein; 250 AA. Novel human secreted and transmembrane protein PRO1279 (18,2003.087112.4).
INC. 48.19% 29.94%	; protein; ted and to	INC. 48.19% 29.94%	; protein; tide #253	INC. 48.19% 29.94%	; protein; tide #253	48.19%	; protein; ted and ti	48.19%	; protein; und recept	INC. 48.19\$ 29.94\$; protein; tide #253.	INC. 48.19% 29.94%	; protein; tide #253.	INC. 48.19% 29.94%	; protein; tide SEQ]	INC. 48.19% 29.94%	; protein; ted and to
PN US2003073129-A1. PD 17-APR-2003. PA (GETH) GENENTECH Best Local Similarity: Query Match:	ADA88741 standard; protein; 250 Novel human secreted and transme US2003073213-A1.	PD 17-APR-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.19% Query Match: 29.94%	746 standard PRO polypep 3082686-A1. Y-2003.	(GETH) GENENTECH st Local Similarity: sry Match:	DE Human PRO polypeptide #253. PN US200302229-A1.	# Ç.	ID ADB22436 standard DE Novel human secret PN US2003087344-Al.	ED US-MAI-2003. Best Local Similarity. Query Match:	ID ABJ72150 standard, DE Human membrane bou PN US2003065147-A1.	03-APR-2003. (GETH) GENENTECH it Local Similarity: rry Match:	KESULY 467127 standard; protein; DE Human PRO polypeptide #253. PN US2003068793-A1. PD 10-APR-2003.	ENTECH arity:	ESOUL *2001; protein; DE Human PRO polypeptide #253. PN US200307711.A1. PD 24-APR-2003.	7 7 5	ADB3761 standard; protein; 250 Human PRO polypeptide SEQ ID NO US2003077712-Al.	PA (GETH) GENENTECH INC. Best Local Similarity: 48.19% Query Match: 29.94%	ADA92483 standard Novel human secret

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48.19% 29.94%	protein; 250 ide #253. INC. 48.19\$ 29.94\$	7	ndard, protein, 250 er-associated prote: -A2. BIOTECHNOLOGY INC. rity: 48.19%	rotei	INC. 48.19% 29.94%	protein; ed and tr	INC. 48.19% 29.94%		INC. 48.19% 29.94%	otein; #93.	INC. 48.19% 29.94%	indard; protein; 29 secreted and trans?-A1.	INC. 48.19% 29.94%	undard; protein; 2: secreted and tran -A1. NTECH INC.
Best Local Similarity:	standard; to polypept 12698-Al. 1003. GENENTECH	0 standard; RO polypept 82762-Al. 2003. GENENTECH	RESULT 482 ID ADB80596 standard; protein; 250 AP DE Ovarian cancer-associated protein PN W02002102235-A2. PD 27-DEC-2002. PA (EOSB-) EOS BIOTECHNOLOGY INC. Best Local Similarity; 48.19\$ Churry Match:	RESULT 483 ID ADB39631 standard; p: DE Novel human secreted PN US2003082764-A1.	01-MAY-2003. (GETH) GENENTECH st Local Similarity: sry Match:	9 standard; uman secret 92886-Al.	PD 15-MAY-2003. PA (GETH) GENENTECH Best Local Similarity: Opery Match:	DE Human PRO polypeptide #93. PN US2003088067-A1. PD 08-MAY-2003.	PA (GETH) GENENTECH Best Local Similarity: Query Match:	DE ADB84807 standard; pro DE Human PRO polypeptide PN US2003092890-Al. PD 15-MAY-2003.	PA (GETH) GENENTECH Best Local Similarity: Query Match:	487 B47254 sta vel human 2003082687	01-MAY-2003. (GETH) GENENTECH st Local Similarity: ery Match:	RESULT 488 ID ADB83922 standard; DE Novel human secret PN US200306397-A1. PA (GETH) CENENTECH PA (GETH) CENENTECH PA (GETH) CENENTECH Best Local Similarity:

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DE AD577466 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PR01279.

PN US2003082696-A1.

PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.19% Mismatches: 89

Query Match:

RESULT 492.
                                                                                                                                                                      DE ADB73077 standard; protein; 250 AA.

DE ADB73077 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.

PO 15-MAY-2003.

PD 15-MAY-2003.

PA (GETH ) GENENTECH INC.

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PA (19 **) Mismatches: 89

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US2003077720-Al.
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ADB34623 standard; protein; 250 AA.
Human PRO polypeptide SEQ ID NO 506.
US2003077717-A1.
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DB Prostate cancer marker protein.

DB WOZ00030814-AZ.

PD 06-FBB-2003.

PA (MILL-) MILLENNIUM PHARM INC.

PBST LOCAL Similarity: 48.19% Millery Match:

29.94% Ir
Query Match: 29.94% I.
RESULT 489
ID ADBRESUL standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082697-A1.
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19%
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PA (GETH ) GENENTECH INC.

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PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19%
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PD 01-MAY-2-003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19.
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ADC49652 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003088071-A1.
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                     ADB46674 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US220031082692-A1.
01-MAY-2003.
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Novel human secreted and transmembrane protein PRO1279.
US2030921106-Al.
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Novel human secreted and transmembrane protein PRO1279.
US2003092105-A1.
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Novel human secreted and transmembrane protein PRO1279.
US2003088064-A1.
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Novel human secreted and transmembrane protein PRO1279.
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Human PRO polypeptide #93.
US2003096969-A1.
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                                                                                                                                         ADC18039 standard; protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC72094 standard; protein; 250 AA
RESULT 498

ID ADB46674 standard; protein; 2

DE Novel human secreted and trar
PN US2003082692-A1.

PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.19%
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(GETH ) GENENTECH INC.
Local Similarity: 48.19$
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US2003064925-A1.
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(GETH ) GENENTECH INC.
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(GETH) GENENTECH INC.
Local Similarity: 48.
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(GETH ) GENENTECH INC.
Local Similarity: 48.
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(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein Seg ID506.
US2003087365-A1.
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Novel human secreted and transmembrane protein Seg ID506.
US2003087366-A1.
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Novel human secreted and transmembrane protein Seg ID506.
US2003087363-A1.
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Novel human secreted and transmembrane protein Seq ID506.
US2003087364-A1.
                                                                                                                                          Novel human secreted and transmembrane protein PRO1279.
US2003088072-A1.
08-MAY-2003.
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Novel human secreted and transmembrane protein PRO1279.
US2003087367-A1.
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Novel human secreted and transmembrane protein PRO1279.
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US2003087362-A1.
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PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19%
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Best Local Similarity: 48.19%
Query Match: 29.94%
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Best Local Similarity: 48.19%

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PA (GETH) GENENTECH INC.
Beet Local Similarity: 48.1
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.
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Best Local Similarity: 48.
ID ADC49652 standard; ID Novel human secretee PN US2003088071-A1. PD 08-MAY-2003. PA (GETH ) GENENTECH II Best Local Similarity:
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ID ADC65627 standard;
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ADC47513 standard;
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RESULT 509
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RESULT 514
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RESULT 516
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32003096972-A1.

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8 9 8 9	Seg ID506.	65 kg	Seq ID506.	S 89	PRO1279.	8 8 9	PRO1279.	8 S	PRO1279.	89 5		8 S		8 8 5		5 5
Mismatches: Indels:	protein	Mismatches: Indels:	protein	Mismatches: Indels:	1. 3.19 Novel human secreted and transmembrane protein US2003105288-Al.	Mismatches: Indels:	ln; 250 AA. transmembrane protein	Mismatches: Indels:	T. 521 MDC90323 standard; protein; 250 AA. Novel human secreted and transmembrane protein US2003087348-A1.	Mismatches: Indels:	AA.	Mismatches: Indels:	AA.	Mismatches: Indels:	АА.	Mismatches: Indels:
INC. 48.19% 29.94%	protein; 250 ed and transm	INC. 48.19% 29.94%	protein; 250 AA. ed and transmembrane	INC. 48.19% 29.94%	protein; 250 ed and transm	INC. 48.19% 29.94%	protein; 250 ed and transm	INC. 48.19% 29.94%	protein; 250 ed and transm	INC. 48.19% 29.94%	protein; 250 ide #253.	INC. 48,19% 29.94%	protein; 250 ide #253.	INC. 48.19% 29.94%	protein; 250 ide #253.	INC. 48.19% 29.94%
PD 08-MAY-2003. PA (GETH) GENENTECH Best Local Similarity: Query Match:	ADC56087 standard, protein; 250 AA. Novel human secreted and transmembrane US2003087360-A1.	ENTECH arity:	AD 218 AD 258657 standard; protein; Novel human secreted and tra US2003087346-Al.	(GETH) GENENTECH Local Similarity: Match:	KESULI 319 ID ADC47258 standard; DE Novel human secret PN US2003105288-A1.	GENENTECH milarity:	AD00331 standard, protein, Novel human secreted and tra US2003092104-A1.	(GETH) GENENTECH Local Similarity: Match:	RESULT 521 ID ADC90323 standard; DE Novel human secret PN US2003087348-A1.	oos. GENENTECH milarity:	ADC69742 standard; protein; Human PRO polypeptide #253. US2003194770-A1.	PA (GETH) GENENTECH Best Local Similarity: Query Match:	ADC48631 standard; protein; Human PRO polypeptide #253. US2003194773-A1.	ENENTECH Llarity:	RESULI 3-2010160 standard; protein; DE Human PRO polypeptide #253. PN US2003194776-A1. PD 16-OCT-2003.	ENTECH arity:

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DC80691 standard, protein, 250 AA.
Veel human secreted and transmembrane protein PRO1279.
S2003092103-A1.
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DC80139 standard; protein; 250 AA.
vvel human secreted and transmembrane protein PRO1279.
S2003087358-A1.
                                                               upu4735 standard; protein; 250 AA.
2vel human secreted and transmembrane protein PRO1279.
32003087354-A1.
                                                                                                                                                                                           DD06368 standard; protein; 250 AA.
ovel human secreted and transmembrane protein PRO1279.
52003073816-A1.
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DC77887 standard; protein; 250 AA.
vvel human secreted and transmembrane protein PRO1279.
S2003088066-A1.
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DD10497 standard, protein; 250 AA.
Uman secreted/transmembrane PRO polypeptide #104.
S200315611-A1.
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ADD11457 standard; protein; 250 AA.
Human secreted/transmembrane PRO polypeptide #104.
US2003105013-A1.
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uman PRO polypeptide #253.
32003194774-A1.
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uman PRO polypeptide #253.
S2003194771-A1.
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GETH ) GENENTECH INC.
Local Similarity: 48.19*
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GETH ) GENENTECH INC.
Local Similarity: 48.19*
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2-MAY-2003.
GETH ) GENENTECH INC.
Local Similarity: 48.19$
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Mismatches: Indels:	250 AA.	Mismatches: Indels:	.n, 250 AA. transmembrane protein PRO1279	Mismatches: Indels:	in; 250 AA. transmembrane protein	Mismatches: Indels:	250 AA.	Mismatches: Indels:	n; 250 AA. transmembrane protein	Mismatches: Indels:	250 AA. protein PRO1279.	Mismatches: Indels:	250 AA. : protein PRO1279.	Mismatches: Indels:	250 AA.	Mismatches: Indels:	in; 250 AA. transmembrane protein PRO1279
INC. 48.19% 29.94%	protein; ide #253.	INC. 48.19% 29.94%	protein; ed and tra	INC. 48.19% 29.94%	protein; ed and tra	INC. 48.19% 29.94%	protein; ide #253.	INC. 48.19% 29.94%	protein; ed and tra	INC. 48.19% 29.94%	protein; nsmembrane	INC. 48.19% 29.94%	protein; nsmembrane	INC. 48.19% 29.94%	protein; ide #253.	INC. 48.19% 29.94%	protein; ed and tra
PA (GETH) GENENTECH Best Local Similarity: Query Match: RESULT 535	ADD09608 standard; protein; Human PRO polypeptide #253. US2003194775-A1.		RESOLI 336 ID ADD50850 standard; protein; DE Novel human secreted and tr: PN US2003105291-Al.	05-JUN-2003. (GETH) GENENTECH Local Similarity: " Match:	KESULI 33.1 Standard; protein; DE Novel human secreted and triph USF003203438-A1.	PA (GETH) GENENTECH : Best Local Similarity: Query Match:	DD52460 standard, protein; 2 Human PRO polypeptide #253. US2003194769-A1.	PA (GETH) GENENTECH Best Local Similarity: Query Match:	1 539 MADD51096 standard; protein; Novel human secreted and tr US2003105290-A1.	PD 05-00N-2003. PA (GETH) GENENTECH : Best Local Similarity: Query Match:	ADD70685 standard; protein; 250 AA. Human secreted/transmembrane protein PRO127 US2003099655-A1.	ENTECH arity:	ADD39762 standard; protein; 250 AA. Human secreted/transmembrane protein PRO127 US2003083462-A1.	PD 01-MAY-2003. PA (GETH) GENENTECH : Gest Local Similarity: Query Match: RESULT 542	ADD53200 standard; protein; Human PRO polypeptide #253. US2003194792-A1. 16-OCT-2003.	PA (GETH) GENENTECH : Best Local Similarity: Query Match:	of 543 ADD53752 standard; protein; 250 AA. Novel human secreted and transmembr

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TLT 552
ADD54323 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003203432-A1.
30-OCT-2003.
(GETH ) GENENTECH INC.
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Result And Add
Local Standard; protein; 250 AA.

ID ADD70208 standard; protein; 250 AA.

ID ADD70208 standard; protein PR01279.

PN US2003054406-A1.

PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.

Rest Local Similarity: 29.94% Indels:
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AESULT 546
ID ADD38329 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PD 22-MAY-2003.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% Mismatches:
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Indels:
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US2003096954-A1.
22-MAY-2003.
LOCATH ) GENENTECH INC.
LOCAT Similarity: 48.19$ Mismatches:
// MAtch: 29.94$ Indels:
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Human PRO polypeptide #253.

16-07-2003.

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ADD02707 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003203431-A1.
30-OCT-2003.
(GETH ) GENENTECH INC.
St Local Similarity: 48.19% Missery Match:
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(GETH) GENEWTECH INC.

(GETH) GENEWTECH INC.

29.94% Indianch:

(SULT 551

(Aman PRO Polypeptide #253.

(US2003203430-A1.

(GETH) GENEWTECH INC.

(GETH) GENEWTECH INC.

St. Local Similarity: 48.19% Missiery Match:
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ADD50577 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003096971-A1.
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JLT 547
ADD39285 standard; protein; 250 AA.
(GETH ) GENENTECH INC.
Local Similarity: 48.19%
Match: 29.94%
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29.94%
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LT 548
ADD51908 standard;
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 indels: Indels: Indels: In PRO1279. In PRO1279. In PRO1279. In PRO1279. In PRO1279. In Gels: Indels:	RESULT 162.	# 72 E	PD 23-OCT- PA (GETH) Best Local S Guery Match: RESULT 564 ID ADD7960	3 tr	# F.E	DE Human Pl PD 13-0CT-: PD 23-0CT-: PA (GETH) Best Local S. RestLocal S. RestLocal S. Th Anneyson	DE Human Pl PD 03-003-1 PD 23-0CT-1 PA (GETH) Best Local S Query Match: RESULT 568 ID ADE3355	PN US20031 PD 16-0CT- PA (EETH) Best Local S Query Match: RESULT 569 ID ADB3410 DE NOVEL h PD 16-0CT-	it SULY SULY
 Indels: 250 AA. Protein PR01279. Mismatches: Indels: 250 AA. Protein PR01279. Mismatches: Indels: 250 AA. Mismatches: Indels: 250 AA. 250 AA.							a	50	o,
29.94% ide #93. ide #93. lNC. 29.94%	Indels: AA.	<i></i> .	••				AA. Mismatches: Indels:	Mismatches: Indels: AA.	matches: els: PRO1279.

ss.	in PRO1279.		68	ស				ເທ					ហ				68					68					88		in PRO1279.		•	:: 68 L		in PRO1279.			. 89					
Indels:	250 AA. ansmembrane protein		Mismatches	Indels:	50 AA.		Mismatches	Indels:	250 AA.			Mismatches	Indels:	250 AA.			Mismatches	Indels:	50 AA.			Mismatches	Indels:	50 AA.			Mismatches	Indels:	n; 250 AA. transmembrane profein			Mismatches Indels:		50 AA. smembrane protein			Mismatches	Indels:	250 AA.			
29.94%	protein; ed and tr	; ; ;	INC. 48.19%	5	protein; 2:		Νά Δ	29.94%	protein;	de #253.	Ş	1NC. 48.19%	94	protein;	de #253	č	48.19	94	protein; 2	de #25	È	48.19%	σ.	protein; 2			_	æ	•~		INC.	48.19%		; protein; 2 -ed and tran		INC.	٦.	29.94*	protein; de #253.		JNL	
;;.	, sta	5-A1.	(GETH) GENENTECH Local Similarity:	ah:	ADE22379 standard; Human PRO polypeptic	3199056-A1. TT-2003.	f) GENENTECH	זווודדמדדווה	1 9603 standard;	Human PRO polypepti	T-2003.	1) GENENTECH Similarity:	ظ. نور	2139 standard	Human PKO polypepti US2003194772-A1.	CT-2003.	Similarity:	д	7956 standard	Human PRO polypeptions US2003199023-A1.	T-2003.	Similarity:	:h: 7	2088 standard	Human PRO polypeptide # US2003199053-A1.	CT-2003.	d) GENENTECH Similarity:	ah: B	3551 standard	03194767-A1.	H) GENENTECH	l Similarity:		4103 standard human secrei	US2003194791-A1.	CT-2003.	Similarity:	ch:	0155 standard; n PRO polypepti	03207417-A1.	U) CENENWECH	I SELECTION OF THE PERSON OF T
Query Matc	ID ADE32447 DE Novel hu		ξ	Query Match:	ID ADE22 DE Human		PA (GETH	>	RESULT 564 ID ADD79			PA (GETH Best Local	Query Match:	ID ADE42		PD 16-0C	3t		,	DE Human PN US200		PA (GEIN Best Local	Query Match: RESULT 567	ID ADD92			PA (GETH Best Local	Query Match: RESULT 568	ID ADE33			Best Local	31,	ID ADE34		PD 16-OCT PA (GETH	Best Local	Query Match RESULT 570	ID ADD80155 DE Human PR	PN US2003:	100	

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250 AA. e protein PR01279. Mismatches: Indels: 250 AA.	Mismatches: Indels: 250 AA.	Mismatches: Indels: 250 AA. e protein PRO1279.	Mismatches: Indels: 250 AA.	Mismatches. Indels: 250 AA.	Mismatches: Indels: 250 AA.	Mismatches: Indels: 250 AA.	Mismatches: Indels: 250 AA.	Mismatches: Indels:
protein; namembran INC. 48.19% 29.94% protein; ide #253.	INC. 48.19% 29.94% protein; ide #253.	CH INC. 29.94% rd; protein; transmembrane	INC. 48.19% 29.94% protein; ide #253.	48.19% 29.94% protein; ide #253.	29.94% 29.94% protein; ide #253.	48.19% 29.94% protein; ide #253.	INC. 48.19\$ 29.94\$ protein; ide #253.	INC. 48.19% 29.94%
RESULT 571 ID ADE9983 standard; protein; 250 AA. DE Human secreted/transmembrane protein PR01279 PN US200308256-A1. PD 01-MAY-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.19% Mismatches Query Match: 29.94% Indels: RESULT 572 ID ADD93192 standard; protein; 250 AA. DE Human PRO POILYPeptide #253. PN US2003194768-A1.	16-OCT-2003. (GETH) GENENTECH St Local Similarity: ary Match: SULT 573 ADE19612 standard; Human PRO polypept US2003199025-A1.	(SETH) CENENTE Strocal Similarit ery Match: SULT 574 ADE21541 standa Human secreted/ US2003082628-A1	GETH) GENERATECH st Local Similarity: rry Match: SULF 575 ADE19060 standard; Human PRO polypept US2003199026-A1. CERTH) CENTERPORT	st Local Similarity: ery Match: SULT 576 ADE43256 standard; Human PRO polypept US2003199033-A1. 23-OCT-2003. (GETH) GENENTECH	st Local Similarity: ery Match: SULT 577 ADD96045 standard; Human PRO polypept US2003199059-A1.	t Local Similarity: ary Match: SULT 578 ADE22931 standard; Human PRO polypept US2003199064-A1.	(GETH) GENENTECH st Local Similarity: Nutr 579 ADD79049 standard; Human PRO polypept US2003203429-A1.	PA (GETH) GENENTECH ; Best Local Similarity; Query Match; RESULT 580

protein PRO1279.	88 22		88 5		5 89		5 8 9		88 5		8 S 5 S		8 8 9	•	2 8		8 S
	Mismatches: Indels:	AA.	Mismatches: Indels:	AA.	Mismatches: Indels:	AA.	Mismatches: Indels:	AA.	Mismatches: Indels:	AA.	Mismatches: Indels:	AA.	Mismatches: Indels:	250 AA. protein PRO1279.	Mismatches: Indels:	250 AA. protein PRO1279.	Mismatches: Indels:
ndard; protein; 250 AA. secreted and transmembrane -Al.	INC. 48.19% 29.94%	protein; 250 ide #253.	INC. 48.19% 29.94%	protein; 250 de #253.	INC. 48.19% 29.94%	protein; 250 de #253.	INC. 48.19% 29.94%	tein; 250 #253.	INC. 48.19% 29.94%	orotein; 250 le #253.	INC. 48.19% 29.94%	250	INC. 48.19% 29.94%	protein; 250 . nsmembrane pro	INC. 48.19% 29.94%	`` o	INC. 48.19% 29.94%
999 Bta human 3194766 T-2003.	GETH) GENENTECH cocal Similarity: Match:	2691 standard; n PRO polypept 03199032-A1. CT-2003.	GETH) GENENTECH cocal Similarity: Match:	707 standard; PRO polypept 3207418-A1.	GENENTECH imilarity:	5 standard; RO polypept 99028-Al.	TH) GENENTECH : al Similarity: tch:	ADE41019 standard; proi Human PRO polypeptide : US2003199031-A1.	23-OCT-2003. (GETH) GENENTECH LOCAL Similarity: 'MAECh:	standard; polypept 034-A1.	23-OCT-2003. (GETH) GENENTECH : Local Similarity: Match:	92947 standard; protein; an PRO polypeptide #253. 003194777-Al.	GETH) GENENTECH : Local Similarity: Match:	ADF29966 standard; protein; 25 Human secreted/transmembrane p (W22003204653-A1.	TH) GENERATECH : al Similarity:	1.558 ADF55859 standard; protein; Human secreted/transmembran; US2003204054-Al.	Similarity:
	PA (GETH Best Local Query Matc) RESHIT 581	ID ADE DE Hum PN US2 PD 23-	PA (GETH Best Local Query Matc RESULT 582	ID ADD DE Hum	ar st	ID ADD DE Hum PN US2	ar at	ID ADE DE Hum PN US2	3 H 2 H	ID ADE DE HUM PN US2	9 8 4	18 E S 2	# 25	ID ADF DE Hum PN US2	# G 6	ID ADE OE Hum PN US2	Sty St

US2003207386-A1.

	89 S	PRO1279.	89 5		· & 13		89 5		89 5	PRO1279.	യ ഗ സ	PRO1279.	89 5		89 60 FC	PRO1279.	8 S
	Mismatches: Indels:	in; 250 AA. transmembrane protein	Mismatches: Indels:	50 A.A	Mismatches: Indels:	250 AA.	Mismatches: Indels:	250 AA.	Mismatches: Indels:	n; 250 AA. transmembrane protein	Mismatches: Indels:	ein; 250 AA. d transmembrane protein	Mismatches: Indels:	250 AA. protein PRO1279.	Mismatches: Indels:	in; 250 AA. transmembrane protein	Mismatches: Indels:
UNI	48.19% 29.94%	protein; 2 ed and trar	INC. 48.19% 29.94%	protein, 2 ide #253.	INC. 48.19% 29.94%	protein; 2	INC. 48.19% 29.94%		INC. 48.19% 29.94%	protein; sed and tran	INC. 48.19% 29.94%	protein; 2 ed and tran	INC. 48.19% 29.94%	protein; insmembrane	INC. 48.19% 29.94%	protein; sed and tran	INC. 48.19% 29.94%
06-NOV-2003.	denemiech imilarity:	T 590 ADG23297 standard; protein Novel human secreted and t US2003207384-Al.	03. ENENTECH ilarity:	RESULT 591 ADP97632 standard; protein; DE Human PRO polypeptide #253. PN US2003207370-A1.	PD 06-NOV-2003. PA (GETH) GENENTECH 1 Best Local Similarity: Query Match:	596 standard; PRO polypept 1207373-A1.	ENTECH arity:	ADG80144 standard; protein; Human PRO polypeptide #253. US2003207372-Al.	GETH) GENENTECH INC Local Similarity: 48	RESULT 594 DD ADH55436 standard; protein; DE Novel human secreted and tr	US-NOV-2003. (GETH) GENENTECH 1 Local Similarity: Match:	KESULI 3998 standard; protein DE ADH5598 standard; protein DE Novel human secreted and the US2003207379-A1.	06-NOV-2003. (GETH) GENENTECH 1 Local Similarity:	1. 596 ADH99363 standard; protein; i Human secreted/transmembrane US200365142-A1.	PD 03-AFK-2003, PA (GETH) GENENTECH 1 Best Local Similarity: Query Match:	T 597, Novel human secreted and tr. US2003207385-Al.	PD 06-NOV-ZOUS. PA (GETH) GENENTECH : Quert Match: PRESITY 58

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ADN39242 standard; protein; 250 AA.
Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:560.
WO2003042661-A2.
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                                                                        DE Novel human secreted and transmembrane protein PRO1279.

BN US2003207388-A1.

PA (GFTH) GENEWITECH INC.

Best Local Similarity: 48.19$ Mismatches: 89

Next Match: 29.94$ Indels: 5

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Novel human secreted and transmembrane protein PRO1279.
US2003207387-A1.
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Novel human secreted and transmembrane protein PRO1279.
US2003087385-A1.
08-MAY-2003.
                                                                                                                                                                                                                                    ADHB1517 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207377-A1.
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Novel human secreted and transmembrane protein PRO1279.
US2003087355-A1.
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Novel human secreted and transmembrane protein PRO1279.
US2003087356-A1.
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D 08-MAY-2003.
A (GETH) GENENTECH INC.
38est Local Similarity: 48.19%
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A (GETH ) GENENTECH INC.
BEST Local Similarity: 48.19%
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Best Local Similarity: 48.19%
herv Match: 29.94%
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Best Local Similarity: 48.19%
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A (GETH ) GENENTECH INC.
Hest Local Similarity: 48.1
OG-NOV-2003.
A (GETH ) GENENTECH INC.
Sest Local Similarity: 48.
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ESULT 604
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Mismatches: Indels:

V-2003.	\ (PA (GETH) GENENTECH INC. Best Local Similarity: 48.19%
រី <u>ត</u> ្	Mismatches: Indels:	88 S	Query Match: 29.94 RESULT 617
ADC48889 standard; protei Novel human secreted and	in; 250 AA. transmembrane protein	PRO1279,	ID ADEZUBI4 BEGINGATO; protein; DE Novel human secreted and tr DD 022003100734-A1.
FN 022003002000-A1. PD 15-MAY-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.19% Onery March 29.948	Mismatches: Indels:	68 W	# 1. 1
RESULT 609 1D ADC81243 standard; protein be Novel human secreted and novel nov	50 AA smemb	PRO1279.	ID ADE39111 standard; protein; DE Novel human secreted and tx PN US20030965262-A1.
PN USZUOVOZOZIES-AI. PN 15-MAY-2003. PA (GETH) GRNENTECH INC. Best Local Similarity: 48.19% Query March:	Mismatches: Indels:	8 6 5 7	# 2,2
KESULT 610 ID ABOLO Standard; protein; 250 AA. DE Novel human secreted and transmembrane protein PN US2003100735-A1.	n; 250 AA. transmembrane protein	PR01279.	S standard; RO polypept 92113-A1. 2003.
PD 25-MAX-2003. BAR (GETH) GENENTECH INC. Best Local Similarity: 48.19% Query Match: 29.94%	Mismatches: Indels:	5 8 9	# 2.5
RESULT 611 ID ADBE05904 standard; protein; DE Human PRO polypeptide #93. PN US2003100728-A1.	n; 250 AA.		ID ADD86459 standard; protein; DE Human PRO polypeptide #253. PN US2003203440-Al. PD 30-OCT-2003.
PD 29-MNY-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.19% Query Match: 29.94%	Mismatches: Indels:	8 S	# K E
RESULT 912 ID ADD76631 standard; protein; DE Human PRO polypeptide #253. PN US2001100087-Al.	n; 250 AA. 3.		D ADDOSSAS BERHARAT, PIOLELII, DE Human PRO POLYPEPLIGE #93. PN US2003100727-A1. PD 29-MAX-2003.
# £	Mismatches: Indels:	. 68	FA (GEIH) GENENTECH INC. Best Local Similarity: 48.19% Query Match: RESULT 622
RESULT 613 LD ADD75133 standard; protein; DE Human PRO polypeptide #93. PN US2003100712-A1.	n; 250 AA		1D ADD/3643 standard; protein; DE Human PRO polypeptide #93. PN US2003100711-A1. PD 29-MAY-2003.
PD 29-MNY-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.19% Query Match: 29.94%	Mismatches: Indels:	8 S	Str.
KESULT 614 DE NADD15879 standard; protein; 250 AA. DE Novel human secreted and transmembrane protein PN US2003100717-A1.	n; 250 AA. transmembrane protein	PRO1279.	ADE/5907 Human PF US200321 13-NOV-2
PD 29-MAY-2003. Rest Local Similarity: 48:19% Query Match: 29:94%	Mismatches: Indels:	68 21	Sir at
1 sta uman 00722	ndard; protein; 250 AA. secreted and transmembrane protein :-Al.	PRO1279.	D ADD/0483 BERHERET; protein; DE Novel human secreted and tr PN US2003100737-A1. PD 29-MAX-2003. DA (COPTU) CENTRANDOUT INC
PA (GETH) GENERATECH INC. Best Local Similarity: 48.19% Query Match: 29.94%	Mismatches: Indels:	89 5	Siry st
5 4 4	n; 250 AA. tranвmembrane protein	PR01279.	ADE41458 SCA Human secret US2003100497 29-MAY-2003.

29-MAY-2003

В

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Query Match:

RESULT 617

ID ADE20814 standard; protein; 250 AA.

ID ADE20814 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.

PD 29-MAY-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 48.19$ Mismatches: 89

Query Match: 29.94$ Indels: 5

RESULT 618

ID ADE301095362-A1.

PN US2003096362-A1.

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Novel human secreted and transmembrane protein PRO1279.
US2003100737-A1.
29-MAY-2003.
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Human secreted/transmembrane PRO polypeptide #104.
025003100497-A1.
29-MAY-2003.
(GETH ) GENENTECH INC.
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Indels:
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PD 29-MAY-ZO03.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19$ Misme
Query Match:
RESULT 623
ID ADB75907 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN USZ003211571-A1.
PD 13-NOV-Z003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19$ Mis
                                                                                                                                                                                                                                                                                                                                                                          Query Match:
RESULT 619
ID ADD88055 standard; protein; 250 AA.
DE Human PRO Polypeptide #253.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19$ Mis
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DE Human PRO polypeptide #253.

PN US2003440-A1.

PD 30-CCT-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 48.19% Mism Query Match: 29.94% Inde RESULF 621

ID ADE05658 standard; protein; 250 AA.

PN US2003100727-A1.

PD 29-MAY-2003.

PA (GETH) GENENTECH INC.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD73643 standard, protein; 250 AA. Human PRO polypeptide #93. US2003100711-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE Novel human secreted and traup W US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENEWIECH INC.
Best Local Similarity: 48.19%
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RESULT 625
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RESULT 620
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Query Mat RESULT 63	DE Huma PN US20 PD 15-iv	gry st	DE Huma	PD 15-N PA (GET Best Loca	Query Mat RESULT 63	ID ADD8 DE Huma PN US20	# K E	ID ADEC	PD 29-N	gg g	1D ADD DE Hune PN US20-10	PA (GET Best Loca Query Mat	DE NOVE PN US20 PN US20	gir it	ID ADD8 DB NOVE PN US20 PD 29-P	# 5.2	1D ADE DB Huma PN US20 PD 23-C	# £ £	ID ADD7 DB NOVE PN US2C	븄
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Mismatches: Indels:	250 AA.	Mismatches: Indels:	n; 250 AA. transmembrane protein		Mismatches: Indels:	otein; 250 AA. and transmembrane protein	Mismatches: Indels:	250 AA ansmemb	4	Mismatches: Indels:	250 AA.	Mismatches: Indels:	250 AA.	Mismatches: Indels:	250 AA.	Mismatches: Indels:	.n; 250 AA. transmembrane protein	Mismatches: Indels:	n; 250 AA. transmembrane protein	
48.19% 29.94%	protein; ide #253.	INC. 48.19% 29.94%	protein; ed and tr	INC.	48.19% 29.94%	protein; ed and tr	INC. 48.19% 29.94%	protein;		INC. 48.19\$ 29.94\$	protein; ide #93.	INC. 48.19% 29.94%	protein; ide #93.	INC. 48.19% 29.94%	protein; ide #93.	INC. 48.19% 29.94%	undard; protein; secreted and tra 3-A1.	INC. 48.19% 29.94%	protein; ed and tr	INC.
Best Local Similarity: Query Match: RESULT 626	ADE23483 standard; protein, Human PRO polypeptide #253. US2003092108-A1.	PD 15-MAY-2003. PA (GETH) GENENTECH 1 Best Local Similarity: Query Match:	ADE21306 standard; protein Novel human secreted and to	PN US2003100736-A1. PD 29-MAY-2003. PA (GETH) GENENTECH 1		T 628 ADD77421 standard; protein; Novel human secreted and tri	PD 29-MAY-2003. PA (GETH) GENENTECH 1 Best Local Similarity: Ouery Match:	red	US2003100733-A1.	ENTECH 1 arity:	.r 630 ADD75633 standard, protein, Human PRO polypeptide #93. US2003100064-Al.	PD 29-MAY-2003. PA (GETH) GENENTECH 1 Best Local Similarity: Query Match:	1. 641 ADD74149 standard, protein, Human PRO polypeptide #93. US2003100708-Al.	PD 29-FM1-2003. PA (GETH) GENENTECH I BEST LOCAL SIMILARITY: Query Match:	/T 632 ADD74395 standard; protein; Human PRO polypeptide #93. US2003100709-Al.	FD (GETH) GENENTECH) PA (GETH) GENENTECH) Query Match:	S sta uman 00718	29-MAY-2003. (GETH) GENENTECH 1 Local Similarity: Match:	RESULT 634 ID ADD85617 standard; protein; 2: DE Novel human secreted and tran PN HS200310071-21	(GETH) GENENTECH
Best Query RESUL	PN	PD PA Best Query	DE DE SOL	7 0 4 8 0 4	Best Query	RESUL ID DE	PD PA Best	RESUL ID DE		PA Best Query	ID DE DE	PD PA Best Query	NESCOL DE DE	PA PA Best J Query	RESUL ID DE PN	π̈́ğ	RESUL ID DE	PD PA Best Query	RESUL ID DE	P P P

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29.94% ; protein; 250 tide #253.	INC. 48.19% 29.94%	; protein; 250 tide #253. INC. 48.19%	29.94% ; protein; 250 tide #253.	NC. 18.19% 29.94%	; protein; 250 tide #93. INC. 48.19% 29.94%	; protein; 250 tide #93.	INC. 48.19% 29.94%	ndard; protein; 250 AA. secreted and transmembrane -A1.	INC. 48.19% 29.94%	ndard; protein; 250 AA. secreted and transmembrane -A1.	INC. 48.19% 29.94%	; protein; 250 tide #253.	INC. 48.19% 29.94%	; protein; 250 ted and transm	INC. 48.19% 29.94%
.March: T 635 ADE24035 standard; protein. Human PRO polypeptide #253.	US2003092110-A1. 15-MAY-2003. (GETH) GENENTECH Local Similarity: Match:	AD 8-36 AD 8-24678 standard; 1 AD 8-24678 standard; 1 US 2003 09 2111-A1. 15-MAY-2003. (GETH) GENENTECH II GACA Similarity: 1	y Match: LT 637 ADD87503 standard; Human PRO polypeptic	30-OCT-2003. (GETH) GENENTECH Local Similarity: Match: T 638	ADE05166 standard; protein; Human PRO polypeptide #93. US2003100726-Al. 29-MAY-2003. (GETH) GENENTECH INC. Local Similarity: 48.19\$ March: 29.94\$	ADD75379 standard; protein; 2 Human PRO polypeptide #93. US2003100714-Al.	(GETH) GENENTECH Local Similarity: Match:	LI 640 ADD76923 standard Novel human secre US2003100715-A1.	(GETH) GENENTECH Local Similarity: Match:	D86691 sta vel human 2003100719	29-MAY-2003. (GETH) GENENTECH Local Similarity: Match:	ADE89369 standard; protein; Human PRO polypeptide #253. US2003199062-Al.	23-OCT-2003. (GETH) GENENTECH Local Similarity: Match:	.1 04.3 ADD78159 standard; protein; 250 AA. Novel human secreted and transmembrane US2003100731-A1.	29-MAY-2003. (GETH) GENENTECH Local Similarity: Match:
ST.	PN US PD 15 PA (G Best Lo Query N	TESOLITION OF THE PROPERTY OF	Query Match: Query Match: RESULT 637 ID ADD8750 DE Human P	PD 30-OCT- PA (GETH) Best Local S Query Match: RESULT 638	ID AL DE HU PN US PD 29 PA (G	ñ	PA (G Best Lo Query N	ID AL DE NO PN US	e tr	ID AL DE NG	PD 25 PA (G Best Lo Query N	Š	PD 23 PA (G Best Lo Query N	7	PD 29 PA (G Best Lo Query M

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250 AA.	Mismatches: Indels:	50 AA.	Mismatches: Indels:	50 AA. smembrane protein	Mismatches: Indels:	n; 250 AA. transmembrane protein	Mismatches: Indels:	50 AA. smembrane protein	Mismatches: Indels:	50 AA.	Mismatches: Indels:	50 AA.	Mismatches: Indels:	50 AA. smembrane protein	Mismatches: Indels:	50 AA. smembrane protein	Mismatches: Indels:
	INC. 48.19% 29.94%	protein; 2 ide #253.	INC. 48.19% 29.94%	protein; 250 AA. ed and transmembrane	INC. 48.19% 29.94%	protein; 2 ed and tran	INC. 48.19% 29.94%	protein; 250 AA. ed and transmembrane	INC. 48.19% 29.94%	protein; 2 ide #93.	INC. 48.19% 29.94%	protein; 2 ide #93.	INC. 48.19% 29.94%	protein; 250 AA. ed and transmembrane	INC. 48.19% 29.94%	protein; 2 ed and tran	INC. 48.19% 29.94%
JT 644 ADE18508 standard; protein; Human PRO polypeptide #253. US2003194794-A1.	18-CC1-2003. (GETH) GENENTECH . Local Similarity: / Match:	E88817 standard; man PRO polypept 2003199054-A1.	-OCT-2003. BTH) GENENTECH cal Similarity: atch:	D77667 standard; vel human secret 2003100729-A1.	(GETH) GENENTECH (GETH) GENENTECH (Y Match:	ADD77913 standard; protein; 2 Novel human secreted and tran US2003100730-A1.	29-MAY-2003. (GETH) GENENTECH . Local Similarity: 'Match:	035 D85371 standard; vel human secret 2003100725-A1	-MAY-2003. ETH) GENENTECH cal Similarity:	ADD73903 standard, protei Human PRO polypeptide #93 US2003100710-A1.	PD 29-MAY-2003. PA (GETH) GENENTECH : Query Match: PREST CO :	ADD74641 standard; protei ADD74641 standard; protei Human PRO polypeptide #99 US2003100713-A1. 29-MAY-2003.	(GETH) GENENTECH : Local Similarity: / Match:	651 D77169 standard; vel human secret 2003100716-A1.		AD055863 standard; protein; 250 AA. Novel human secreted and transmembrane US2003100720-AI.	
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250 AA. Mismatches: Indels: 250 AA.	Mismatches: Indels: 250 AA. protein PRO1279.	Mismatches: Indels: 250 AA.	Mismatches: Indels: 250 AA.	Mismatches: Indels: 250 AA. protein PRO1279.	Mismatches: Indels: 250 AA.	Mismatches: Indels: 250 AA.	Mismatches: Indels: 250 AA. protein PRO1279.	Mismatches: Indels: 250 AA.
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ADE05412 standard; protein; Human PRO polypeptide #93. US2003100723-Al. 29-MAY-2003. (GETH) GENENTECH INC. (GETH) GENENTECH INC. 29-MATCh. 19% 20.94% ILT 654 ADD74887 standard; protein; Human PRO polypeptide #93. US2003100724-Al.	29-MAX-2003. (GETH) GENENTECH INC. (Incal Similarity: 48.19% by Match: 29.94% JLT 655 ADE96543 standard; protein; 25 Human secreted/transmembrane pus2003195347-A1.	16-OCT-2003. (GETH) GENENTECH INC LOCAL Similarity: 48 Y Match: 29 LT 656 ADE94837 standard; pro Human PRO polypeptide US2003199027-A1.	23-0CT-2003. 23-0CT-2003. GGFH) GENENTECH II. Local Similarity: Y Match: LT 657 ADE91248 standard; Human PRO Polypeptil	23-OCT-2003. Local Similarity: 48.19% Local Similarity: 48.19% In 658 AD ADPESSES standard; protein; US203199675-A1.	23-001-2003. (GF-M) GENENTECH II LOCAL Similarity: Y Match: LT 659 ADE95389 standard; Human PRO polypeptit	-CCT-2003. ETH) GENENTECH I cal Similarity: atch: atch: E93499 standard; man PRO polypepti 200319906-A1.	i) GENENTECH INC. Similarity: 48.19# th: 29.94# I753 standard; protein; 31 secreted/transmembrane 17-2003.	<pre>1) GENENTECH 1 Similarity: th: 2 2 489 standard;</pre>
56.5	PD 29-MAY- PA (GETH) PA (GETH) Best Local S Query Match: RESULT 655 ID ADE9654 DE Human B PN US20031	# 2 12	SGR	ery SUI	st SUI	PD 23-CCT-2 PA (GETH) Best Local Si Query Match: RESULT 660 ID ADE93499 DE Human PR PN US200319 PN 23-CCT-2	GG Bt Lo ery M SULT AD AD Hu Hu US	PA (GETH) G Best Local Sin Query Match: RESULT 662 ID ADF29489

DE	Human secreted/tran	івтетргапє	secreted/transmembrane protein PRO1279.		
	T-2003. CENENTECH	INC.	Mismatches:	or co	
Query	Best Local Similarity: Query Match:	29.94%	Indels:	ກັດ	•
ID TO	ADF35080 standard; protein; Human PRO nolymentide #253.	protein;	250 AA.		
N C	US2003199029-A1.				<u>.</u>
ŭ	(GETH) GENENTECH I Local Similarity:	INC. 48.19%	Mismatches:	68	
Query	h:	29.94%	Indels:	ro L	
	ADE97020 standard;	protein;	120 standard, protein; 250 AA.		
321	DS2003195334-Al.	Tome Tome			
		INC.		;	
Best Query	cal Similarity: latch:	48.19%	Mismatches: Indels:	ט מט	
Ĕ	T 665 ADE92395 standard; protein;	protein;	1	9201000	
	Novel numan secrete US2003199051-A1.	ed and cr	cransmembrane process	FROIZ / 3 .	
04		INC.			
Best	cal Similarity:	48.19%	Mismatches: Indels:	98 N	
RESUL	T 666			1	
018	ADE90696 standard; Human PRO polypept;	protein; ide #253.	250 AA.		
PN US	US2003199063-Ā1.				
PA	(GETH) GENENTECH	INC.		C	
Best Query	cal Similarity: atch:	48.19% 29.94%	Mismatches: Indels:	u v	
ğ	667 E01943 eta	nrotein.	250 AA		
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	309695				
P P	(GETH) GENENTECH	INC.			
Best	Similarity: h:	48.19%	Mismatches: Indels:	യ വ	
RESUL	RESULT 669				
	ADG27253 standard; protein; Human PRO polypeptide #93.	protein; ide #93.	250 AA.		
	US2003096962-A1.				
•) GENENTECH	INC.			
Best Lo Query N	Best Local Similarity: Query Match: prem.r 620	48.19% 29.94%	Mismatches: Indels:	50 LC	
日日	ADG02422 standard; protein; Human PRO polypeptide #253.	protein; ide #253.	250 AA.		. <u>-</u>
	US2003207352-A1. 06-NOV-2003.				
PA Best Ouery	(GETH) GENENTECH Local Similarity: Match:	INC. 48.19% 29.94%	Mismatches: Indels:	6 60 60	
RESULT	IT 671 APG22208 standard:	protein:	250 AA.		
E E	Novel human secret	ed and tr	Novel human secreted and transmembrane protein PRO127	PRO1279.	_

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ADG24401 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207426-A1.
06-NOV-2003.
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ID ADG01586 standard; protein; 250 AA.
ID Human PRO polypeptide #253.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48:19$ Miss Onery Match: Ind
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO polypeptide #253.
US2003208055-A1.
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US2003207375-A1.
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Human PRO polypeptide #253.
US2003207353-A1.
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Human PRO polypeptide #253.
US2003207425-A1.
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1D Human PRO polypeptide #253.

PN US2003207359-A1.

PD 06-NOV-2003.

PA (GETH ) GENEWTECH INC.

PA (GETH ) GENEWTECH INC.

Query Match:

29.94% I
                                                                                                  ADG20278 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003207376-A1.
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DE Human PRO polypeptide #253.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19% M
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
BEST LOCAL SIMILATITY: 48.19$
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PA (GETH ) GENENTECH INC.
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Best Local Similarity: 48.19%
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PA (GETH) GENENTECH INC.
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(GETH ) GENENTECH INC.

Best Local Similarity: 48.19%

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29:94%
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RESULT 680
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Mismatches: 150 AA. Mismatches: Indels: 250 AA.	89 5	PRO1279.	8 8 5		6 8 S	PRO1279.	5 8 8		8 8 S		80 r. 20	1		8 B B		80 KJ	PRO1279.	8 S	
larity: 48.19\$ trandard; protein; nn secreted and trands. NENTECH INC. larity: 29.94\$ trandard; protein; polypeptide #253. NENTECH INC. larity: 29.94\$ trandard; protein; nn secreted and trands. larity: 48.19\$ trandard; protein; polypeptide #253. NENTECH INC. larity: 48.19\$ trandard; protein; polypeptide #253. NENTECH INC. larity: 48.19\$ trandard; protein; nn secreted and trands. NENTECH INC. larity: 48.19\$ trandard; protein; polypeptide #253. NENTECH INC. larity: 48.19\$ trandard; protein; polypeptide #253. NENTECH INC. larity: 48.19\$ trandard; protein; polypeptide #253. NT-Al. NENTECH INC. larity: 48.19\$ trandard; protein; polypeptide #253. NT-Al. 29.94\$ trandard; protein; polypeptide #253. NT-Al. 20.94\$ trandard; protein; nn secreted and trandard; protein; larity: 29.94\$	Mismatches: Indels:		Mismatches: Indels:	250 AA.	Mismatches: Indels:	250 AA. nsmembrane protein	Mismatches: Indels:	00			Mismatches: Indele:	250 AA.		Mismatches: Indels:	250 AA.	Mismatches: Indels:	250 AA. nsmembrane protein	Mismatches: Indels:	250 AA.
llarity: llarity: llarity: larity:	INC. 48.19% 29.94%	protein; ed and tra	INC. 48.19% 29.94%	stein; #253.	INC. 48.19% 29.94%	protein; ed and tra	INC. 48.19% 29.94%	protein; ide #253.	INC. 48.19% 29.94%	protein; ed and tra	INC. 48.19%	protein;	ide #253.	INC. 48.19% 29.94%	protein; ide #253.	INC. 48.19% 29.94%	protei ed and	INC. 48.19% 29.94%	protein; ide #253.
PA (GETH) GEN Best Local Simil Query Match:	(GETH) GENENTECH : Local Similarity: Match: T 681	316 hum 3096	2003. GENENTECH imilarity:	ADG13455 standard; pro Human PRO polypeptide US2003207357-A1.	V-2003.) GENENTECH Similarity: h:	T 683 ADG08512 standard; Novel human secrete	2003. GENENTECH imilarity:	682 standard; PRO polypept. 3219885-A1.	W-2003.) GENENTECH Similarity: h:	095 standard; human secret	US2003096963-A1. 22-MAY-2003. (GETH) GENENTECH : LOCAL Similarity:	080 standard;	Human PRO polypept US2003207371-A1. 06-NOV-2003.	GENENTECH imilarity:	265 standard; PRO polypept. 3207374-A1.	V-2003. I) GENENTECH Similarity: h:	KESULI 688 ID ADG23849 standard; DE Novel human secrete PN US2003207389-A1.	2003. GENENTECH imilarity:	T 689 ADG04138 standard; protein; Human PRO polypeptide #253. IIS2001207423-A1

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5039 standard; protein; 250 AA.
1 human secreted and transmembrane protein PRO1279.
03207427-A1.
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1 human secreted and transmembrane protein PRO1279.
03096964-A1.
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1 human secreted and transmembrane protein PRO1279.
33207350-A1.
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L human secreted and transmembrane protein PRO1279.
33207336-A1.
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1 human secreted and transmembrane protein PRO1279.
03194778-A1.
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1 human secreted and transmembrane protein PRO1279.
103207390-A1.
103207390-A1.
10 GENERTECH INC.
11 Similarity: 48.19$ Mismatches: 89
11 ch: 100 Ch:
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1 human secreted and transmembrane protein PRO1279.
03207428-A1.
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Human secreted/transmembrane protein PRO1279.
US2003216562-A1.
(GETH ) GENENTECH INC.
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man PRO POLypeptide #93.
0003096966-Al.
MAY-2003.
TH ) GENENTECH INC.
2TH ) GENETY 48.19$ Miss
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TH ) GENENTECH INC.
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TH ) GENENTECH INC.
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TH ) GENENTECH INC.
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H ) GENENTECH INC.
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Query Match: 29.94% Indels: 5 RESULT 708 ID ADGS0143 standard; protein; 250 AA. DE Novel human secreted and transmembrane protein PRO1279.	PN US2003207363-A1. PD 06-NOV-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.19% Mismatches: 89 Query Match: 29.94% Indels: 5	RESULT 709 ID ADG53727 standard; protein; 250 AA. DE Novel human secreted and transmembrane protein PRO1279. PN US2003207415-A1.	at Sury	613 standard; protein; 250 AA. human secreted and transmembrane protein PR 3207421-A1. 7-2003. PENENTECH INC.	7 £ E	DE Human PRO polypeptide #253. PN US2003207805-Al. PD 06-NOV-2003. Best Local Similarity: 48.19* Mismatches: 89 Query Match: 29.94* Indels: 5	2 standard; RO polypept: 77723-A1.	3 tr	129 standard human secre 3207419-A1. W-2003.	r KE	embrane protein PR	Match: 29.94* Indels: A7 715 ADG54279 standard; protein; 250 AA. Novel human secreted and transmembrane prote:	07416-A1. 2003. GENENTECH INC. imilarity: 48.19% Misma	SULT 716 SULT 716 ADG81248 standard; protein; 250 AA. Human PRO polypeptide #253.	PN US200194793-A1. PD 16-0071-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.19% Mismatches: 89	Indels:
Sty St	RO polypeptide #253. 0738-Al. 2003. GENENTECH INC. imilarity: 48.19%	Indels: 1, 250 AA. :ransmembrane protein PR	US2003207362-A1. 06-NOV-2003. (GETH) GENENTECH INC. 5t Local Similarity: 48.19\$ Mismatches: 5r ymatch: 29.94\$ Indels:	9 standard; protein; 250 AA. uman secreted and transmembrane protein PR 07364-Al.	Str.	<pre>ID ADG55935 standard; protein; 250 AA. DB Novel human secreted and transmembrane protein PRO1279. PN US2003207365-A1. PD 06-NOV-2003. PA (GETH) GENENTECH INC.</pre>	Best Local Similarity: 48.19% Mismatches: 89 Query Match: 29.94% Indels: 5 RESULT 703 ID ADG38695 standard; protein; 250 AA.	Novel human secreted and transmembrane protein PR US2003207368-A1. 06-NOV-2003. (GETH) CENENTECH INC.	y Match. 19.94% Indels: 10.704 ADG71061 standard; protein; 250 AA. Novel Numan secreted and transmembrane protein PRO	US2003207420-A1. 06-NOV-2003. (GETH) GENENTECH INC 3t Local Similarity: 48	2 standard; protein; 250 AA. ecreted/transmembrane protein PRO1279.	ir gry	ADH03535 standard; Human secreted/trs US2003224478-A1. 04-DEC-2003.	t Local Similarity: 48.19% sry Match: 29.94% SULT 707	ADH390 Novel US2003 22-MAY	PA (GETH) GENENTECH INC. Best Local Similarity: 48.19% Mismatches: 89

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5-A1.	48.19%	protein; ed and tra	INC. 48.19%. 29.94%	protein; ed and tra	INC. 48.19% 29.94%		INC. 48.19% 29.94%	protein; ed and tra	INC. 48.19% 29.94%	protein; ed and tra	INC. 48.19% 29.94%		INC. 48.19% 29.94%	protein; ed and tra	INC. 48.19% 29.94%	protein; ısmembrane	INC. 48.19% 29.94%
US2003207366-A1. 06-NOV-2003. (GETH) GENENTECH	imilarity:	ADH12753 standard, protein, Novel human secreted and tr US2003207378-Al.	₩;	ADG61599 standard; Novel human secrete US2003207429-Al	PD 06-NOV-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 48.19% QUETY MATCH: 29.94%	KESOLI /20 ID ADH28686 standard; protein; DE Human PRO polypeptide #253. NI 19270120131.	PD 30-JAN-2003. PA (GETH) GENENTECH : Best Local Similarity: Query Match:	KESULI 721 ID ADG54831 standard; Dovel human secrete PN US2003207367-A1. PD 06-NOV-2003) GENENTECH Similarity: h:	KESULI 722 ID ADG59871 standard; protein; 250 AA. E Novel human secreted and transmembrane protein PRO1279 DN 1620013073160.81	=	ADH43641 standard; protein; Human PRO polypeptide #104. US2003224984-A1.	PA (GETH) GENENTECH 1 Best Local Similarity: Querry Match:	ID AD034182 standard; protein; 250 AA. Novel human secreted and transmembrane protein PRO1279 N US2004006206-AI.	ENTECH arity:	89	PD 08-JAN-2004. PA (GETH) GENENTECH J Best Local Similarity: Query Match:

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ADG10038 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2004009548-A1.
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Novel human secreted and transmembrane protein PRO1279.
US2003207382-A1.
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DB ADG0386 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.

PN US2004009547-A1.

PD 15-JAN-2004.

PA (GETH) GENERTECH INC.

Best Local Similarity: 48.19% Mismatches: 89

Query Match: 29.94% Indels: 5
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Novel human secreted and transmembrane protein PRO1279.
US2003207383-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO1279
US2003096961-A1.
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Novel human secreted and transmembrane protein PRO1279.
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Human secreted/transmembrane protein PRO1279
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                                                                                                                        ID AD133652 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 48.19$
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DE Human PRO polypeptide #93.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENNATTECH INC.
Best Local Similarity: 48.19% M.
Query Match:
DE Human PRO polypeptide #253.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19$
Query Match:
RESULT 727
          Human PRO polypeptide #253. US2003207361-Al.
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19%
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PA (GETH ) GENENTECH INC.
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.1
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22-JAN-2004.
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RESULT 732
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Mismatches: Indels:	in; 250 AA. transmembrane protein PRO1279	Mismatches: Indels:	in; 250 AA. transmembrane protein	Mismatches:	250 AA.	Mismatches: Indels:	250 AA.	Mismatches: Indels:	250 AA.	Mismatches: Indels:	250 AA.	Mismatches: Indels:	Mismatches:	50 AA.	Mismatches: Indels:	250 AA. e protein PRO1279.
INC. 48.19% 29.94%	prote: ed and	INC. 48.19% 29.94%	prote: ed and	INC. 48.19%	; protein; tide #253.	INC. 48.19% 29.94%	; protein; tide #104.	INC. 48.19% 29.94%	; protein; tide #93.	INC. 48.19% 29.94%	; protein; tide #253.	INC. 48.19% 29.94%	; protein; tide #253. I INC.	l; protein; tide #253.	INC. 48.19% 29.94%	l; protein; ansmembrane
PN US2003207349-A1. PD 06-NOV-2003. PA (GETH) GENEWTECH Best Local Similarity: Query Match:	4 8t6 uman 44179	PD 04-MAR-2004. PA (GETH) GENENTECH Best Local Similarity: Query Match:	7 stë uman	PD 26-FEB-2004. PA (GETH) GENENTECH Best Local Similarity:	VECULT 738 ID AD/77612 standard; protein; DE Human PRO Polypeptide #253. DN TROPOGRASALAL	£ 5	KESULI 139 ID ADK82986 standard; protein; DE Human PRO polypeptide #104. DN IRSOA4041977-1	# J	KESOLI /40 ID ADK66662 standard; protein; DE Human PRO polypeptide #93. PN US2004044180-A1.	17 E	ID ADJ65734 standard, pro DE Human PRO polypeptide PN US2004038335-Al.	ř.	RESULT 742 ID ADNA7870 standard; protein; DE Human PRO polypeptide #253. PN US2004048333-A1. PD 11-MAR-2004. PA (GETH) GENENTECH INC. Best Local Similarity: 48.19\$	Cutery Macton: RESULT 743 ID ADM42594 standard; protein; 2 DE Human PRO polypeptide #253. DN 1720AAA65424-1	in in in	RESULT 744 ID ADL9689 standard; protein; 250 AA. DE Human secreted/fransmembrane protein PRO1279 , PN US2004073015-Al.

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ADR72890 standard; protein; 250 AA.
Human ovarian cancer-related tumour marker kallikrein 11 (hK11) protein2.
WO2004075713-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID ADR72632 standard; protein, 250 AA.

ID Human renal cell carcinoma-related kallikrein 11 (hKl1) protein 2.

BN WO2004077060-A2.

BD 10-SRP-2004.

PA (MOUN ) MOUNT SINAI HOSPITAL.

Best Local Similarity: 48.19$ Mismatches: 89

Query Match: 59.94$ Indels: 5
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Novel human secreted and transmembrane protein PRO1279.
US2003207354-A1.
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Human autoimmune disease-related protein - SEQ ID 106.
WQ2004083403-A2.
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RESULT 753
ID AAY43636 standard; protein; 282 AA.
DE A human prostate-associated serum protease (PRASP).
PN W09941387-A2.
PD 19-AUG-1999.
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DE Aubil 122 standard; protein; 282 AA.

DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO:2.

PN W020031257-A1.

PD 02-JUN-2000.

PA (FUSO) PRISO PRARM IND LTD.

Best Local Similarity: 48.19% Mismatches:

Query Match: Logical Similarity: 29.94% Indels:
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PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Guest Local Similarity: 48.19* Mismatches:
Query Match: 29.94* Indels:
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US2003077659-A1.
                                                                                   ID APM28456 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2004077064-A1.
PA GETAPR-2004.
PA GETH) GENENTECH INC.
Best Local Similarity: 48.19% M
Query Match:
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CASB12 amino acid sequence.
WO9949055-A1.
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PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Best Local Similarity: 48.19%
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PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 48.19%
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19%
QUERY MATCh: 29.94%
RESULT 745
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 48.19%
                                                                                                                                                                                                                                                                                                                                                           29.94$
                                                                                                                                                                                                                           JT 746
ADI95938 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
RESULT 750
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RESULT 746
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RESULT 747
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RESULT 748
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RESULT 751
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478.

91

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AAB36483 standard; protein; 289 AA.
Fusion gene with human serine protease catalytic domain protein #14.
WO200066709-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB67543 standard; protein; 289 AA.
Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.
WO200116289-A2.
08-MAR-2001.
(ORTH ) ORTHO-MCNEIL PHARM INC.
                                                                                   ID AAB67542 standard; protein; 288 AA.

DE Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.

PN W0200116289-A2.

DO 8-MAR-2001.

PA (ORTH ) ORTHO-WCNEIL PHARM INC.

PAST LOCAL Similarity: 51.10% Mismatches: 87

Query Match: 29.16% Indels: 3
                                                                                                                                                                                                                                                                                                                                                  ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB11714 standard; protein; 275 AA.
Human serine protease BSSP6 (hBSSP6) SEQ ID NO:6.
W0200031257-A1.
02-UNN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADN10932 standard; protein; 256 AA.
Human kallikrein 15, marker of endocrine cancer.
WO2004029285-A2.
                                                                                                                                                                                                                                                                                                                  AAY36093 standard; protein; 250 AA.
Extended human secreted protein sequence, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD 09-NOV-2000.
PA (ORTH ) ORTHO-MCNEIL PHARM RES INC.
Best Local Similarity: 28.14% Mismatches:
  Mismatches:
Indels:
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WO200268649-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP19401 standard; protein; 250 AA.
Human secreted polypeptide #252.
US2004110939-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU79390 standard; protein; 256 AA.
Novel human kallikrein KLK15.
WO200214485-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI17075 standard; protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PN WO2004029285-AZ.
PD 08-ARR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
BEST Local Similarity: 47.08%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 47.08%
Query Match: 28.99%
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DE Amino acid sequence of cata
PN W0200116289-A2.
PD 08-MAR-2001.
PA (ORTH ) ORTHO-MCNEIL PHARM
Best Local Similarity: 49.14%
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PA (CURA-) CURACEN CORP.
Best Local Similarity: 49.78%
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  Best Local Similarity:
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Best Local Similarity:
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Best Local Similarity:
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RESULT 770
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36482 standard; protein; 288 AA.
Fusion gene with human serine protease catalytic domain protein #13.
WO200066709-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR72631 standard; protein; 282 AA.
Human renal cell carcinoma-related kallikrein 11 (hKll) protein 1.
WO2004077060-A2.
10-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV42440 standard; protein; 281 AA.
CASB12 polypeptide derived from Expressed Sequence Tag products.
WO9949055-A1.
                                                                                                                                                                                                                                                                                                                                                                                SEQ ID 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human autoimmune diBease-related protein - SEQ ID 107.
WO2004083403-A2.
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                                                                                                          DE Human kallikrein-11, marker for prostate cancer.

NO2004029616-A2.

PD 08-APP-2004.

MOUNN MOUNT SINAI HOSPITAL.

Best Local Similarity: 48.19% Indels:

Ouery Match:
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                                                                                                                                                                                                                                                                                                                                                                       DE Human soft tissue sarcoma-upregulated protein Wo20064048938-A2.
PN WO20064048938-A2.
PD 10-UTN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
PAST Local Similarity: 48.19% Mismatches: 29.94% Indels: RESULT 756
                                Mismatches:
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(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
Local Similarity: 47.98% Misme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T 760
AAU82732 standard; protein; 320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
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Human protease, PRTS-3 protein.
WO200208396-A2.
31-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR72889 standard; protein; 282 AA.
                                                                                                                                                                                                                                                                                                                       r 755
ADQ17587 standard; protein; 282 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-2000.
(ORTH ) ORTHO-MCNEIL PHARM RES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOUN ) MOUNT SINAI HOSPITAL.
Local Similarity: 48.19%
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Local Similarity: 48.19%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-2004.
(APPL-) APPLERA CORP.
Local Similarity: 48.19%
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v Match: 29.55%
PA (INCY-) INCYTE PHARM INC.
Best Local Similarity: 48.19%
Query Match: 29.94%
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Best Local Similarity:
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                                                        Query Match:
RESULT 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
RESULT 761
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RESULT 757
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30

2 2

86 2

88 16

88 16

79

Query Match RESULT 762

PA Best

Query Ma

Best

Query Match: 27.66% Indels: RESULT 781 ID AAB21306 standard; protein; 251 AA. DE Human KLK-Leb protein #2. PN WOODGESTAGES	14-582-2000. (MOUN) MOUNT SINAI HOSPITAL. St Local Similarity: 46.85% Mismatc STY Match: 27.57% Indels: SULT 782 ADN10930 standard; protein; 251 AA. Human kallikrein 14. marker of endocrine	Human Kallikren 14, marker or WO2004029285-A2. 08-APR-2004. (MOUN) MOUNT SINAL HOSPITAL. st Local Similarity: 46.85\$ ary Match: 3LT 783	AMBALOS BEGINGARG; procein; 250 Human KLK-L3 protein #2. WO200053776-A2. 14-SEP-2000. (MOUN) MOUNT SINAI HOSPITAL. st Local Similarity: 46.67% ery Match: SULT 784	ID ABP64969 standard; protein; 250 AA. DE Human protein SEQ ID 629. PN W0200259260-A2. PD 01-AUG-2002. PA (HYSE-) HYSEQ INC. Best Local Similarity: 46.67% Mismatches Ouery Match: 27.52% Indels:	ID ABR55400 standard; protein; 250 AA. DE Amino acid sequence of human kallikrein 9 (hK9) PN W02003033731-A2. PD 24-APR-2003. PA (MOUN) MOUNT SINAI HOSPITAL. Best Local Similarity: 46.67% Nismatches: Query Match: 27.52% Indels:	ID ADN05516 standard; protein; 250 AA. DE Antipsoriatic protein sequence #924. PN W0204028479-A2. PD 08-APR-2004. PA (GETH) GENENTECH INC. Best Local Similarity: 46.67% Mismatches Query Match: RESULT 787 ID AAB21300 standard; protein; 277 AA. DE Human KLK-L4 protein #2.	st ery SUL	P.D. 20-74R.2003. P.A. (HYSE) INC. Best Local Similarity: 46.77% Mismatches Query Match: 27.44% Indels: RESULT 789 ID ADL/1094 standard; protein; 277 AA. DE Human Kallikrein 13 protein SEQ ID NO:1.	at ery
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ហ	7.2	 9 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	100 13	79 14	.77 4	83 10	83 10		
28.97% Indels: 5 undard; protein; 248 AA. consensus protein sequence.	Mismatches: 87 Indels: 7 276 AA. (mBSSP6) SEO ID NO:4.	ised in NO:4.	Mismatches:	ADC31389 standard; protein; 298 AA. Human novel polypeptide sequence, SEQ ID NO:1471. 10-APR-2003. (HYSE-) HYSEQ INC. Local Similarity: 48.12% Mismatches: 79 Match: 28.80% Indels: 14	228 AA. Mismatches: '77 Indels: 4	247 AA. Mismatches: 83 Indels: 10	GMBH. & CO AG F. Mismatches: 83 Indels: 10	on or one	ches: 88

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	80 16	eqID576.	80 16	89 71		90 15		5 3		23		83		53		5.5
277 AA. ice #287.	Mismatches: Indels:	177 AA. :iated protein S	CO. Mismatches: Indels:	251 AA. , SEQ ID 212. Mismatches:	247 AA. .ide #303.	Mismatches: Indels:	293 AA. protease (KDP).	Mismatches: Indels:	293 AA.	EUTICS INC. Mismatches: Indels:	293 AA. ed by gene No. 27.	Mismatches: Indels:	293 AA. ed by gene No. 27.	Mismatches: Indels:	293 AA. 32.	Mismatches: Indels:
T 790 ADNO4184 standard; protein; 27 Antipsoriatic protein sequence	WOZU04028479-AZ. 08-APR-2004. GETH) GENENTECH INC. Local Similarity: 46.77% Match:	731 R14575 standard; proti man NF-kappaB pathway 2004065577-A2.	05-AUG-2004. (BRIM) BRISTOL-MYERS SQUIBB Local Similarity: 46.77% MATCh:	792 UJ6971 standard; protein; UJ6971 secreted protein; 200155441.A2AUG-2001. UMA-) HUMAN GENOME SCI INC call Similarity: 46.85\$	793 U23217 standard; protein; vel human enzyme polypept 200155301-A2	02-AUG-2001. (HUMA-) HUMAN GENOME SCI INC Local Similarity: 46.85% Match: 27.32%	rotein; erived	-APF ROC Cal atch	Y30524 standard; protein; man PDSP-1 protein. 9946391-A2.	16-SEP-1999. (MILL-) MILLENNIUM BIOTHERAPEUTICS Local Similarity: 45.34% 27.32%	AAY38412 standard; protein; 293 Human secreted protein encoded k WO9935158-Al.	15-JUL-1999 Local Similarity: 45.34 Match: 27.32*	AXY8426 standard; protein; 293 Human secreted protein encoded WO9935158-A1.	15-JUL-1999. (HUMA-) HUMAN GENOME SCI INC Local Similarity: 45.34% Match: 27.32%	AAY66726 standard; protein; 293 Membrane-bound protein PRO1132. WO9963088-A2.	(GETH) GENENTECH INC. Local Similarity: 45.34% March: 27.32% T 799
3ď.	PN WC PD 08 PA (G Best Lo Query M	ID AL DE HU	PD 05 PA (B Best Lo Query M	RESULT ID AA ID AA DE HU PN WC PD 02 PA (H	RESULT ID AA DE NO PN WO	PD 02 PA (F Best Lo	ID AR DE HU	m 13 m	ID AP	er st	DE HO	ery	DE DE PN	# 14 15	ID AA DE Mei	st I

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•	Mismatches: Indels:	•••	Mismatches: Indels:	uence SEQ ID	Mismatches: Indels:	•	Mismatches: Indels:	:	Mismatches: Indels:	protein	Mismatches: Indels:	in PRO1132.	Mismatches: Indels:	rane protein	Mismatches: Indels:	•	Mismatches: Indels:	·
tein; 293.AA	SPITAL. 34% 32%	tein; 293 AA ide sequence	8 8 2 8 8 8	protein; 293 AA 370) protein seq	32* 32*	protein; 293 AA	3328 328	tein; 293 AA #96.	348 328	protein; 293 AA.	328 328	protein; 293 AA. smembrane protein	.328	protein; 293 AA. ed and transmembrane	34% 32%	otein; 293 AA n #257.	SCI INC. .34% .32%	protein; 293 AA :ein #257.
AAB21296 standard; protein; Human KLK-L2 protein.	-AZ. NT SINAI HOSI arity: 45.34	T 800 AAU12399 standard; prot Human PRO1132 polypepti WO200140466-A2.	-2001.) GENENTECH INC. Similarity: 45.		INC. 45. 27.		INC. 45. 27.	standard; prol polypeptide : 163-A1.	45.	andard; pro secreted o 2-Al.	NC 45 27	C	45		-2003.) GENENTECH INC. Similarity: 45.	rd, pr protei	ENOME Y: 45	ndard; ed prot -A2.
AAB21296 st Human KLK-L	PN MOZOUSSY 78-A PD 14-SEP-2000. PA (MOUN) MOUNT Best Local Similar Querry Match:	AAU12399 Bt AAU12399 Bt Human PRO11 WO200140466	PD 07-30N-2001 PA (GETH) GEN Best Local Simil	LT 801 AAB65249 standard; Human PRO1132 (UNQ 70200073454-A1.	PA (GETH) GEN Best Local Simil Query Match:	AAU81966 standard; Human PRO1132. WO200109327-A2.	PD 08-FEB-2001 PA (GETH) GEN Best Local Simil Query Match:	3US8064 IMAN PRO 32003027	Local Simil Match:	ABUS9142 standard;) Novel human secrete US2002132252-A1.	PD 19-SEP-2002 PA (GETH) GEN Best Local Simil Query Match:	ABU82654 standard; Human secreted/tra: US2003032023-Al.	13-FEB-2003 Local Simil Match:	ABO17843 standard; Novel human secrete	13-FEB-2003 (GETH) GEN Local Simil Match:	28 B 5	Z7-DEC-2002. (HUMA-) HUMAN Local Similari Match:	ADA56974 Juman sec VO2002102
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2002. HUMP	ecret 02994 2002. HUMA	8 9 0 0 2 H	73 standar secreted/t 1-160384-Al. -2002.) GENENTEC Similarity	5 sta RO113 03125 2002. GENE	097 standar PRO polype 1004311-Al. 1-2003.) GENENTEC Similarity	40 standar human secr 1003531-A1. 1-2003.) GENENTEC	97 standard PRO polypep 1036180-A1. -2003.) GENENTECH Similarity:	3 sta ecret 02993 2002. HUMA HUMA imila 5 sta ecret 02993
PD 27-DEC-2002. PA (HUMA-) HUMAN GENOME BEST LOCAL Similarity: 49 Query Match: 27 RESULT 809	ID ADA57427 standard; protein; DE Human secreted protein #257 N W02002102994-A2. PD 27-DEC-2002. PA (HUMA-) HUMAN GENOME SCI IN(Best Local Similarity: 45.34% QUEZY MACCh: 27.32%	DE Human secreted DE Human secreted DE W02002102994-A2 PD 27-DEC-2002. PA (HUMA-) HUMAN G Best Local Similarity Query Match:	RESULT 811 D ABU60573 standard; protein; 2 DE Human secreted/transmembrane PN US2002160384-A1. PD 31-CTT-2002. PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Query Match:	Jur B125 standard; protein; ABU11955 standard; protein; Human PRO1132 polypeptide. US2002103125-A1. (GETH) GENENTECH LTD. CLOCAL Similarity: 45.34%	RESULT 813 ID ABU81097 standard; protein; DE Human PRO polypeptide #228. PN US2003004311-A1. PD 02-JAN-2003. PA (CETH) GENENTECH INC. PA (CETH) GENENTECH INC. Onerv Match:	RESULT 814 ID ABU72540 standard; protein; DE NOVEL human secreted and tr. PN US200303531-A1. PD 02-UAN-2003. PA (GETH) GENENTECH INC. PB SEST LOCAL Similarity: 45.34%		ADA41303 standard; pr Human secreted protei WC200210293-A2. 27-DEC-2002. (HUMA-) HUMAN GENOME LOCAL Similarity: 45 Watch: LT 817 ADA41305 standard; pr Human secreted protei WC2002102993-A2.
PD 27-DE PA (HUMA Best Local Query Matc RESULT 809	ID AD DE HU PN WO PD 27 PD 27 PA (H Best Lo Query M	i i	SULT AB AB Hu US 31 (G St Lo	KESULT 812 ID ABU13 DE Human DN US200 PN 01-AU PA (GETH PA (GETH PATCE)	AB AB Hu US US (G	No BB ULT IN B BB ULT IN B BB IN B B IN B I	RESULT 815 ID ABUGE DE Human PN US200 PD 20-FE PA (GETH Best Local Query Matc	
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LT 825
ABU92373 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003022187-A1.
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PN US2003027985-A1.
PD 06-FEB-2003.
Chest Local Similarity: 45.34$ Mismatches: 83
Chery Match: 27.32$ Indel8: 5
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Novel secreted and transmembrane protein PRO1132.
US2003017563-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted/transmembrane protein (PRO) #228. US2003036179-A1.
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Query Match: 27.32%

RESULT 81

ID ABU59289 standard; protein; 293 AA.

DE Human secreted/transmembrane protein, #130.

PN US2003027162-A1.

PD 06-FEB-2003.

PD 06-FEB-2003.

Best Local Similarity: 45.34%

Mismatches:
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Indels:
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Human sectreted/transmembrane protein, #130.
US2002142961-A1.
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DB Human secreted protein.
PN W02002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 45.34% Misn Query Match:
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ID ABO25986 standard; protein; 293 AA.
ID Human PRO1132 polypeptide.
PN U52002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34% Misr Query Match:
RESULT 823.
                                                                       ADA40825 standard; protein; 293 AA.
Human secreted protein.
WOZ00210293-AZ.
27-DEC-2002.
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                                                                     ID ADA40825 Brancarr,
DE Human secreted protein.
PN W0200210299-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 45.34%
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 45.34%
Query Match: 27.32%
RESULT 818
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DE Novel secreted and transmemb
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENEWIECH INC.
Best Local Similarity: 45.34%
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PN US2003036179-A1.
PD 20-FBB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34%
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PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34%
Query Match:
RESULT 825
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PD 30-JAN-2003.
BEST LOCAL Similarity: 45.34%
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RESULT 819
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RESULT 826
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RESULT 824
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	ID 456.	8 8 3	PRO1132.	5 33		5 33	PRO1132.	8 2 3	PRO1132.	8 2 3		2 3	PRO1132.	8 2 3		2 3		8 2 3	
	293 AA. e, PRO, protein SEQ	Mismatches: Indels:	.n; 293 AA. transmembrane protein	Mismatches: Indels:	293 AA.	Mismatches: Indels:	n; 293 AA. transmembrane protein	Mismatches: Indels:	AA. polypeptide	Mismatches: Indels:	293 AA.	Mismatches: Indels:	n; 293 AA. transmembrane protein	Mismatches: Indels:	293 AA.	Mismatches: Indels:	293 AA.	Mismatches: Indels:	293 AA.
	protein; smembrane	INC. 45.34% 27.32%	indard; protein; secreted and tra	45.34%	protein; de #96.	INC. 45.34% 27.32%	indard; protein; secreted and tra i-Al.	INC. 45.34% 27.32%	protein; 293 i transmembrane	INC. 45.34% 27.32%	ein; de.	45.34%	indard; protein; secreted and tra	INC. 45.34% 27.32%		45.34%		INC. 45.34% 27.32%	protein;
•	andard; ted/trar 5-A1.	03. ENENTECH ilarity:	RESULT 828 ID ABU92204 standard; DE Novel human secrete	USZUOSOL/*/O-AL. 23-JAN-2003. Local Similarity:	RESULI 829 ABU110910 standard; protein; 2 DE Human PRO polypeptide #96. PN US200123463-A1.	US-SEF-ZUUZ. (GETH) GENENTECH 1 Local Similarity:	JT 830 ABU81662 sta Novel human US2002177164	28-NOV-2002. (GETH) GENENTECH Local Similarity: // Match:	LI 831 ABU88601 standard; Human secreted and US2002197615-A1.	PD 26-DEC-2002. PA (GETH) GENENTECH I Best Local Similarity: Query Match:	LI 832 ABO34115 standard; prot Human PRO1132 polypepti US2003017981-Al.	23-JAN-2003 Local Similarity: y Match:	75 sta human 1022328	J3. ENENTECH Llarity:	TESUL 3A76406 standard; protein, DE Human PRO polypeptide #228. PN US2003073212-A1. PD 17-APR-2003. PA (GETH) GENEWECH INC.	ilarity:	KESULT 8155 ID ADA19056 standard; protein; DE Human PRO polypeptide #228. PN US2003054517-A1.		9 standard; piens. 49816-A1.
	ID PN	PD PA Best Query	RESUL ID DE	PD Best Query	ID DE CO	PA Best Query	RESUI 1D DE PN	PD PA Best Query	KESOT ID DE PN	PD PA Best Query	KESOL 1D DE PN	PD Best Query	NESOL DE DE	PD PA Best Query	DE D	Best	RESUI ID DE PN	PA Past Query	ID ID DE PN

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ADB19464 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003068796-A1.
                                                                                                                                                                                                                                                                                                                                                     ADA86484 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003082711-A1.
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Human secreted/transmembrane polypeptide PRO1132.
US2003054404-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA10293 standard; protein; 293 AA.
Human secreted/transmembrane protein, PRO1132.
US2003059831-A1.
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Indels:
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DB Human secreted/transmembrane protein PRO1132.
DB Human secreted/transmembrane protein PRO1132.
DD 9-JAN-2003.
DA (GETH) GENEWTBCH INC.
DB (GETH) GENEWTBCH INC.
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DE Human PRO polypeptide #228.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34% Mi
Query Match:
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DE Human PRO polypeptide #228.

PN US200307315-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 45.34% Mi
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DE Human PRO polypeptide #228.

PN US2003068795-A1.

PN UG-87-2003.

PA (GETH ) GENEWTECH INC.

Best Local Similarity: 45.34% M.
                                                                                                                                                                                                                        ADB28005 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003082704-A1.
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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34%
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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34*
27.32*
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34%
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PA (GETH) GENENTECH INC.
Best Local Similarity: 45.34%
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Best Local Similarity: 45.34%
Onerv Match: 27.32%
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RESULT 842
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RESULT 837
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RESULT 840
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RESULT 839
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RESULT 841
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RESULT 845
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RESULT 843
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	8 3 3	PRO1132.	8 8 8		83 5		83 5		5 33	PRO1132.	5 8 5 3		8 5		83 5	PRO1132.	83 5
3 AA.	Mismatches: Indels:	AA. embrane protein	Mismatches: Indels:	3 AA.	Mismatches: Indels:	3 AA.	Mismatches: Indels:	3 AA.	Mismatches: Indels:	n, 293 AA. transmembrane protein	Mismatches: Indels:	3 AA.	Mismatches: Indels:	3 AA. rotein PRO1132.	Mismatches: Indels:	in; 293 AA. transmembrane protein PRO1132	Mismatches: Indels:
protein; 293 ide #228.	INC. 45.34% 27.32%	protein; 293 ed and transme	INC. 45.34% 27.32%	protein; 293 peptide.	45.34%	protein; 293 ide #228.	INC. 45.34% 27.32%	protein; 293 ide #228.	INC. 45.34% 27.32%	protein; 29 ed and trans	INC. 45.34% 27.32%	protein; 293 ide #228.	INC. 45.34% 27.32%	protein; 293 nsmembrane pro	45.34%	ndard; protein; 293 secreted and transme:-Al.	INC. 45.34% 27.32%
RESULT 846 ID ADB30636 standard; protein; DE Human PRO polypeptide #228. PN US2003068794-A1.	PA (GETH) GENENTECH : Best Local Similarity: Query Match:	KEEULT 847 ID ADA8592 standard, protein; DE Novel human secreted and tr PN US2003082593-A1.	Ħ:	J. 0%0 ADA17837 standard; protein Human PRO1132 polypeptide US2003054987-Al. 20-MAR-2003.	Best Local Similarity: Query Match: RESULT 849	ID ADA97144 standard; protein; DE Human PRO polypeptide #228. PN US2003082705-Al. PD 01-MAY-2003.	PA (GETH) GENENTECH : Best Local Similarity: Query Match: PRSHIT RAG	ADA79448 standard, protein, Human PRO polypeptide #228. US2003082763-A1.	PD 01-MAY-2003. PA (GETH) GENENTECH 1 Best Local Similarity: Query est	AD 82587 standard, protein, Novel human secreted and tr. US2003087345-A1.	Ξ	ADB16789 standard, protein, Human PRO polypeptide #228. US2003087349-A1.	PD · 08-MAY-2003. PA (GETH) GENENTECH) Best Local Similarity: Query Match: RESULT, 853	ADA27945 standard; protein; 293 AA. Human secreted/transmembrane protein US2003054399-A1.	Best Local Similarity: Query Match:	8ta Iman 12694	ENTECH arity:

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ADB18905 standard; protein; 293 AA.

Novel human secreted and transmembrane protein PR01132.
US2003073211-A1.
17-APR-2003.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
27.32* Mismatches: 83
SULT 857
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Novel human secreted and transmembrane protein PR01132.

1 US2003082691-A1.

0 01-MAY-2003.

(GETH ) GENENTECH INC.

(GETH ) GENENTECH INC.

27.32$ Mismatches: 83

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SULT 859
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Novel human secreted and transmembrane protein PRO1132.
US2003044945-A1.
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Indels:
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Indels:
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Indels:
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Human secreted/transmembrane protein PRO1132.

US2003059832-A1.

27-MAR-2003.

St Local Similarity: 45.34$ Mismatches: lery Mach: 27.32$ Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 10-APR-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 45.34* Mism Ouery Match: 27.32* Inde RESULT 863

ID ADB24815 standard; protein; 293 AA.

DE Human PRO polypeptide SEQ ID NO 456.

PD 24-APR-2003.
                                                                                                                                                                                                                                                                                                          ID ADA94120 standard; protein; 293 AA.

DE Human PRO POLYpeptide #228.

DD 24-APR-2003.

PA (GETH ) GENENTECH INC.

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US2003082701-A1.
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Human PRO polypeptide #228.
US2003082710-A1.
01-MAY-2003.
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Human PRO polypeptide #228.
US2003068798-A1.
DE Human PRO polypeptide #228.
W US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.34%
Duery Match:
RESULT 856
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st Local Similarity: 45.34%
ery Match: 27.32%
SULT 860
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Best Local Similarity: 45.34\$ Mismatches: Query Match: 27.32\$ Indels: RESULT 87.551 standard, protein; 293 AA. DE Human PRO polypeptide #228.	PD 24-XPR-2003. PD 24-XPR-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 45.34\$ Mismatches: Query Match: RESULT 875 ID ADB2691 standard; protein; 293 AA. DE Human DRO nollymentide #228	# ÇE	Human PRO polypeptide #228. US2003096386-Al. 22-MAY-2003. (GETH) GENENTECH INC. st Local Similarity: 45.34* SULT MATCH: ADA22871 standard; protein; 293	ed/transmembrand -Al. rity: 45.34% 27.32% ndard; protein;	g g g	Human PRO polypeptide SEQ.ID NO US200307714-A1. 24-APR-2003. (GETH) GENENTECH INC. (GETH) GENENTECH INC. 27.324 STL Local Similarity: 45.344 STLT 880 ADA96592 standard; protein; 293 Human PRO polypeptide #228. US2003085690-A1.	# Ç.E	# # £ E	PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Mismatches: Query Match: 27.32% Indels:
	83.3	PRO1132. 83 5	PRO1132. 83 5	89	ņ	ა გა	83.3	8 S	_
Mismatches: Indels:	Mismatches: EIndels:	n; 293 AA. transmembrane protein PRC Mismatches: Indele:	ane protein ismatches: ndels:	Mismatches: 6	••		protein PRO1132. Mismatches: Indels:	Mismatches: Indels: AA.	
01-MAY-2003. (GETH) GENENTECH INC. st Local Similarity: 45.34% sry Match: 27.32%	1D ADA7310 Standard; process; DE Human PRO polypeptide #228. PN US2003073216-Al. PPD 17-APR-2003. PA (GETH) GENEWIECH INC. Best Local Similarity: 45.34% PRENIM A66.	human secreted and 308269-A1. Y-2003. GENENTECH INC. GENENTECH 1NC. Similarity: 45.34%	B standard; protein; uman secreted and tra 2003. GENEWTECH INC. imilarity: 27.32\$	RESULT 868 ID ADB30084 standard; protein; 2 DE Human PRO polypeptide #228. PN US2003073214-A1. PD 17-APR-2003. PA (GETH) GENEWTECH INC. PA (GETH) GENEWTECH INC. APR-CALL SIMILARILY: 45.34%	2 standard; protein; RO polypeptide #228. 82761-Al. GENENTECH INC.	V Match: 27.32% LT 8704 ADA75864 standard; protein; Human PRO polypeptide #228. US2003082703-Al. Ol-MAY-2003. Local Similarity: 45.34% V Match: 27.32%	750 standard; protein; secreted/transmembrane; 3059780-Al. R-2003. Similarity: 45.34% h: 27.32%	Human PRO polypeptide #228. US2003073210-A1. 17-APR-2003. GETH) GENENTECH INC. St Local Similarity: 45.34* SULT 873 ADB25375 standard; protein; Human PRO polypeptide SEQ ID	PN USZUGJO77715-A1. PD 24-APR-2003. PA (GETH) GENENTECH INC.

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293 AA.	Mismatches Indels:	n; 293 AA. transmembrane p	Mismatches Indels:	293 AA.	Mismatches Indels:	293 AA.	Mismatches Indels:	293 AA. ansmembrane p	Mismatches Indels:	293 AA. ansmembrane p	Mismatches Indels:	293 AA. ansmembrane p	Mismatche Indels:	293 AA.	Mismatches Indels:	293 AA.	Mismatches
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T 883 ADB26349 standard; protein; Human PRO polypeptide #228. US2063082760-A1.	GENENTECH imilarity:	T 884 ADB21834 standard; protein; Novel human secreted and tr US2003082765-A1.	GENENTECH imilarity:	JT 885 ADA77613 standard; protein; Human PRO polypeptide #228. US2003068797-Al.	H) GENENTECH 1 Similarity: ch:	ADB18353 standard; protein; Human PRO polypeptide #228. US2003077710-Al.	FK-2003. H) GENENTECH I Similarity: Ch:	1 887 ADA87036 standard; protein; Novel human secreted and tr	2003. GENENTECH imilarity:	9 standard uman secre	2003. GENENTECH imilarity:	7 sta	USZUUJOSHSIB-AI. 20-MAR-2003. (GETH) GENENTECH Local Similarity: Match:	ADD28557 standard; protein; Human PRO polypeptide #228. US2003082699-A1. 01-MAY-2003.	H) GENENTECH 1 Similarity: ch:	ADB29109 standard, protei ADB29109 standard, protei Human PRO polypeptide #22 US2003082706-A1. 01-MAY-2003.	H) GENENTECH Similarity:
Ĕ	PA (GETH) Best Local S: Query Match:	RESULT 884 ID ADB21 DE Novel PN US200	ř,	RESULT 885 ID ADA77 DE Human PN US2000	7 7 5	ID ADB18 DE Humar PN US200	PD 24-AFK- PA (GETH) Best Local S: Query Match:	ID ADA87 DE Novel	ary H	ID ADA88 DE Novel	# 7 H	ID ADA46 DE Novel	PN USZUUSUS PD 20-MAR-2 PA (GETH) Best Local Si Query Match:	ID ADB28 DE Human PN US200 PD 01-MP	# £	ID ADB29 DE Humar PN US200 PD 01-MA	= =

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D ADB22386 standard; protein; 293 AA.

E Novel human secreted and transmembrane protein PRO1132.

V US2003087344-A1.

SO B-MAY-2003.

SE Local Similarity: 45.34% Mismatches: 83

SULT 899
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Novel human secreted and transmembrane protein PRO1132.
US2003073213-A1.
17-APR-2003.
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US2003040473-A1.
27-FEB-2003.
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Human secreted/transmembrane PRO polypeptide #96.
US2003049638-A1.
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Indels:
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Indels:
ABO53201 standard; protein; 293 AA.
Human secreted/transmembrane protein PRO1132.
US2003044806-A1.
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Indels:
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Human secreted/transmembrane protein PRO1132.
US203017982-A1.
23-JAN-2003.
Ex Local Similarity: 45.34% Mismatches:
ery Match:
SULT 900
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US203059782-Al.
                                                                                                                                                                                                                           Indels:
                                                                                                                  ID ADA77061 standard; protein; 293 AA.

DE Human PRO polypeptide #228.

DE ORGAN-2003-09-A1.

PD 27-MAR-2003.

PA (GETH) GENENTECH INC.

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Human PRO polypeptide #228.
US2003082686-A1.
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sst Local Similarity: 45.34%
tery Match: 27.32%
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GETH ) GENENTECH INC.

St Local Similarity: 45.34%

ery Match: 27.32%
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est Local Similarity: 4
uery Match:
ESULT 901
D ADA39291 standard; p
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est Local Similarity:
uery Match:
ESULT 902
                                                                  st Local Similarity:
ery Match:
SULT 893
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ery Match:
SULT 895
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PN US20030 PD 01-MAY- PA (GETH)	Query Match: Query Match: RESULT 912 ID ADB9048 DE Human F	J.	Vecly macon: RESULT 913 ID ADB8049 DE Ovarian		Best Local S Query Match: RESULT 914 ID MB13958	PN US20030 PD 01-MAX	ery Sur		H LE H	DE HUMAN PN US20030 PD 01-MAY-	ary GL	DE NOVEL D PN US20030 PD 01-MAY- PA (GETH)	Query Match: RESULT 918		PA (GEIN) Best Local S Query Match: RESULT 919		PA (GETH) Best Local S Query Match: RESULT 920 ID ADB1402	DE Human F
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	5 3		2 83		5 33	PR01132	2 3		5 3	PR01132	5 33		83 5	PR01132	8 2 3	PRO1132	5 3	
233 AM.	Mismatches: Indels:	293 AA.	Mismatches: Indels:	293 AA. NO 456.	Mismatches: Indels:	rane protein	Mismatches: Indels:	293 AA.	Mismatches: Indels:	ADB38748 standard; protein; 293 AA. Novel hus secreted and transmembrane protein	Mismatches: Indels:	293 AA.	Mismatches: Indels:	protein	Mismatches: Indels:	rotein; 293 AA. and transmembrane protein	Mismatches: Indels:	293 AA.
	INC. 45.34% 27.32%		45.34% 27.32%	protein; ide SEQ ID	INC. 45.34% 27.32%	protein; 293 AA ed and transmemb	INC. 45.34% 27.32%		INC. 45.34% 27.32%	protein; ed and tra	INC. 45.34% 27.32%		45.34%	protein; ed and tra	INC. 45.34% 27.32%	protein; ed and tra	INC. 45.34% 27.32%	
Human PRO polypeptide #228. US2003068793-A1.	PA (GETH) GENENTECH I Best Local Similarity: Query Match: RESULT 903	standard; O polypept 7711-A1. 003.	Best Local Similarity: Query Match: RESULT 904	ADB23711 standard; protein; 293 Human PRO polypeptide SEQ ID NO US2003077712-Al.	PD 24-APR-2003. PA (GETH) GENENTECH I Best Local Similarity: Query Match:	ADA92433 standard; Novel human secrete	# :*	MDB15496 standard; protein; Human PRO polypeptide #228. US2003087352-A1.	PD 08-MAY-2003. PA (GETH) GENENTECH I Best Local Similarity: Query Match:	KESULI 907 ID ADB38748 standard; DE Novel human secrete DN 1103003003766.NI	003. SENENTECH	KESULI 908 ID ADB96317 standard; protein; DE Human PRO polypeptide #96. PV US2003069403-A1.	Best Local Similarity: Query Match:	KESOLI 309 ADS 1946 standard; protein; 293 AA. DE Novel human secreted and transmembrane PRN 192001987347-A1.	US-MAY-2003. (GETH) GENENTECH I Local Similarity: / Match:	RESOLI 310 DB ADB66668 standard; protein; DB Novel human secreted and tra PN US2003082689-A1.	PD 01-MAY-2003. PA (GETH) GENENTECH I Best Local Similarity: Query Match: RESHT, 911	ADB89748 standard; protein;

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581 standard; protein; 293 AA.
Muman secreted and transmembrane protein PRO1132.
3082764-Al.
Y-2003.
GENENTECH INC.
Similarity: 45.34% Mismatches: 83
Similarity: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 standard; protein; 293 AA.
human secreted and transmembrane protein FRO1132.
3082687-A1.
Y-2003.
) GENENTECH INC.
Similarity: 45.34* Mismatches: 83
h: 27.32* Indels: 5
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human secreted and transmembrane protein PRO1132.
1082696-A1.
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Indels:
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rian cancer-associated protein #27.
102.102235-A2.
DEC-2002.
BE-1 EOS BIOTECHNOLOGY INC.
11 Similarity: 45.34% Mismat
11 Similarity: 27.32% Indels
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IN PRO polypeptide #228.
103082697-A1.
1047-2003.
1047-2003.
1051 inilarity: 45.34*
1061 inilarity: 27.32*
1061 inida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB34021 standard; protein; 293 AA. Human PRO polypeptide SEQ ID NO 456. US2003077716-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 standard; protein; 293 AA. PRO polypeptide SEQ ID NO 456.077719-A1.
                                                                                              180 standard; protein; 293 AA.
PRO polypeptide #228.
1082762-A1.
03082698-A1.
AY-2003.
TH ) GENENTECH INC.
A1 Similarity: 45.34%
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TH GENENTECH INC.
Al Similarity: 45.34%
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H) GENENTECH INC.
Al Similarity: 45.34$
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AY-6003.

H) GENENTECH INC.

I Similarity: 45.34%
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H) GENENTECH INC.
A1 Similarity: 45.34%
27.32%
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Mismatches: Indels:	AA. 7 456. Mismatches: Indels:	AA.) 456. Mismatches: Indels:	n; 293 AA. transmembrane protein PRO1132 Mismatches: 83 Tndels: 5	₹	Mismatches: Indels:	Mismatches: Indels: 293 AA. protein PRO1132.	Mismatches: Indels:	Mismatches: Indels: 293 AA. protein PRO1132.	Mismatches: Indels: AA.	.34% Mismatches: 83 .32% Indels: 5
INC. 45.34% 27.32%	ide SEQ ID NO INC. 45.34%	ide SEQ ID NO: INC. 25.34%	protei ed and INC. 45.34%	protein; 293	45.34% 27.32% protein; 293		45.34% 27.32% : protein; 293	(4 0)	45.34% 27.32% ; protein; 293 ansmembrane pro	K-2003. Similarity: 45.34% h: 27.32% 497 standard, protein; 293 AA
PD 4-ARK-2003. PA (GETH) GENERALINC. Best Local Similarity: 45.34* QUETY March: 27.32*	KESULT 921 ID ADB35125 standard; DE Human PRO polypept: PN US2003077718-A1. PD 24-APR-2003. Best Local Similarity: Query Match:	9 standard, RO polypept 77720-Al. 2003. GENENTECH	4 standard uman secret 82692-A1. 2003. GENENTECH imilarity:	RESULT 924 ID ADCS7789 standard; protein; DE Human PRO polypeptide #96. PN US2003027754-A1.	Best Local Similarity: 45.34% Query Match: 27.32% RESULT 925 ID ADC55153 standard; protein; DE Human PRO polypeptide #96. PN US2003045463-A1.	Best Local Similarity: 45.34% Query Match: 27.32% RESULT 926 ADC12020 standard; protein; 3 DE Human secreted/transmembrane PN US203049681-A1.	Best Local Similarity: 45.34% Query Match: 27.32% RESULT 927 ID ADG56442 standard; protein; DE Human PRO polypeptide #96.000	Best Local Similarity: 45.34% Query Match: 27.32% RESULT 928 ED ADCOT497 standard; protein; 3 DE Human secreted/transmembrane PN US2003068647-A1.	3. larity: tandard eted/tr 03-A1.	PD 10-APK-2003. Best Local Similarity: Query Match: RESULT 930 TD ADC50497 standard;

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ID ADC53030 standard; protein; 293 AA.

DE Novel human secreted and transmembrane protein Seq ID456.

PN US2003087365-Al.

PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.

PA Mismatches: 83

Query Match: 5
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DE Novel human secreted and transmembrane protein Seq ID456.

PN US2003087366-A1.

PD 08-WAY-2003.

PA (GETH ) GENEWINCH INC.

Best Local Similarity: 45.34$ Mismatches: 83

Query Match: 5
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DE Novel human secreted and transmembrane protein Seq ID456.

BN US2003087363-A1.

PD 08-WAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 415.34 Mismatches: 83

Query Match: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC53636 standard, protein, 293 AA.
Novel human secreted and transmembrane protein Seq ID456.
US2003087364-A1.
                                                                                                                          DE ACC72044 standard; protein; 293 AA.

DE Novel human secreted and transmembrane protein PRO1132.

PN US2003092107-A1.

PD 15-MAY-2003.

PA (GETH) GENETHECH INC.

Best Local Similarity: 45.34% Mismatches: 83

Query Match: 27.32% Indels: 5
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DE Novel human secreted and transmembrane protein PRO1132.

PN US2003087367-A1.

PD 08-MAY-2003.

PA (GRTH) GENEWTECH'INC.

Best Local Similarity: 45.34% Mismatches: 83

Query Match: 27.32% Indels: 5
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DE Novel human secreted and transmembrane protein PR01132.

PN US2003087361-A1.

PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 45.34% Mismatches: 83
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DB Novel human secreted and transmembrane protein PRO1132.

PN US2003092105-A1.

PD 15-MAY-2003.

PA (GETH ) GENEWTECH INC.

Best Local Similarity: 45.34* Mismatches: 83

Query Match: 5
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RESULT 934
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RESULT 949 ID ADC48581 standard; protein; 2 DE Human PRO polypeptide #228. PN US203194773-A1.	PD 16-OCT-2003. PD (GETH) GENENTECH INC. Best Local Similarity: 45.34% Query Match: 27.32%	RESULT 950 RESULT 910 ID ADD10110 standard; protein; 2 DE Human PRO polypeptide #228. PN US200319476-A1.	PO 16-70L1-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Query Match: 27.32%	RESULT 95608 standard; protein; 2 DE Novel human secreted and tran	يُرْ تَد	RESULT 952 ID ADD04685 standard; protein; 2 DE Novel human secreted and tran	at ary	KESULI 953 ID ADC82499 standard; protein; 2 DE Human PRO polypeptide #96.	PN USZUGJOSPS483-41. PD 77-MAR-2003. Best Local Similarity: 45.34% Query Match:	RESULT 954 ID ADC80641 standard; protein; 2 B Novel human secreted and tran	אָר	Query Match: 27.32	PD 16-0CT-2003. PA (GETH) GRNENTECH INC. Best Local Similarity: 45.34* Query Match: 27.32*	RESULT 956 ID ADC48029 standard; protein; 2 DE Human PRO polypeptide #228. PN 1152003194771-31	the first	9 standard; uman secrete	US2003073090-A1. 17-APR-2003. st Local Similarity: 45.34; sry Match: 27.32	RESULT 958 ID ADC80089 standard; protein; 2 DE Novel human secreted and tran
5 5 3	Seq ID456.		Seq ID456.	83 5	Seg ID456.	83 5	PRO1132.	83 5	PRO1132.	83 5	PRO1132.		PRO1132.	5 5 33		83 5		5 83
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ID ADD76641 standard; protein; 293 AA.	Human PRO polypeptide #228. US2003100087-A1. 29-MAY-2003.		ID ADD88005 standard; protein; 293 AA. DE Human PRO polypeptide #228. PP US2003092113-A1. PD 15-MAY-2003.		409 standard; PRO polypept; 3203440-A1. T-2003.) GENENTECH]	ar Egy	Human PRO POLYPEPTIGE #228. US2003211571-A1. 13-NOV-2003. (GFTH) GENERVIECH INC.	st Local Similarity: 45.34% ery Match: 27.32% SULT 1027	ID ADE2343 standard; protein; 293 AA. DE Human PRO polypeptide #228. PN US2003092108-A1. PD 15-MAY-2003.	7 L E	Human PRO polypeptide #228. US2003092110-Al.	(GETH) GENERATECH INC. st Local Similarity: 45.34% sry Match: 27.32% SULT 1029	ide #228.	t Local Similarity: 45.34\$ sry Match: 27.32\$ SULT 1030	1D ADD8/453 Standard; procent; 293 AA. DE Human PRO polypeptide #228. PN US2003203439-A1. PD 30-OCT-2003. DA (GETT) GENERATE INC	# Ç.Ę	Human PRO polypeptide #228. US2003199062-Al. 23-CCT-2003. (ceru) CENDAMPOLU INC	Tocal Similarity: Bry Match: SULT 1032 ADE18458 standard
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Best Local Similarity: 45.34% Query Match: 27.32% RESULT 1060	10 A0G23799 standard; protein; 293 AA. DE Novel human secreted and transmembrane PN US2003207389-A1.	PA (GETH) GENENTECH INC. Best Local Similarity: 45.34* Query Match: 27.32* RESULT 1061 ID ADG04088 standard; protein; 293 DE Human PRO polypeptide #228.	PN US2003207423-A1. PN US-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 45.34* Query Match: RESULT 1062 ID ADG24989 standard: protein: 29	# KE	DE NOVOLZEB Brandard; procenn; 293 AA. DE NOVOLZEB Brandard; procenn; 293 AA. DN US2003207350-A1. PD 06-NOV-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 45.34% Mismatches: Query Match: 27.32% Indels:	RESULT 1064 ID 1064 ID Novel human secreted and transmembrane PN US2003207356-A1. PD 06-NOV-2003. PA (GETH) GENEWIECH INC. Best Local Similarity: 45.34\$	Query Match: RESULT 1065 ID ADG55333 standard; protein; 293 AA. DE Novel human secreted and transmembrane PN US2003194778-A1. PD 16-OCT-2003. PA (GETH) GENENTECH INC.	BEST LOCAL SIMILATICY: 45.34* Query Match: RESULT 1066 ID ADG60997 standard; protein; 293 AA. DE Novel human secreted and transmembrane PN US2003207390-A1. PD 06-NOV-2003. PA (GRTH) GRNEWPRCH INC.	Best Local Similarity: 45.34% Misma Query Match: 27.32% Indel RESULT 1067 A ADGE2101 standard; protein; 293 AA. DE Novel human secreted and transmembrane by 082003207428-A1.	st sury st
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Cherry Match: 27.32\$ Indels: 5 RESULT 1069 RESULT 1069 ROVEL human secreted and transmembrane protein PRO1132 PA (GETH) GENEWINECH INC. Best Local Similarity: 45.34\$ Mismatches: 83 Cherry Match: 27.32\$ Mismatches: 83 Cherry Match: 27.32\$ Mismatches: 83 Cherry Match: 45.34\$ Mismatches: 83 Cherry Match: 77.32\$ Milarity: 45.34\$ Mismatches: 83 Cherry Match: 45.34\$ Mismatches: 83 Cherry Match: 45.34\$ Mismatches: 83 Cherry Match: 67 Cherry Match: 45.34\$ Mismatches: 83 Cherry Matc
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standard; nan secret 250.5-A1. 003. Standard; nan secret 3364-A1. 003. STANDATECH nilarity: standard; nan secret 7365-A1. 003. STANDATECH nilarity: standard; nan secret 17369-A1. 003. STANDATECH nilarity: standard; nan secret 17363-A1. 003. STANDATECH nilarity: standard; nan secret 17363-A1. 003. STANDATECH nilarity: standard; nan secret 17363-A1. 003. STANDATECH nilarity: standard; nan secret 17363-A1. 003. STANDATECH nilarity: standard; nan secret 17415-A1. 003. STANDATECH nilarity: standard; nan secret 17415-A1. 003. STANDATECH nilarity: standard; nan secret 17415-A1. 003.

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6437 standard; protein; 293 AA.

1 human secreted and transmembrane protein PRO1132.
03207366-A1.
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H) GENETYECH INC.
H) GENETYECH INC.
Similarity: 45.34% Mismatches: 83
ch: 27.32% Indels: 5
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el human secreted and transmembrane protein PRO1132.
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1 human secreted and transmembrane protein PRO1132.
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L human secreted and transmembrane protein PRO1132.
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1 human secreted and transmembrane protein PRO1132.
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n secreted/transmembrane protein PRO1132.
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n secreted/transmembrane protein PRO1132.
03224358-A1.
                                                                                                     0712 standard; protein; 293 AA.
n PRO polypeptide #228.
03077723-A1.
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n PRO polypeptide #228.
03194793-A1.
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cal Similarity: 45.34%
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I) GENENTECH INC.
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Mismatches: Indels:	293 AA. protein PRO1132.	Mismatches: Indels:	293 AA.	Mismatches: Indels:	in; 293 AA. transmembrane protein	Mismatches: Indels:	rotein; 293 AA. and transmembrane protein	Mismatches: Indels:	293 AA.	Mismatches: Indels:	988 standard; protein; 293 AA. human secreted and transmembrane protein	Mismatches: Indels:	159 standard; protein; 293 AA. human secreted and transmembrane protein 2207382-A1.	Mismatches: Indels:	cotein; 293 AA. and transmembrane protein	Mismatches: Indels:	293 AA. nsmembrane protein
INC. 45.34% 27.32%	protein; nsmembrane	INC. 45.34% 27.32%		INC. 45.34% 27.32%	protein; ed and tra	INC. 45.34% 27.32%	protein; ed and tra	INC. 45.34% 27.32%		INC. 45.34% 27.32%	protein; ed and tra	INC. 45.34% 27.32%	protein; ed and tra	INC. 45.34% 27.32%	protein; ed and tra	INC. 45.34% 27.32%	protein; ed and tra
PN US2003207429-A1. PD 06-NOV-2003. PA (GETH) GENENTECH Best Local Similarity: Query Match: RESULT 1088	D ADH20088 standard; protein; 293 AA. DE Human secreted/transmembrane protein PRO113: PN US2003119856-A1. DD 37-NOW-2003	PA (GETH) GENENTECH Best Local Similarity: Query Match:	RESOLT 1089 ID ADH28636 standard; protein; DE Human PRO polypeptide #228. PN US2003022331-A1.	PD 30-0AN-Z003. PA (GETH) GENENTECH : Best Local Similarity: Query Match:	ABSOLI 1990 ID ADG54781 standard; prote: DE Novel human secreted and DN 1192001367-21	06-NOV-2003. (GETH) GENENTECH st Local Similarity:	resold 1091 ID ADG5981 standard; protein; DE Novel human secreted and tra PN US2003207369-Al	7,7,7	ID ADI81245 standard; protein; DE Human PRO polypeptide #228. PN US2003207361-A1.	# K.	ID ADG09988 standard; DE Novel human secrete PN ISS2004009548-Al	15-JAN-2004. (GETH) GENENTECH st Local Similarity: sry Match:	ADI15 Novel US200	PD 06-NOV-2003. PA (GETH) GENENTECH : Best Local Similarity: Query Match:	DE Novel human secreted and tr	# ::	RESULT 1791 1 standard; protein; 293 AA. DE Novel human secreted and transmembrane protein PRO1132 PN US2003207383-A1.

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06-NOV-2003. (GETH) GENENTECH Local Similarity: Y Match: LIT 198386 standard; AD118386 standard; NOVEL human secret.	06-NOV-2003. (GETH) GENE Local Simila Match: T 1098	AbJ63667 standard; Novel human secrete. US2004039164-A1. 26-FEB-2004. (GETH) GENENTECH I. Local Similarity: Y Match:	ADJ77562 standard; I Human PRO polypeptic US2004038336-A1. 26-FEB-2004. (GETH) GENENTECH II Local Similarity: 4 Y Match: LT 1100 ADJ65684 standard; I	Human PRO polypeptide US200403835-A1. 26-FEB-2004. (GETH) GENENTECH INC. Local Similarity: 45 LT 1101 ADMATSE20 standard; prol Human PRO polypeptide: US2004048333-A1.	(GETH) GENENTECH 1 Local Similarity: Match: LT 1102 ADK52481 standard; Human kallikrein 5 Human kallikrein 5 11-MAR-2004.	(MOUN) MOUNT SINAI (YOUS)/ YOUSEF G. Local Similarity: y Match: LT 1103 ADMA2544 standard; Human PRO POlypepti US2004058424-A1.	(GETH) GENENTECH I) Local Similarity: YM March: LT 1104 ADM28406 standard; Human PRO polypepti US2004077064-Al.	(GETH) GENENTECH INC. Local Similarity: 45.34% Antch: 27.32% T 1105 AD195888 standard; protein; Human PRO polypeptide #228. US2003077659-A1.
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(EOSB-) EOS BIOTECHNOLOGY INC.
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ADR72673 standard; protein; 293 AA..

Human ovarian cancer-related tumour marker kallikrein 5 (hK5) protein.

MW02004075713-A2.

10-SEP-2004.

(MOUN ) MOUNT SINAI HOSPITAL.

Local Similarity: 45.34*

Match:

Match:
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Best Local Similarity: 27.32*
Query Match: 27.32*
DESTITE 1107
ID ADR72621 standard; protein; 293 AA.
ID ADR72620 standard; protein; 293 AA.
ID ADR72620 standard; protein; 293 AA.
ID ADR72620 standard; protein; 293 AA.
ID ADR72621 standard; protein; 293 AA.
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Novel human secreted and transmembrane protein FRO1132.
US2003207354-A1.
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Amino acid sequence of novel human protease #28
WO200200860-A2.
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PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
Best Local Similarity: 45.91% Mismatches:
27.30% Indels:
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Ovarian cancer-associated protein #46.
WO2002102235-A2.
27-DEC-2002.
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Human BS247 specific epitope.
W09922077-A1.
06-MAY-1999.
(ABBO ) ABBOTT LAB.
st Local Similarity: 45.34* Miss
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Human ovarian cancer marker OV32.
WO200271928-A2.
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AAB21327 standard; protein; 276 AA.
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PA (MILL-) MILLENNIUM PHARM INC.
BEST LOCAL Similarity: 45.91%
Query Match: 27.30%
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Best Local Similarity: 45.34%
Query Match:
27.32%
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  24-APR-2003.
(GETH ) GENENTECH INC.
Local Similarity: 45.34%
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(GETH) GENENTECH INC.
Local Similarity: 45.
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Best Local Similarity:
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WO200053776-A2.
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RESULT 1108
ID ADRICATOR
DE Human Over
PN WO200407E
PD 10-SEP-20
PA (MOUN) N
Best Local Sin
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RESULT 1111
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Query Match:
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RESULT 1110
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PA
Best
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Ouery Match: 27.30% Indels: 18
RESULT 1120
ID ADR72886 standard; protein; 276 AA.
B Human ovarian cancer-related tumour marker kallikrein 10 (hK10) protein.
                                                                                                                                                                                      AUN39880 standard; protein; 276 AA.
Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C250.
WO2003042661-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADR72628 standard; protein; 276 AA.
Human renal cell carcinoma-related kallikrein 10 (hK10) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ89070 standard; protein; 276 AA.
Human urological disorder related protein 2045 SEQ:22.
WO2004065576-A2.
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                                                                    ADE40473 standard; protein; 276 AA.
Human kallikrein 10 (gene ID 2045) protein.
WO2003070883-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB21305 standard; protein; 237 AA.
Human KLK-L6 protein #1.
WO200053776-A2.
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RESULT 1122
ID AAB21299 standard; protein; 256 AA.
DB Human KLK-L4 protein #1.
PN WO200053776-A2.
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(MOUN ) MOUNT SINAI HOSPITAL.
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PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 45.91%
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PD 10-ESP-2004.
PA (MOUN ) MOUNT SINAI HOSPITAL.
Best Local Similarity: 45.91%
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D 14-SEP-2000.
PA (MOUN ) MOUNT SINAI HOSPITAL.
Best Local Similarity: 48.10%
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Best Local Similarity: 45.91%
Query Match: 27.30%
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PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 49.12%
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Best Local Similarity: 45.91%
Query Match: 27.30%
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OB-APR-2004.
(GETH) GENENTECH INC.
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Query Match: 27.30%
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PA (EOSB-) EOS BIOTECHNO BESET LOCAL Similarity: 41 Query Match: 2 RESULT 1115 ID ADE40473 standard; p) DF Human kallikrein 10 PN WO2003070883-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
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RESULT 1121
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RESULT 1116
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RESULT 1117
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RESULT 1118
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Mismatches: Indels:

Beet Local Similarity: 46.67% Mism Query Match: 27.15% Inde	RESULT 1133 ADNO4074 standard; protein; 244 AA. DE Antipsoriatic protein sequence #232. PN WO2004028479-A2.	US-AFK-ZUU4. (GETH) GENENTECH I St LOCAl Similarity: STY Match:	ID ADN29289 standard; protein; 244 AA. DE Human Kallikrein 6 associated protein. PD US2004097452-Al. PD 20-MAY-2004. PA (ISIS-) ISIS PHARM INC.	휴	ADQ890/0 Standard; process; 244 AA. DE Human urological disorder related prot PN W02004065576-A2. PD 05-AUG-2004. PA (MILL-) MILLENNIUM PHARM INC. Best Local Similarity: 46.67% Mism	27.15% SULT 1136 ADR72624 standard; protein; 244 AP Human ronal call carrinoma.related	MO2004077060-A2. 10-SEP-2004. (MOUN) MOUNT SIN	r rij		MOUNT SINAI HOSPITAL. nilarity: 46.67% 27.15%	1D ABG9525/ Etamdard; protein; 244 AA. DE Human ovarian cancer marker OV33. PN WC200271928-A2. PD 19-SEP-2002. PA (MILL-) MILLERNIUM PHARM INC.	nilarity: standard;	DE Human KLK-L3 protein #1. PN 40200053776-A2. PD 14-SEP-2000. PA (MOUN) MOUNT SINAL HOSPITAL. Best Local Similarity: 46.12% Mism	252 AA	PA (CURA-) CURAGEN CORP. Best Local Similarity: 44.66\$ Query Match: 26.89\$ RESULT 1141 ID ADN62898 standard; protein; 252 AA.	V18b. 8223-Al. 004. SMITHSON G.
80		77 8		83 10		83 10		83 10		83 10		83 10		83 10	83 10	de, SEQ ID NO:530.
ery b	To safe	PD US-AUG-2002. PA (HOFF) ROCHE DIAGNOSTICS GMBH. PA (HOFF) HOFFMANN LA ROCHE & CO AG F. Beet Local Similarity: 46.72% Mismatches: Query Match: 177.15% Indels:	RESULT 1125 ID AAB21310 standard; protein; 239 AA. DE Human zyme. PN WO20053776-A2. PD 14-SEP-2000.	PA (MOUN) MOUNT SINAI HOSPITAL. Best Local Similarity: 46.67% Mismatches: Query Match: 27.15% Indels:	RESULT 1126 DE 2Vme APP-cleaving protein; 244 AA. DE Zyme APP-cleaving protease. PN EP576152-A1. PA (EJLL) LILLY & CO ELI.	Similarity: 46.675: : 27.155 sc crandard: prote	0.00	PA (SUNK) SUNTOKY LTD. BEBT LOCAL Similarity: 46.67% Mismatches: Query Match: 27.15% Indels:	Į,	PD 19-MAR-1998. PA (DAND) DANA FARBER CANCER INST INC. BEST LOCAL Similarity: 46.67% Mismatches: Query Match: 27.15% Indels:	KESULI 1129 DE Aluman zyme. DE Human zyme. PN WO200053776-A2. PD 14-58P-2000.	(MOUN) MOUNT SINAI HOSPITAL. Local Similarity: 46.67% 'Match: 27.15%	n; 244 AA INC.	Best Local Similarity: 46.67% Mismatches: Ouery Match: 27.15% Indels: RESULT 113.1 Indels: ID ADB80567 standard; protein; 244 AA. DE Ovarian cancer-associated protein #66. PN W02002102235-A2.	PD 27-DEC-2002. PA (EOSB-) EOS BIOTECHNOLOGY INC. Best Local Similarity: 46.67% Mismatches: Query Match: 27.15% Indels: RESULT 113.2	ID ADN39212 standard; protein; 244 AA. DE Cancer/angiogenesis/fibrosis-related polypeptide, PN W02003042661-A2. PD 22-MAY-2003. PA (EOSB-) EOS BIOTECHNOLOGY INC.

83 10 83 10 SEQ: 28.	83 10 6 (hKG) protein.		83 10	83 10 79	00 88 88 88
46.67% Mismatches: 27.15% Indels: 1 protein; 244 AA. 6 associated protein. 46.67% Mismatches: 27.15% Indels: 1; protein; 244 AA. disorder related protein 2047	M PHARM INC. 46.67% Mismatches: 27.15% Indels: protein; 244 AA.	L. Mismatches: Indels: 244 AA.	HOSPITAL. Mismatches: 27.15% Indels: protein; 244 AA. marker OV33.	296 AA	Drotein; 252 AA. In SEQ ID NO:94. (P. Mismatches: 26.89% Indels: protein; 252 AA.
PD 08-APR-2004. PA (GETH) GENENTECH II BEST LOCAL SIMILARITY: QUERY MATCH: RESULT 1134 ID ADN29289 standard; ID Human kallikrein 6 PN US2004099452-A1. PD 20-MAY-2004. PA (ISIS-) ISIS PHARM BEST LOCAL SIMILARITY: QUERY MATCH: RESULT 1135 ID ADQ89076 standard; ID ADQ89076 standard; ID ADQ80076 576-A2.	PD 05-AUG-2004. PA (MILL-) MILLENNIUM Best Local Similarity: , Query March: RESULT 1136 ID ADR72624 standard; DE Himan renal call call	WO2004077066-A2. 10-SEP-2004. (MOUN) MOUNT SIN st Local Similarity: ST Match: SULT 1137 ADRY2876 standard Human ovarian car WO200407571-A2.	ary Sury	Milbennium imilarity: 7 standard; LK-L3 prote: 2000. MOUNT SINAI	QUELY MACCA: RESULT 1140 ID ADA05734 standard; protein; DE Human NOV18b protein SEQ ID PN WO2003029424-A2. PD IO-APR-2003. PA (CURA-) CURAGEN CORP. BEST Local Similarity: 44.66% QUETY MACCh: RESULT 1141 ID ADN62898 standard; protein; DE Human NOV18b. PN US200403823-A1. PD 26-FEB-2004. PA (SMIT/) SMITHSON G. PA (MILL/) MILLET I.

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RESULT 1152
ID ABRS8471 standard; protein; 253 AA.
DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
PN WO2003029468-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human heat mitochondrial protein as a therapeutic target SeqID639.
WO2003087768-A2.
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ADN39180 standard; protein; 253 AA.
Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:498.
WO2003042661-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  .T 1150
ABU07440 standard; protein; 253 AA.
Protein differentially regulated in prostate cancer #43
WO200281638-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU07471 standard; protein; 253 AA.
Protein differentially regulated in prostate cancer #74.
W0200281638-A2.
                               ABB84421 standard; peptide; 253 AA.
Human SCCE protein N-terminal fragment SEQ ID 48.
WO200262135-A2.
                                                                                                                                                                                                                                                                                                        RESULT 1149

ID AAU82740 standard; protein; 253 AA.

DE Amino acid sequence of novel human protease #39.

PN WO200200860-A2.
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Indels:
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RESULT 1153
RESULT 1153
DE Ovarian cancer associated protein #24.
                                                                                                                                                                             ABB84406 standard; protein; 253 AA.
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Best Local Similarity: 44.57%
Query Match: 26.86%
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Best Local Similarity: 44.57%
Query Match: 26.86%
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PA (EOSB-) EOS BIOTECHNOLOGY INC.
Best Local Similarity: 44.57%
26.86%
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PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Best Local Similarity: 44.57%
26.86%
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PA (CORI-) CORIXA CORP.
Best Local Similarity: 44.57%
26.86%
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Query Match: 26.86%
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 26.86%
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WO200262135-A2.
                                                                               15-AUG-2002.
(EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                      PA (SUGE-) SUGEN INC.
Best Local Similarity:
                                                                                                                                                                                                                                         (EGEL/) EGELRUD T. (HANS/) HANSSON L.
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RESULT 1154
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Human kallikrein 12, marker of endocrine cancer.
WO2004029285-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 1144
AARG788 standard, protein, 253 AA.
ANG7808 standard, protein, 253 AA.
WO9500651-A1.
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AAW05383 standard; protein; 253 AA.
Human amyloid precursor protein protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY08025 standard, protein; 253 AA. Mouse protease-related protein (PVP). DE19736198-C1.
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(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
Local Similarity: 42.52% Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB21302 standard; protein; 111 AA.
Human KLK-L5 protein #2.
MO200053776-A2.
14-SEP-2000.
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WOUN ) MOUNT SINAI HOSPITAL.
Local Similarity: 55.78%
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LOCAL Similarity: 55.78%
MATCh: 26.86%
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05-001-1995
(SYMB-) SYMBICOM AB.
Local Similarity: 44.57%
26.86%
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(ELIL) LILLY & CO ELI.
Local Similarity: 44.57%
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RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKERS R A.
ROTHENBERG M E.
                                                                                                          EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                    AGEE M L.
BERGHS C.
DIPIPPO V A.
EISEN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GANGOLLI E A.
                                                                              PATTURAJAN M.
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SPADERNA S K.
                                                                                                                                                                                          ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                          CATTERTON E.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity:
                                                                                                                                                                         GORMAN L.
                                                                                                                                                                                                                          ZHONG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9631122-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EISE/)
(GANG/)
(RIEG/)
(SPAD/)
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(BERG/)
                                                                                                            (ELLE/
(MALY/
                                                                                                                                                                                                                                                                          (MILL/
(RAST/
(STON/
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RESULT 1143
                                                                                                                                                                             GORM/
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                                                                                              SPYT/
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Best
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PA (PROD-) PRODIGENE INC. Best Local Similarity: 46.29* Mismatches: 77 Query Match: 26.72* Indels: 6	ur 1161 Boxine trypsinogen. Boxine trypsinogen. BES97681-A1. (ELIL) LILLY & CO ELI.	řŘŘ	DE RECOMDAINAIL EIYPBIN. PN WO20017332-A1. PD 30-MAR-2000. PA (ELIL) LILLY & CO ELI. Best Local Similarity: 46.29% Mismatches: 77 Query Match: 26.72% Indels: 6	RESULT 1163 ID AAB80953 standard; protein; 231 AA. DE Bovine met phe-trypsinogen. PN WO200119970-A2.	M 4) 10	ID ADA05732 standard; protein; 250 AA. DE Human NOV18a protein SEQ ID NO:92. PN WO2003029424-A2.	7,7,5	ID ABB84420 standard; peptide; 249 AA. DE Porcine SCCE protein N-terminal fragment SEQ ID 47. PN W0200262135-A2.	PD 15-AUG-2002. PA (GGEL/) EGELNUD T. PA (HANS/) HANSON L. Best Local Similarity: 45.35* Mismatches: 82 Query Match: 26.67* Indels: 26	RESULT 1166 ID AAB35701 standard; protein; 247 AA. DE Human trypsin hi amino acid sequence. PN 47200253887-A.	# K	ID AAU86677 standard; protein; 247 AA. DE Novel human connective tissue related polypeptide #243. PN W0200155343-AI.	ក់ក្ន	ID AAU23752 standard; protein; 247 AA. ID Novel human enzyme polypeptide #838. PN WO200153911-A2. PD 02-AHG-2001	الله به	ID AAU17043 standard; protein; 247 AA. ID Human novel secreted protein, SEQ ID 284. PN W0200155441-A2. PD 02-AUG-2001.
PA (EOSB-) EOS BIOTECHNOLOGY INC. Best Local Similarity: 44.57* Mismatches: 90 Query Match: 26.86* Indels: 16	Alloson to the protein, 253 AA. Human tumour-associated antigenic target (TAT) po w0200401625-A2. 26-FEB-2004. (GETH) GENENTECH INC.	Tr. Local Similarity: 44.5/* Pry Match: SULT 1157 ADNO4182 Standard; protein; 253	DE ANTIPOSTATIC Protein Bequence #286. PN W02004028479-A2. PD 08-APR-2004. PA (GETH) GENENTECH INC. Best Local Similarity: 44.57% Mismatches: 90 Query Match: 26.68% Indels: 16	RESULT 1158 ID ADR72880 standard; protein; 253 AA. DE Human ovarian cancer-related tumour marker kallikrein 7 (hK7) protein. PN 402004075713-A2.	ert SUL	ID ADN62896 standard; protein; 250 AA. DE Human NOV18a. PN US2004038223-A1.		(JUDJ/) (LILL/) (GUOX/)	(PATT/) (SPYT/) (EDIN/) (ELLE/) (MALY/)	(GORM/) (GORM/) (ZERH/) (ANDE/)	PA (CATT/) CATTERTON E. PA (JNWW/) JI W. PA (MILL/) MILLER C E. PA (PARTERTON E.	(STON) STONE D C (PENA/) PENA C E (SHENA/) SHENOY S	(ROTH/) SOTHERERG (LEAC/) LEACH M D. (AGEE/) AGEE M L.	FA (BENG) BENGIN C. PA (DIPI/) DIPIPPO V A. PA (EISE/) EISEN A. PA (GANG) ANOGULI E A. PA (RIEG) RIFERE D K	(SPAD/) SPADERNA st Local Similarity: ery Match:	NESULI 1164 standard; protein; 229 AA. DE Bovine trypsinogen. PN W0200005384-A1. PD 03-FEB-2000.

PD 04-NOV-2003. PA (UYAR-) UNIV BEST LOCAL SIMILA	Query March: RESULT 1179 ID AD137158 sta DE Human protea PN US2003199010 PD 23-OCT-2003.	PA (UYAK-) UNIV Best Local Simila Query Match: RESULT 1180	ID AAY78974 sta DE Canine catio PN WO200009739-	PD 24-FEB-2000. PA (FUJY) FUJI BEST LOCAL Simila	RESULT 1181 ID ADA05742 sta DE Human NOV18f	PN 10-APR-2003: PA (CURA-) CURA- Best Local Simila	Query Match: RESULT 1182 ID ADN62906 sta DB Human NOV18£	PN US2004038223 PD 26-FEB-2004. PA (SMIT/) SMIT PA (MILL/) MILL	-	(LILL/) (GUOX/) (PATT/)	(SPYT/) (EDIN/) (ELLE/)	(MALY/) (ORTT/) (GORM/) (ZERH/)	PA (ANDE) ANDE PA (ZHON/) ZHON PA (CATT/) CATT PA (JIWW/) JI W PA (MILL/) MILL PA (RAST/) RAST		(SHIM/) (ROTH/) (LEAC/) (AGEE/)	PA (DIPI/) DIPI PA (BISE/) BISE PA (GANG/) GANG PA (RIEG/) RIEG PA (CRANC) GANG	t Local Siery Match:	ID AAB98502 sta DE Human Stratu PN WO200129056-
92 15		92 15		77 6		77 6	structure analysis method.	7			7.7		77 6		77		77 6	
Mismatches: Indels:	AA. #243.	Mismatches: 9 Indels: 1 223 AA		KENKYUSHO KK. Mismatches: 7 Indels: 6	223 AA.		protein; 223 AA. used in three-dimensional struc	Mismatches:	Indels:	E E	Mismatches: 7		Mismatches: 7 Indels: 6	224 AA.	Mismatches: 7 Indels: 6	233 AA.	Mismatches: Indels:	244 AA. :ein.
PA (HUMA-) HUMAN GENOME SCI INC. Best Local Similarity: 46.06% Ducry March: 26.50%	1 standard; ive tissue 6 54375-A1. 2003. HUMAN GENO	46.06% 26.50%		(IYAK-) IYAKU BUNSHI SEKKEI it Local Similarity: 46.05% iry Match: 26.48%	andard, protein; 1. 1.	PD 02-DEC-1999. PA (MEDI-) INST MEDICINAL MOLECULAR DESIGN INC Best Local Similarity: 46.05% Mismarche Query Match: 26.48% Indels:	l standard; protein #3 7954-Al.	PD 25-JUL-2002. PA (MITU) MITSUBISHI CHEM CORP PA (UMEY) UNEXPARA H. Best Local Similarity: 46.05\$	ory Match: 26.48% ULT 1174 abc73287 grandard: protein:	ein - SEQ	AJINOMOTO C UMEYAMA H. imilarity:	zry Match: 26.48% SULT 1175 ADD35545 standard; protein; Cationic bovine trypsinogen	PN WO2003040033-A2. PD 15-MAY-2003. PA (FARB) BAYER AG. Best Local Similarity: 46.05% DOURTY MATCH: 26.48%	7 standard; protein; trypsin.	1 tr	s standard; protein; ogen analogue. 7332-A1.	ily it	4 standard; protein; rotease M (proM) prot 13-B1.

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AAB98502 standard; protein; 225 AA.
Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.
WO200129056-A1.
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16
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16
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12
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onic trypsinogen amino acid sequence.
-A1.
v ARKANSAS MEDICAL SCI.
arity: 45.83% Mismatches:
26.43% Indels:
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Indels:
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if protein SEQ ID NO:102.
4-A2.
                                                                                                                                andard; protein; 244 AA. ase m (Protm).
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arity: 45.56%
26.43%
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IV ARKANSAS.
larity: 45.83%
26.43%
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RAGEN CORP.
.larity: 45.45%
.26.43%
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SEMUAN L.

SERHANN B D.

UDERSON D W.

WITERTON E.

LILLER C E.

KATELLI L.

SATELLI L.

SNACH D J.

SNA C B A.

SIENOY S G.

SIENOY S G.

SIENOY S G.

STHWEISER M.

THENBERG M. E.

SEGH M. D.

SEGH M. D.

SEGH M. D.

SEGH M. D.

SEGH M. C.

SEGH M. C
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O X.
TTURAJAN M.
YTEK K A.
INGER S R.
LERMAN K.
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LLET I.
YMAN J A.
KUDA R.
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Query Match: RESULT 1185

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ABB04644 standard; protein; 240 AA.
Engraulis japonicus trypsinogen (aTry I) SEQ ID NO:1.
JP2001269173-A.
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine SCCE protein N-terminal fragment SEQ ID 46.
WO200262135-A2.
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WO200262135-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match: 25.15% In
RESULT 1198
LD ADLIS205 standard; protein; 232 AA.
DE Pancreatic Kallikrein #1.
PN CN1384199-A.
                                                                                                                                                                                    T1191
ABB78122 standard; peptide; 223 AA.
Amino acid sequence of trypsin.
US2002072863-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW64261 standard; protein; 232 AA. Kallikrein substrate binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB84423 standard; peptide; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR96164 standard; protein; 261 AA.
Human NOV13a protein SEQ ID NO:70.
WO200290568-A2.
                                                                                                                                                                                                                                                                                                                                   ABB83322 standard; protein; 223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DE KALLLANDEN.
PN WO9824866-A1.
PD 11-UNV-1998.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
Best Local Similarity: 43.64%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 15-AUG-2002.
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON I.
Best Local Similarity: 43.70%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PN OF COCT - 2001.
PD 02-OCT - 2001.
PA (NISB ) JAPAN TOBACCO INC.
Best Local Similarity: 45.71%
                                                                                                                                                                                                                                                  PD 13-JUN-2002.

PA (FUIT) FUJITSU LTD.

Best Local Similarity: 45.61%
26.04%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PN W0200290568-A4.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
BEST Local Similarity: 40.00%
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PA (FULT ) FUJINGU LTD.

Best Local Similarity: 45.61%
26.04%
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                                                                                                                                                      44.35%
                                                                                                                                                                                                                                                                                                                                                   Partial trypsin sequence.
US2002035434-A1.
21-MAR-2002.
        COLMAN S D.
WOLENC A R.
PENA C E A.
FURTAK K.
GROSSE W M.
                                                       (FURI/) FURTAK K.
(GROS/) GROSSE W M.
(GLSO/) ALSOBROOK J P
(LEPL/) LEPLEY D M.
(RLEG/) LEPLEY D M.
(RLEG/) BURGESS C E.
(BURG/) BURGESS C E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-2002.
(EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
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RESULT 1193
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RESULT 1194
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RESULT 1197
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RESULT 1195
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RESULT 1192
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RESULT
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RESULT
                                                                                                                                                      Best
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Human NOVX protein to treat human pathological conditions SeqID222.
WO200268649-A2.
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14
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                                           818
                                                                                                                                                                                                                                                                                                                                                                  Human amyloid beta-protein precursor inhibitor. WO9824886-A1.
                                                                                     AAY78975 standard; protein; 246 AA.
Canine anionic trypsinogen amino acid sequence.
24-FEB-2000.
                                         Mismatches:
Indels:
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Indels:
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Indels:
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Stereostructure-related 2PTC_E protein.
WOO003060065-A1.
24-UUL-2003.
(AJIN ) AJINOMOTO CO INC.
(UMEY/) UMEYAMA H.
Et Local Similarity: 26.19% Mismatch ery Match:
                                                                                                                                                                                                                  AAB21326 standard; protein; 257 AA. Human HSCEB.
WQ200053776-A2.
14-SEP-2000.
(WOUN ) WOUNT SINAI HOSPITAL.
St Local Similarity: 44.11$ Mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC73301 standard, protein; 279 AA.
Stereostructure-related 2PTC protein.
WA22003060765-A1.
                                                                                                                                                                                                                                                                                                                                              AAW64260 standard; protein; 246 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 1190
ADN42340 standard; protein; 259 AA.
Human novel proteinNOV 62.
US2004033493-A1.
                                                                                                                                                                                                                                                                                                                                                                                          MOJENS HOSPITAL.
(BGHM ) BRIGHAM & WOMENS HOSPITAL.
Local Similarity: 44.53%
26.28%
                                                                                                                                              PD (FUJY) FUJI YAKUHIN KOGYO KK. Best Local Similarity: 44.22%
Ouery Match: 26.38%
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(CURA-) CURAGEN CORP.
Local Similarity: 44.35%
PD 26-APR-2001.
PA (UYAR-) UNIV ARKANSAS.
Best Local Similarity: 46.52%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-UUL-zvus.
(AJIN ) AJINOMOTO CO INC.
(UMEY) UMEYAMA H.
Local Similarity: 46.85%
March: 26.19%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-2004.
(TCHE/) TCHERNEV V T.
(SPYT/) SPYTEK K A.
(ZERH/) ZERHUSEN B D.
(PATT/) PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GANGOLLI E A.
PADIGARU M.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPYTEK K A. ZERHUSEN B D. PATTURAJAN M. SHIMKETS R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MILLER C E.
GERLACH V.
TAUPIER R J.
GUSEV V Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RASTELLI L.
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Best Local Sir Query Match: RESULT 1189

Query M RESULT

(TAUP/) (GUSE/)

(LILL/ (GANG/ (PADI/ ANDE/ (RAST/ (MILL/

Query Match: RESULT 1188

Best

73 14		95 20		77 36		114· 34	ID NO:2.	92		91 10		91 10	91 10		GEN. 91 10	orotein.
SHENZHEN CITY. 14% Mismatches: 2% Indels:	AA.	Mismatches: Indels:	AA. protein.	Mismatches: Indels:	ide; 464 AA. trypsinogen-3aa-sp55.	C. Mismatches: Indels:	AA. (aTry II) SEQ	Mismatches: Indels:	AA. #5.	Mismatches: Indels:	, AA. #265.	Mismatches: Indels:	AA. .0. INC. Mismatches: Indels:	AA. 1 II precursor.	r. NAT HUMAN Mismatches: Indels:	, 530 standard; protein; 261 AA. DITHP protein modification/maintenance protein
	protein; 268	M INC. 42.42% 25.10%	rotein; 247 e TLSP-like	42.51 % 24.98 %	pept	THERAPEUTICS INC B. 38.56% 24.54%	rotein, 241 trypsinogen	CCO INC. 45.87% 24.39%	; protein; 247 tumour protein	24.25%	tein; 247 sequence	INC. 43.27% 24.25%	orotein; 247 sequence #41 HERAPEUTICS 13.27 4.25	ein; 247 - trypsin	THE & CO LTD CHII 27% 25%	protein; 261 n modification
-DEC-2002. EMI-) REMIN HOSPITAL cal Similarity: 44. atch: 25.1	il 1199 AAW94493 standard; Human kallikrein. WO9842849-A1.	01-OCT-1998. (INCY-) INCYTE PHARM Local Similarity: 4: Match: 2:	Serine Protes 55702-A2. -2002.		7 standard; cid sequenc 19878-A2. 2004.	COMPOUND AFEYAN N imilarity:	Lr 1202 ABB04645 standard; p: Engraulis japonicus † JP2001269173-A.	2001. JAPAN TOBA imilarity:	3 standard ancreatic 2331-A2.	14-FEB-2002. (CORI-) CORIXA CORP Local Similarity: Match:	ADNO4140 standard; pro Antipsoriatic protein WO2004028479-A2.	2004. GENENTECH imilarity:	ADM99594 standard; I Novel human protein Novel human protein Novel human protein 06-MAX-2004. (FIVE-) FIVE PRIME ? (COSAL SIMILARITY: *	T 1206 ADQ30589 standard; prot Pancreas cancer marker WO2004055519-A2.	UL-2004. F) HOFFMANN LA O-) SINOGENOMAX 1 Similarity:	T 120, ABR41530 standard; Human DITHP protei
PD 11-DEC-2 PA (REMI-) Best Local Si Query Match:	200	PD 01-0CT-: PA (INCY-) Best Local S: Query Match:	TESOLI 1200 ID ABG7027 DE Human S PN WO20025 PD 18-JUL-	ery	DE AMINO ACION WOOD ACION NO A	PA (COMP-) PA (AFEY/) Best Local S Query Match:	KESULT 120 ID ABBO. DE Engra	# # # # # # # # # # # # # # # # # # #	ID AAU87693 DE Human pai	PD 14-FEB- PA (CORI-) Best Local S Query Match:	į.	PD 08-APR- PA (GETH) Best Local S Query Match:	RESULT 1205 ID ADN99594 DE NOVEL hur PN WO2004030 PD 06-MAY-20 PA (FIVE-) Best Local Sir		PD 01-JUL- PA (HOFF) PA (SINO-) Best Local S Querry Match:	KESULI 120 ID ABR419 DE Human

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112
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Human prostate-specific amino acid seguence P703P.
WO200151633-A2.
                                                                            Duery Match:

RESULT 1208

ID ADL27346 standard; peptide; 461 AA.

ID ADL27346 standard; peptide; 461 AA.

DE Amino acid sequence of trypsinogen-0aa-sp55.

PN W02004019878-A2.

PD II-MAR-2004.

PA (COMP-) COMPOUND THERAPEUTICS INC.

PA (APEY/) AFEYAN N B.

Best Local Similarity: 38.24* Mismatches:
                                                                    Mismatches:
Indels:
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Indels:
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PN 19-JUL-2001.
PD 19-JUL-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.10% Mismatches Query Match: 24.10% Indels: RESULT 1213
ID A4069819 standard; protein; 254 AA.
DE Human prostate cDNA encoded protein #27.
PD WQ-OCI73032-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.10% Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1214
ID AAG99059 standard; protein; 254 AA.
ID AAG99059 standard; protein; 254 AA.
DE Human prostate-specific amino acid of P703P.
DN W0200134802-A2.
PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.10% Mismatcher Anerv Match:
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Prostate cancer specific antigen P703P #7.
US2002192763-A1.
                                                                                                                                                                                                                                                                     UNELY CHACLE.

VUELY CHACLE.

ID ALB03862 standard; protein; 223 AA.

ID Human neurosin amino acid sequence.

PN W020031284-AA.

PD 02-JUN-2000.

PA (FUSO) FUSO PHARM IND LTD.

Best Local Similarity: 43.46$

Missimatch:

24.20$ Ind
                                                                                                                                                                                                                                                                                                                                                                                                                                            MESOLI 1211
DB Amino acid sequence of trypsinogen.
DB Amino acid sequence of trypsinogen.
DB Amino acid sequence of trypsinogen.
DB MARZ-2004
DB ACOMP-) COMPOUND THERAPEUTICS INC.
DA (AFEY/) AFEYAN N B.
Best Local Similarity: 41.03$ Mism Query March:
RESULT 1211
D AAB21294 standard; protein; 254 AA.
DB Human KLK-LI protein #2.
DB Human KLK-LI protein #2.
DD 14-SEP-2000.
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Best Local Similarity: 43.10%
Query Match: 24.10%
PD 05-DEC-2002.
PD 05-DEC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 43.27*
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(XUJJ/) XU J.
(DILL/) DILLOU D C.
(MITC/) MITCHAM J L.
(HARL/) HARLOCKER S L.
(JIAN/) JIANG Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
RESULT 1214
ID AAG99059
DE Human pro
PN WO201348
PD 17-MAY-27
PA (CORI-)
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RESULT 1210
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RESULT 1212
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RESULT 1215
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ABB95279 standard; protein; 254 AA.
Human P703P putative full length protein SEQ ID NO 525.
US2002022248-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABRS4391 standard; protein; 254 AA.
Prostate tumour specific protein sequence SEQ ID 525.
WO200289747-A2.
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Indels:
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PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.

Best Local Similarity: 43.10% Mismatches:

Onerv Match: Indels:
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Indels:
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Human prostate specific protein P703P.
US2003185830-A1.
(CCT-2003.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 1217
ABPS4560 standard; protein; 254 AA.
Human KLK4 protein SEQ ID NO:13.
WO200277243.A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 03-UCT-2002.

A (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
Best Local Similarity: 43.10%
Merv Match: 24.10% I
                                                                                                                                    PA (HURA/) HUKALL V.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (BASS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
Best Local Similarity: 43.10%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID ABR54391 standard; protein;
DE Prostate tumour specific proposes w02029747-A2.
PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.10%
RESULT 1220
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PA (WANG/) WANG A.

PA (SKEI/) SKEIKY Y A W.

PA (HEDL/) HEPLER W T.

PA (HEDL/) HENDERSON R A.

Best Local Similarity: 43.10%

RESULT 1217
                                                                                                                                                                                                                                                                                    DILLON D C.
MITCHAM J L.
HARLOCKER S L.
                                                                           LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                                                                         HENDERSON R A. HURAL J.
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RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
                                STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
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KALOS M D.
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                                                                                                                                                                                                                                                                                                           (HARL/)
(JIAN/)
(KALO/)
                                                                                                             (HEPL/)
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RESULT 1219
                                                                            (LISX/)
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RESULT 1218
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                                                      VEDV/
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AAB74830 standard; protein; 1079 AA.
Prostate tumour antigen amino acid sequence for a fusion protein.
WO200125272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI17268 standard; protein; 230 AA.
Polypeptide homologous to a human NOVX domain SeqID 804.
WO20026849-A2.
06-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADII7276 standard; protein; 230 AA.
Polypeptide homologous to a human NOVX domain SeqID 812
WO200268649-A2.
 87
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Trypsin-like serine protease protein - SEQ ID 66.
US2003170630-A1.
Mismatches:
Indels:
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Indels:
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Indels:
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Prostate specific antigen fusion protein #2.
US2002192763-A1.
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                                           ADG26391 standard; protein; 254 AA.
Human prostate-specific polypeptide #60.
US2003157089-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HEDL)/ HEPLER W T.

(HEND/) HENDERSON R A.

(HURA/) HURAL J.

(MCNE/) MCNEILL P D.

(HOUG/) HOUGHTON R L.

(BOAZ/) Y DE BASSOLS C V.

(FOYT/) FOY T M.

St Local Similarity: 43.10$
                                                                                PD 21-AGG-2003.
PD 21-AGG-2003.
PA (CORT-) CORIXA CORP.
Best Local Similarity: 43.10%
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PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.10%
24.10%
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PA (CURA-) CURAGEN CORP.
Best Local Similarity: 47.44%
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PA (CURA.) CURAGEN CORP.
Best Local Similarity: 47.44%
Best Local Similarity: 43.10%
Query Match: 24.10%
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TCHERNEV V T.
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                                                                                                                                                                                                                                                                                                                                                                                         MITCHAM J L.
HARLOCKER S L.
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DILLON D C.
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DAY C H.
VEDVICK T S.
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RETTER M W.
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                                                                                                                                      Query Match:
RESULT 1222
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(MITC/)
(HARL/)
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FANG/)
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RESULT 1225
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RESULT 1224
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RESULT
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RESULT 1233

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AAU74932 standard; protein; 254 AA.
Amino acid sequence of prostase protein fragment #3.
WO200200867-A1.
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Local Similarity: 43.10% Mismatches:
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PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

Best Local Similarity: 43.10% Mismatches:

Query March: 140.06% Indels:
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Indels:
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Indels:
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WO2004019878-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU74901 standard; protein; 254 AA.
Protein sequence of prostase homologue #3.
WO200200708-A2.
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PD 18-3ANX -2001.
PA (SMIX ) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.10% Misma
                                                                                                                                                                                                                                                                                                                    ADL27348 standard; peptide; 485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY72525 standard; protein; 254 AA.
Human prostase antigen #3.
WO200104143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB21320 standard; protein; 254 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB21307 standard; protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                          11-MAR-2004.
(COMP-) COMPOUND THERAPEUTICS INC.
(AFBY) APEXAN N B.
Local Similarity: 42.74%
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14-SEP-2000.
(MOUN ) WOUNT SINAI HOSPITAL.
Local Similarity: 43.10%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOUN ) MOUNT SINAI HOSPITAL. Local Similarity: 43.10%
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24.06%
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                                                                                                                             GORMAN L.
GANGOLLI E A.
FERNANDES E R.
                                                 GROSSE W M.
SZEKERES E S.
VERNET C A M.
                                        HIMKETS R A.
PATTURAJAN M.
                                                                                                     CASMAN S J.
BOLDOG F L.
                                                                                                                                                                       RIEGER D K.
             LEPLEY D M.
                                                                                                                                                                                                                                                                             Similarity:
                          BURGESS C
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostase.
WO200053776-A2.
14-SEP-2000.
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WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
RESULT 1229
ID AAB21320
DE Human pro
PN WO-200053:
PD 14-SEP-20
PA (MOUN)
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Query Match:
RESULT 1230
DE Human pro
PN WO20104:
PD 18-JAN-20
PD 18-JAN-2
PD 18-JAN-2
PA (SMIX ) 9
PA (CORI-) (
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RESULT 1232
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RESULT 1231
                                                                                                                                                                                                            (MILL/)
(SCIO/)
(ELLE/)
(MACD/)
(SMIT/)
                                                                                                                                             (GANG/)
(FERN/)
(RIEG/)
(EDIN/)
                                                                                           (LILL/)
(CASM/)
(BOLD/)
(GORM/)
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RESULT 1227
                                      (SHIM/
(GROS/
(SZEK/
(VERN/
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RESULT
ID AA
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PN
PD
PA
PA
Best
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110
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13
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ABU71889 standard; protein; 585 AA.
Prostate cancer specific antigen fusion protein #3.
1D AAW60592 standard; protein; 248 AA.
DE Human prostate-specific kallikrein (HPSK) protein.
PN WO9820117-A1.
PD 14-MAY-1998.
PA (INCY-) INCYTE PHARM INC.
Best Local Similarity: 43.44% Mismatches: 8
Query Match: 24.03% Indels: 1
                                                                                                                                                                                                                                                                                                                                                                                                /T 1236
AAU74931 standard; protein; 248 AA.
AAU70 acid sequence of prostase protein fragment
WO200200867-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 03-27AV-2002.
PD 03-17AV-2002.
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 43.44% Mismacches: 24.03% Indels:
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Indels:
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Prostate tumour-related protein SEQ ID 1020.
WO200289747-A2.
                                                                                                                                                                                                                                                                             AAU74770 standard; protein; 248 AA.
Protein sequence of prostase homologue #2.
92-030-030-038-A2.
03-03NN-2002.
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                                                                                                                                                                          PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
PA (CORI-) A3.44$ Misma
Best Local Similarity: 43.44$ Indel
                                                                                                                                                                                                                                                                                                                                            PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 43.44* Misma
Query Match: 24.03* Indel
                                                                                                                               AAY72524 standard; protein; 248 AA.
Human prostase antigen #2.
WO200104143-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB14470 standard; protein; 585 FOPP/hPAP fusion protein, FOPP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PD 14-NUV-2004.

PA (CORI-) CORIXA CORP.

Best Local Similarity: 40.14%

24.03%
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1: 24.03%
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Y DE BASSOLS C V.
FOY T M.
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HEPLER W T.
HENDERSON R A.
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HARLOCKER S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FANGER G R.
RETTER M W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2002192763-A1.
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WANG A.
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(HURA/) H
(MCNE/) N
(HOUG/) H
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RESULT 1236
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FANG/)
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(DAYC/)
(VEDV/)
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RESULT
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AAU69818 standard; protein; 254 AA.
Human prostate cDNA encoded protein #26.
WO200173032-A2.
                         PN W0200173032-Az.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 42.68*
                                                                                                                                                                          Best Local Similarity: 42.68%
Query Match: 23.91%
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(FOYT/) FOY T M.
Local Similarity: 42.68%
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HARLOCKER S L.
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(WANG/) WANG A.
(SKEI/) SKEIKY Y A W.
(HEPL/) HEPLER W T.
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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DILLON D C.
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DILLON D C.
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DAY C H.
VEDVICK T S
CARTER D.
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RETTER M W.
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RETTER M W.
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                                                                                                                                    WO200134802-A2.
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(DILL/)
(MITC/)
(HARL/)
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(FANG/)
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Human prostate-specific amino acid mature form of P703B.
WO200151633-A2.
                                        110
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18
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(HOFF ) HOFFMANN LA ROCHE & CO AG F.
(SINO-) SINOGENOWAX CO LTD CHINESE NAT HUMAN GEN.
Local Similarity: 41.94* Mismatches:
                                        Mismatches:
Indels:
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Indels:
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Indels:
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Indels:
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Pancreas cancer marker – trypsin I precursor
                                                                                                                                                                                                                                                                                                   Indels:
                                                                              ADG26993 standard; protein; 585 AA.
Human prostate-specific polypeptide #249.
US2003157089-A1.
                                                                                                                                                                                       ABG76997 standard; protein; 262 AA. Human kallikrein protein variant #1.
WO200261131-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABRE4239 standard, protein; 247 AA.
Human NOV35a protein SEQ ID NO:146.
WO2003023001-A2.
                                                                                                                                                                                                                                                                                                                             ADR90673 standard; protein; 246 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 1245
ABR54241 standard; protein; 247 AA.
Human NOV35c protein SEQ ID NO:150.
20-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB21321 standard; protein; 247 AA.
                                                                                                                                                                                                                                                                                                                                           Human trypsinogen partial protein.
WO2004078777-A2.
                                                                                                                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIBB CO. (TSUC/) TSUCHIHASHI Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-SEP-2000.
(MOUN) MOUNT SINAI HOSPITAL.
Local Similarity: 41.94%
. мэтлн. 23.94%
                                                                                                                                                                                                                                                                                                                                                                   16-SEP-2004.
(BIOR-) BIOREXIS PHARM CORP.
                                                                                                          PD 21-ANG-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 40.14%
Query Match: 24.03%
RESULT 1241
                                        40.14%
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(CURA-) CURAGEN CORP.
LOCAL Similarity: 41.94%
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Local Similarity: 41.94%
23.94%
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PA (CORI-) CORIXA CORP.

Best Local Similarity: 42.68%
23.91%
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Ouerv Match: 23.94%
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Query Match: 23.96%
PN US2003185830-A1.
PD 02-OCT-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 40.
Query Macch:
RESULT 1240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human trypsinogen.
WO200053776-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-2000
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RESULT 1246
ID ADQ30580
DE Pancreas
PN WO200405:
PA (HOFF) IP
PA (SINO-)
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RESULT 1242
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RESULT 1243
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RESULT 1247
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Query Me
RESULT 1
ID ABI
DE Hum
PN WO2
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ABRS4190 standard; protein; 254 AA.
Prostate tumour specific protein sequence SEQ ID 523.
WO200289447-A2.
14-NOV-2002.
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888
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8
                                                                      Human prostate-specific mature protein of P703P
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Indels:
Mismatches:
Indels:
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Indels:
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BB95278 Btandard; protein; 254 AA.
Human P703P mature protein SEQ ID NO 523.
US2002022248-A1.
                                                                                                                                                                                              ABU71709 standard; protein; 254 AA.
Prostate cancer associated protein #12.
US2002192763-A1.
19-DEC-2002.
                                     r 1249
AAG99058 standard; protein; 254 AA.
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PA (APPL-) APPLERA CORP. Best Local Similarity: 40.38% Mismatches: 99 Query Match: 23.91% Indels: 18	RESULT 1261 ID ABR54277 standard; protein; 240 AA. DE Human trypsinogen protein SEQ ID NO:341. PN W02003023001-A2. PD 30-MAR-2003.	Dest Local Similarity: 42.56% Mismatches: 93 Query Match: 23.89% Indels: 11	INC. 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	# £	97 standard; oriatic prot 028479-A2. -2004.	PA (GETH) GENENTECH INC. Best Local Similarity: 42.15% Mismatches: 89 Querry Match: 23.86% Indels: 10	ID AB21308 standard; protein; 253 AA. DE Human EMSP. PN W020053776-A2.	PD 14-SEP-2000. PA (MOUN) MOUNT SINAI HOSPITAL. BEST Local Similarity: 42.80% Mismatches: 85 Onerw Match: 12	ULT 1265 AAB21324 standard; protein; 258 AA	human Erasr. WO200053776-A2. 14-SEP-2000. (MOUN) MOUNT SINAI HOSPITAL.	gg g		PD 30-JUL-1998. PA (INCY-) INCYTE PHARM INC. Best Local Similarity: 40.38% Mismatches: 100	JULY 1267 ABP74711 standard, protein, 262 AA. Human glandular kallikrein 1 precursor protein SE	WO200281646-A2. 17-OCT-2002. (CTLI-) CTL IMMUNOTHERAPIES CORP.	St Local Similarity: 40.388 Pry Match: 23.868 SULT 1268	ADL15204 standard; protein; 262 Pancreatic kallikrein #1. CN1384199-A. 11-DEC-2002.	7 K E	ID ADM72846 standard; protein; 263 AA. DE Human glandular kallikrein 1 protein SEQ ID NO:105. PN WQ2004022709-A2. PD 10-MAR-2004. PA (MANN-) MANNKIND CORP.
PA (CORI-) CORIXA CORP. Best Local Similarity: 42.68% Mismatches: 88 Query Match: 23.91% Indels: 8	SULT 1253 ADB13973 stande Human mature pi US2003185830-Ai	PA (COXI-) COXIAA CAR. Best Local Similarity: 42.68% Mismatches: 88 Query Match: 23.91% Indels: 8	ID ADG26389 standard; protein; 254 AA. DE Human prostate-specific polypeptide #59. PN US2001157089-A1. PD 21-AUG-2003.	# 2	Exbour 1235 ID AAB21319 standard; protein; 262 AA. DE Human KLK2. PN WO200053176-A2. PD 14-SEP-2000.	PA (MOUN) MOUNT SINAI HOSPITAL. Best Local Similarity: 40.38% Mismatches: 99 Query Match: 23.91% Indels: 18	2		at ery	RESULT 1257 ID ADL15197 standard; protein; 262 AA. DE Human pancreatic kallikrein. PN CN1384199-A.	2002. REMIN HOSPITAL SHENZHEN CITY. imilarity: 40.38% Mismatches: 9	ery Match: 23.91% Indels: SULT 1258 ADL64969 standard; protein; 262 AA.	DE Human kallikrein protein (KLKI). PN US2004033582-A1. PD 19-FBB-2004.	(FERR/) (PERR/) (POWE/)	(RAMA/) (SWAN/) (TSUC/)	PA (ZERB/) ZERBA K. Best Local Similarity: 40.38* Mismatches: 99 Query Match: 23.91* Indels: 18	RESULT 1259 ID AD039654 standard; protein; 262 AA. DE Human myocardial infarction-associated gene derived protein, SEQ ID 1317. PN W02004058052-A2.	at ery	RESULT 1260 ID ADD34891 standard; protein; 262 AA. DE Human autoimmune disease-related protein - SEQ ID 105. PN WO2004083403-A2. PD 30-SEP-2004.

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RESULT 1280
ID ABM81250 standard; protein; 333 AA.
ID ABM81250 standard; protein; 333 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3499.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 40.00$ Mismatches: 106
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Indels:
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Prostate cancer associated protein #72.
US2002192763-A1.
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AAE00397 standard; protein; 234 AA.
Human serine protease, PROST 07.
WO200125446-A1.
                                                                                                                                                                                                                                                                                                                                                                             (BERG) BERGHS C.
(DIPL) DIPIPPO V A.
(EISE/) EISEN A.
(GANG/) GANGOLLI E A.
(RIEG/) RIEGER D K.
(SPAD/) SPADERNA S K.
(SPAD/) SPADERNA S K.
SPAD/) SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PD 12-APR-2001.
PA (SCHD ) SCHERING AG.
Best Local Similarity: 43.04%
23.69%
                                                                                                                              SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                       ZERHUSEN B D.
ANDERSON D W.
ZHONG M.
CATTERTON E.
                                                                                                                                                                                                                                                                                           STONE DJ.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
                                                                                                   GUO X.
PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                        AGEE M L.
BERGHS C.
DIPIPPO V A.
                                          MILLET I.
PEYMAN J A.
KEKUDA R.
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FANGER G R.
RETTER M W.
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RASTELLI L.
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DILLON D C.
                           SMITHSON G.
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DAY C H.
VEDVICK T S
CARTER D.
LI S X.
WANG A.
                                                                                                                                                                                                                                                                                                                                                            LEACH M D.
                                                                                                                                                                                         GORMAN L.
   JS2004038223-A1.
                                                                                                                                                                                                                                           (CATT/)
(JIWW/)
(MILL/)
(RAST/)
(STON/)
(PENA/)
(SHEN/)
                                                                                                                                         (EDIN/)
(ELLE/)
(MALY/)
(ORTT/)
(GORM/)
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ZHON/)
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RESULT 1280
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(LISX/)
(WANG/)
                                                     PEYM/)
                                                                 KEKU/)
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(KALO/)
(FANG/)
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RESULT
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AABS4293 standard; protein; 267 AA.
Human pancreatic cancer antigen protein sequence SEQ ID NO:745.
W0200055320-A1.
(HUMA-) HUMAN GENOME SCI INC.
Local Similarity: 40.38% Mismatches: 100
   100
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18
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18
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16
                                    ID AAB98503 standard; protein; 225 AA.

DE Human trypsin serine protease catalytic domain.

PN WO200129056-A1.

PN GOAR-2001.

PA (UYAR-) UNIV ARKANSAS.

Best Local Similarity: 43.67% Mismatches:

COBLEY MACCH:

RESULT 1271

Indels:
   Mismatches:
                                                                                                                                                                                                       Mismatches:
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Indels:
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Indels:
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RESULT 1273
ID AAP95121 standard; protein; 262 AA.
ID E Kallikrein encoded by clone lambda HK65a.
PN EP297913-A.
PD 04-JAN-1989.
PA (AMGE-) AMGEN.
Best Local Similarity: 40.38$ Mismatcher
               Indels:
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                                                                                                                                       AAW93488 standard; protein; 230 AA.
Human TRYI trypsinogen variant protein.
WO9910503-A1.
                                                                                                                                                                                                                                                                                                                                                                                                              Best Local June 23.81%
Rusury Match:
Rusur 1274
ID ABG76998 standard; protein; 262 AA.
DE Human kallikrein protein variant #2
PN W0200261131-A2.
PN W0200261131-A2.
PN W6200261131-A2.
PN (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUM) BRISTOL-MYERS SQUIBB CO.
PA (HUIL/) HUI L.
Best Local Similarity: 40.38%
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG76998 standard; protein; 262 AA. Human kallikrein protein variant #2.WO200261131-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1278
ID ADN62908 standard; protein; 224 AA.
DE Human NOV189.
                                                                                                                                                                                                                                            AAB21315 standard; protein; 256 AA.
                                                                                                                                                                                                           Dest. 23.81*
Query Match:
RESULT 1272
ID AAB21315 standard; protein; 256.
DE Human KLKI.
PN WO200053776-A2.
PD 14-SRP-2000.
PA (MOUN ) MOUNT SINAI HOSPITAL.
Best Local Similarity: 23.81*
                                                                                                                                                                      PD 04-MAR-1999.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
Best Local Similarity: 43.67%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-APR-2003.
(CURA-) CURAGEN CORP.
Local Similarity: 45.29*
23.72*
Best Local Similarity: 40.38%
Query Match: 23.86%
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VEDVICK I S.

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96
44
                                                                                                                                                                                                                           80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU71763 standard; protein; 449 AA.
Prostate cancer specific antigen fusion protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAUG9872 standard; protein; 449 AA.
Human prostate serum antigen/P703P fusion protein.
WO200173032-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
Indels:
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Indels:
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Indels:
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Indels:
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Indels:
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P703P and PSA fusion amino acid sequence.
WO200151633-A2.
                                                                                                                                                                Human prostate serine protease protein.
EP936270-A2.
18-AUG-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD 06-MAY-2004.
PD (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (FIVE-) Similarity: 42.32* Mi
Best Local Similarity: 23.62* II
                                                                                                                                                                                                                                                                      ABR96163 standard; protein; 274 AA.
Human NOV12a protein SEQ ID NO:68.
WO200290568-A2.
                                                                                                                                                                                                                                                                                                                                                                                           ADNO4726 standard; protein; 247 AA. Antipsoriatic protein sequence #544 W02004028479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN99593 standard; protein; 247 AA.
                                                                                                                                   T 1282
AAY25510 standard; protein; 231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human protein sequence #409
WO2004038003-A2.
                                        (MCNE/) MCNEILL P D.
(HOUG/) HOUGHTON R L.
(BBAS/) Y DE BASSOLS C V.
(FOYT/) FOY T M.
t Local Similarity: 37.24%
ry Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2001.
(CORI-) CORIXA CORP.
Local Similarity: 44.14*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-2001.
(CORI-) CORIXA CORP.
Local Similarity: 44.14$
23.60$
                                                                                                                                                                                                 PD 18-AUG-122..
PA (BADI ) BASF AG.
Best Local Similarity: 43.95%
                                                                                                                                                                                                                                                                                                             M4-NOV-2002.
(CURA-) CURAGEN CORP.
Local Similarity: 40.82%
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
Local Similarity: 42.32%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MITCHAM J L.
HARLOCKER S L.
               HENDERSON R A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FANGER G R. STOLK J A. DAY C H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
RESULT 1285
ID ADN99593
DE Novel hur
PN WO204038
PD 06-MAY-22
PA (FIVE-)
(HEPL/) H
(HEND/) H
(HURA/) H
(MCNE/) M
(HOUG/) H
(DBAS/) H
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(MITC/)
(HARL/)
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(STOL/)
(DAYC/)
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(KALO/)
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ADB14067 standard; protein; 449 AA.
Human prostate specific protein P703P/PSA fusion protein.
US2003185830-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR54444 standard; protein; 449 AA.
Prostate tumour specific protein sequence SEQ ID 617
WO200289747-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU71890 standard, protein, 801 AA.
Prostate cancer specific antigen fusion protein #4.
US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
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Indels:
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Indels:
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                                                                                                                                                                                                   T 1289
ABB95332 standard; protein; 449 AA.
Human P703P/PSA fusion protein SEQ ID NO 617.
US2002022248-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG26483 standard; protein; 449 AA.
Human prostate-specific polypeptide #113.
US2003157089-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID ADB14067 Standard, Edwan prostate specific prote PN US200185830-A1.
PD 02-0CT-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 44.14%
                                                                  (HURA/) HURAL J.
(MCNE/) MCNEILL P D.
(HOUG/) HOUGHTON R L.
(DBAS/) Y DE BASSOLS C V.
(FOYT/) FOY T M.
t Local Similarity: 44.14%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PN MCZCCCT
PD 14-NOV-2002.
PD 14-NOV-2002.
PPA (CORI-) CORIXA CORP.
Pest Local Similarity: 44.14%
23.60%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 44.14%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity: 44.14% Match: 23.60%
                  SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SKBI/) SKEIKY Y A W. (HEPL/) HEPLER W T. (HEND/) HENDERSON R A.
                                                                                                                                                                                                                                                                                           (XUJJ/) XU J.
(DILL/) DILLON D C.
(MITC/) MITCHAM J L.
(HARL/) HARLOCKER S J.
(JIAN/) JIANG Y.
(KALO/) KALOS M D.
(KALO/) KALOS M D.
(RANG/) PANGER G R.
                                                                                                                                                                                                                                                                                                                                 MITCHAM J L.
HARLOCKER S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEDVICK T S.
CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (JIAN/) JIANG Y.
(KALO/) KALOS M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LI S X.
WANG A.
(WANG/)
(SKEI/)
(HEPL/)
(HEND/)
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RESULT 1290
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Indels:

23.28%

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24-AUG-2000
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RESULT 1307
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
RESULT 1305
  Query Match:
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RESULT 1308
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RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM83249 standard; protein; 261 AA,
Human diagnostic and therapeutic pprotein SEQ ID NO:3498.
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP70568 standard; protein; 262 AA.
Human kallikrein-like substance has hypotensive activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
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9
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19
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Indels:
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                                                                                                                                                                                                                          AAY31160 standard; protein; 224 AA.
Human trypsin serine protease protein domain.
US5948892-A.
                                                                                                                                                                                                                                                                                                                Indels:
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                                                                                                                                                                                                                                                                                                                                                                         11-DEC-2002.
(REMI-) REMIN HOSPITAL SHENZHEN CITY.
Local Similarity: 40.23% Miss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PD 11-DEC-2002.

PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
Best Local Similarity: 39.77% Mis
Query Match: 23.38% Ind
RESULT 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57740 standard; protein; 240 AA. Trypsinogen-like protein. JP10099080-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL15206 standard; protein; 260 AA.
Pancreatic kallikrein #2.
                                                                                                                                                                                                                                                                                                                                     ADL15207 standard; protein; 261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; 237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA (MOUN) MOUNT SINAI HOSPITAL.
Best Local Similarity: 42.24%
                                                                                                                                   HURAL J.
MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-1998.
(SHIS) SHISBIDO CO LTD.
Local Similarity: 42.49$
                                                                                                                                                                                                                                                                PD 07-25-1999.
PD 07-35EP-1999.
PA (AMGE-) AMGEN INC.
Best Local Similarity: 43.42%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2004.
(INCY-) INCYTE CORP.
Local Similarity: 43.50%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.24%
                                                                                                                                                                                               Local Similarity: 44.148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.00%
                                                                                                                                                                                                                                                                                                                                                                                                               23.45%
                                                                                                                                                                                                                                                                                                                                                 Pancreatic kallikrein #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human KLK-Li protein #1.
WO200053776-A2.
14-SEP-2000.
                                                                       LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                                                                          HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP62126980-A.
09-JUN-1987.
(NAKA/) NAKANISHI S.
: Local Similarity: 40.
                        STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB21293 standard;
                                                                                                                                                                                                                                                                                                                                                             CN1384199-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CN1384199-A.
                                                                                                                                   (HURA/)
(MCNE/)
(HOUG/)
(DBAS/)
                                                                                                           (HEPL/)
(HEND/)
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RESULT 1298
                                                                         (LISX/)
                                                                                                                                                                                                                                                                                                            Query Match:
RESULT 1295
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RESULT 1300
                                                                                                 SKEI/)
                                                  VEDV/
                                                            CART/
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DE AMIN4929 standard; protein; 312 AA.
DE Amino acid sequence of wild-type NS1-P703P-His fusion protein.
PN W0200200867-A1.
PD 03-JAN-2002.
PA (SMIX ) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 42.49% Mismatches: 82
                                                                                                                                                                                        AAU74768 standard; protein; 312 AA.
Amino acid seguence of wild-type NS1-p703-His fusion protein.
WO200200708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A human prostate specific antigen variant polypeptide WO200049158-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111
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Amino acid sequence of prostase protein fragment #4.
WO200200867-A1.
                                                                                                                                 82
12
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ABU71886 standard; protein; 344 AA.
Human prostate specific antigen (PSA) epitope #26.
US2002192763-A1.
19-DFC-2002.
(XUJJ/) XU J.
                                                                                                                            Mismatches:
Indels:
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Indels:
                                                                                                                                                                                                                                                 PD 03-JAN-2002.
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 42.49% Mismatches:
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Indels:
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Indels:
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Best Local Similarity: 43.84* Mismatches:
Query Match: 23.11* Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
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Protein sequence of prostase homologue #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indel8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY72526 standard; protein; 226 AA.
Human prostase antigen P703PDE5 sequence.
WO200104143-A2.
ID AAY72522 standard; protein; 312 AA.

DE NSI-P703P-His fusion protein.

PN WC20010413-A2.

PD 18-JAN-2001.

PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

PA (CORI-) CORIXA CORP.

Best Local Similarity: 42.49% Mismat Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD LB-JAN-ZOUL.
PA (SMTK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.84$ Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
Best Local Similarity: 43.84% Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU01290 standard; protein; 216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB08449 standard; protein; 375 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD 05-APR-2001.

PD 65-APR-2001.

PA (SMIX ) SMITHKLINE BEECHAM PLC.

Best Local Similarity: 44.34*

23.11*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human serine protease HETAA37p.
WO200123587-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.49% 23.18%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COMP-) COMPUGEN LTD.
Local Similarity: 37.42%
Match: 23.16%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.11%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
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Human prostate cDNA encoded protein #8.
W0200173032-A2.
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RESULT
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Human immunogenic prostate tumour protein sequence SEQ ID NO:327.
                                                                                                                                                                                                                                                                                                                                                                                                 ABM82601 standard; protein; 239 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2850.
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM02502 standard; protein; 239 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2851.
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM82603 standard; protein; 239 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2852.
25-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAMI1123 standard; protein; 220 AA.
Human prostate-specific amino acid sequence P703PDE6.
WO200151633-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FIVE-) FIVE PRIME THERAPEUTICS INC.
[Acal Similarity: 37.72% Mismatches: 22.89% Indels:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADN99649 standard; protein; 280 AA.
Novel human protein sequence #465.
WO2004038003-A2.
                                                                                                                                                                                     (LISX/)
(WANG) WANG A.
(WANG) WANG A.
(HEPL/) HEPLEN W T.
(HEND/) HENDERSON R A.
(HURA/) HURAL J.
(MURA/) HURALL P D.
(HOUG/) HOUGHTON R L.
(DBAS/) Y DE BASSOLS C V.
(FOYT/) FOY T M.
L LOCAl Similarity: 43.84%
ry Match:
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(INCY-) INCYTE CORP.
Local Similarity: 40.08*
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(INCY-) INCYTE CORP.
Local Similarity: 40.08*
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PD 27-AN-2000.
PA (COR.) CORIXA CORP.
Best Local Similarity: 43.78%
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PD 19-UUL-2001.
PA (CORI-) CORIXA CORP.
OBEL LOCAL Similarity: 43.78%
Query Match: 22.87%
RESULT 1316
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PA (INCY-) INCYTE CORP.
Best Local Similarity: 40.08%
                                                                                                                           STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
                           MITCHAM J L.
HARLOCKER S
                                                                        KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200004149-A2.
          (DILL/)
(MITC/)
(HARL/)
                                                          (JIAN/)
(KALO/)
(FANG/)
(RETT/)
                                                                                                                                                                         CART/)
LISX/)
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DAYC/
VEDV/
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T 1317
AAB74806 standard; protein; 220 AA.
AAB74806 standard; protein; 220 AA.
AAB74806 standard; protein; 220 AA.
MO300125272-A2.
12-APR-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                            ID AAG99008 standard; protein; 220 AA.

DE Human prostate-specific amino acid sequence P703PDES.

PN WC200134802-A2.

PD 17-MAY-2001.

PA (CORI-) CORIXA CORP.

Best Local Similarity: 43.78* Mismatches: 78

Query Match: Indels: 7
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Indels:
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Human P703P inventive antigen SEQ ID NO: 330.
WO200125273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU71659 standard; protein; 220 AA.
Prostate cancer specific antigen P703P #4.
US2002192763-A1.
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Human P703PDE5 protein SEQ ID NO 327
US2002022248-A1.
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(MCNE/) MCNEILL P D.
(HOUG/) HOUGHTON R L.
(DBAS/) Y DE BASSOLS C V.
(FOYT/) FOY T M.
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PD CORI-) CORIXA CORP.
Best Local Similarity: 43.78%
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Query Match: 22.87%
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HARLOCKER S
04-OCT-2001.
(CORI-) CORIXA CORP.
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WANG A.
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HEND/)
HURA/)
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Indels:

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		220 AA tein s			220 AA ein P7		220 AA Peptid			262 AA HK2) p	scı.	262 AA hHk2) ₁		A.	gene.		255 AA		2	(PSA) po	
	A. 43.78% 22.87%	/T 1322 ABR54340 standard; protein; 220 AA. Prostate tumour specific protein sequence	1	43.78\$ 22.87\$	A. 13.20 A. 13.13.77 standard, protein, 220 Human prostate specific protein US2003185830-A1.	43.78\$ 22.87\$	JT 1324 ADG26193 standard; protein; 220 AA. Human prostate-specific polypeptide		43.78% 22.87%	tein; rein (ARKANSAS MEDICAL rity: 38.93% 22.87%	tein; rein (3AS. 38.93\$			40.17% 22.80%		HOSPITAL	22.77%	, protein; Antigen (P	408
T & A H	, α	d; pro specif	CORP		d, pro pecifi	CORP.	d; pro pecifi	ORP.	: 43.	d; pro kallik	ANSAS : 38.	d; pro kallik	ANSAS.	22. d, pro	Kai Li		d; pro	Į,	22.	a, pro c Anti	INC.
DAY C H. VEDVICK CARTER D LI S X. WANG A. SKEIKY Y		tandar umour	WO200289747-A2. 14-NOV-2002. (CORI-) CORIXA CO	larity	tandar tate s 30-A1.	-) CORIXA CO Similarity: h:	tandar tate-s	3-2003. -) CORIXA CO	larıty	ADI39732 standard; protein; Human glandular kallikrein RS642013-81	04-NOV-2003. (UYAR-) UNIV ARKAL Local Similarity: Match:	JT 1326 ADI37156 standard; protein; Human glandular kallikrein	3199010-A1. F-2003. -) UNIV ARKANSAS Similarity: 38	tandar	Auman recombiant Kailikrein EP297913-A. 04-JAN-1989.	(AMGE-) AMGEN. Local Similarity Match:	standard; protein;	PSA. 053776-A2. 2-2000.) MOUNT SIN. Similarity:	,	AAU06276 standard; Prostate specific WO200145728-A2.	-Z001. .) EPIMMUNE INC. Similarity: 40.40%
	Si B:	22 4340 B tate t	028974 OV-200 I-) CO	ı Simi ch:	23 3777 s n pros 031858	I Simi	24 6193 s n pros	ug-200	1 Simi ch: 25	9732 s n glan	04-NOV-2003 (UYAR-) UNI Local Simil Match:	26 7156 s n glan	031990 CT-200 R-) UN	27 2314 8	EP297913-A.	E-) AM 1 Simi ch:	13	. О щ.	29:	AAUU6276 Bta Prostate spe WO200145728-	S. C.
(DAYC/) (VEDV/) (CART/) (LISX/) (WANG/) (SKEI/)	_ ~	ABRS	14-N	Loca	KESULI 1323 ID ADB13777 (DE Human proc PN US2003185(PD 02-OCT-200	(CORI-) (CORI-) Local S Y Match:	RESULT 1324 ID ADG26193 DE Human prod			ADI3: Human	`	RESULT 1326 ID ADI3715 DE Human g		Query Match: RESULT 1327 ID AAP92314	EP29		RESULT 1328 ID AAB21313	Human WO200 14-SE (MOUN		Prost WO20(
A A A A A A A A A A A A A A A A A A A	PA Best Que	REST DE DE	N C A	Quer Quer		PA Best Quer	REST ID DE	888	Quer	2082	PD PA Best Over	RESU ID DE	PN PD PA Best	RESU ID	388	PA Best Quer	TEST TO	PA PA PA	Quer RESU	E E E	PD PA Best

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Human prostate specific membrane antigen SEQ ID NO: 327.
W0200125273-A2.
IL 2-APR-2001.
(CORI-) CORIXA CORP.
Local Similarity: 40.40% Mismatches: 103
Try Match: 22.77% Indels: 13
ULT 1336
AMG62146 standard; protein; 261 AA.
Human prostate specific antigen SEQ ID NO: 329.
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13
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Prostate tumour antigen amino acid sequence for PSA.
W0200125272-A2.
12-APR-2001.
(CORI-) CORIXA CORP.
Local Similarity: 40.40% Mismatches: 103
y Match: Indels: 13
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(CORI-) CORIXA CORP.
(CORIS) Mismatches: 1
Local Similarity: 40.40$ Mismatches: 1
LY MAtch.
ULT 1337
ABU71859 standard; protein; 261 AA.
Human prostatic specific membrane antigen (PSMA).
19-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY77842 standard; protein; 261 AA.
Human prostate-specific antigen (PSA) sequence.
WO9960984-A2.
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Indels:
Dery Match: 22.77% Indels:
ESULT 1330
De AAW13649 standard; protein; 261 AA.
NO9711172-A1.
De 27-MAR-1997.
NO 27-MAR-1997.
A (WONC-) WORCESTER FOUND BIOMEDICAL RES.
Nuery Match: 22.77% Indels:
ESULT 1331
                                                                                                                                                                                                                                                                                                                            Indels:
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E Human prostate-specific antigen.
W09961068-A1.
D 02-DEC-1999.
A (UYPE-) UNIV PENNSYLVANIA.
A (UYPE-) USE 100 A Misnery Macch: 22.77% Independent of the control o
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ESULT 1333

BAB21317 standard; protein; 261 AA.

E Human PSA.

N W0200053776-A2.

N W02000 ST76-A2.

N W0200 ST76-A2.

N W0200 ST76-A2.

N W0200 ST76-A2.

N W0200 ST76-A2.

A (MOUN ) WOUNT SINAI HOSPITAL.

BST LOCAL Similarity: 40.40%

Lery Match:

Ind
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(ENTR-) ENTREMED INC.
Local Similarity: 40.40$
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(XUJJ) XUJ.
(DILL) DILLON D C.
(MITCA) MITCHAM J L.
(HARL) HARLOCKER S L.
(KALO) JIANG Y.
(KALO) KALOS M D.
(FANG) FANGER G R.
(RETT) RETTER M W.
(STOL) STOLK J A.
(DAYC) DAY C H.
(VEDV) VEDVICK T S.
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Mismatches: Indels:

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PA (CORI.) CORIXA CURE.
Best Local Similarity: 40.40%
22.77%
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                        GENENTECH INC.
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Query Match:
WO2004030615-A2.
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RESULT 1354
                                                                    RESULT 1346
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RESULT 1352
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                                                                                                                                                                                                                                                                                                          ADB82777 standard; protein; 261 AA. Human protein sequence useful for the treatment of cancer (SeqID 1558). WO2003050236-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM82166 standard; protein; 261 AA.
Tumour-associated antigenic target (TAT) polypeptide PR02109, SEQ:5591.
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Best Local Similarity: 40.40% Mismatches:
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Local Similarity: 40.40% Mismat
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Human prostate specific antigen (hPSA).
US2003199010-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ59022 standard; protein; 261 AA.
Human PSA precursor protein sequence.
WO2003047506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADW72819 standard; protein; 261 AA. Human PSA protein SEQ ID NO:78. W02004022709-A2. 18-MAR.2004. CMAN.) MANNXIND CORP. L Local Similarity: 40.40% Ind Natch:
                                                                                                                                                                                                                                                                                                                                                                                                                       PSA protein #SEQ ID 78.
WO2003008537-A2.
                                                                                                                                                                                             ABP74202 standard; protein; 261 AA. Human PSA protein SEQ ID NO:78. WO200281646-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2003.
(CTLI-) CTL IMMUNOTHERAPIES CORP.
Local Similarity: 40.40%
                                                                                                                                                                                                                                                   (CTLI-) CTL IMMUNOTHERAPIES CORP.
Local Similarity: 40.40%
Match: 22.77%
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(UYAR-) UNIV ARKANSAS.
Local Similarity: 40.40%
                                                                                              MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
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PA (CHIR ) CHIRON CORP.

PA (HYSE-) HYSEQ INC.

Best Local Similarity: 40.40%
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                                                                                                                                                      Local Similarity: 40.40%
Match: 22.77%
              LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                     HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Locus
Query Match:
RESULT 1345
TD ABM82166 standard; p
                                                                                    HURAL J.
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                                                                                  (HURA/)
(MCNE/)
(HOUG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
RESULT 1343
                                                       (HEPL/)
                                                                                                                           DBAS/)
                                                                                                                                           FOYT/)
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RESULT
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AAB67545 standard; protein; 284 AA.
Amino acid seguence of protease MH2 catalytic domain in PFEK2-6XHIS-TAG.
WO200116289-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU74928 standard; protein; 312 AA.
Amino acid seguence of NS1-P703P mutated-His fusion protein.
WO200200867-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU74767 standard; protein; 312 AA.
Amino acid sequence of NS1-p703 mutated-His fusion protein.
WO200200708-A2.
03-JAN-2002.
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AAU74934 standard, protein; 231 AA.
Amino acid sequence of P703P mutated-His fusion protein.
WO200200867-AI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU74903 standard; protein; 231 AA.
Amino acid sequence of p703 mutated-His fusion protein.
WO200200708-A2.
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Best Local Similarity: 42.06% Mismatches:
Query Match: Indels:
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Best Local Similarity: 40.40% Mismatches:
Query Match: 10618:
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Indels:
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AAG62154 standard; protein; 692 AA.
Human WT1/PSA fusion protein SEQ ID NO: 357.
WO200125273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP81243 standard; protein; 247 AA.
Human spleen trypsin III (trysinogen III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
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Best Local Similarity: 43.38* Misma
                                                                                                                                                                                                                                                                                                                                                                      DE NSI-P703P mutated-His fusion protein.
DE NSI-P703P mutated-His fusion protein.
DN W0200104143-A2.
DD 18-JAN-2001.
DA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
DA (CORI-) CORIXA CORP.
Best Local Similarity: 42.06% Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PA (SMTK ) SMITHKLINB BEECHAM BIOLOGICALS.
Best Local Similarity: 42.06% Misma
Query Match: 10del
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Best Local Similarity: 43.38% Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ59024 standard; protein; 261 AA.
Human PSA precursor protein sequence.
WO2003047506-A2.
                                                                                                                                                                                                                                                08-MAR-2001.
(ORTH ) ORTHO-MCNEIL PHARM INC.
Local Similarity: 43.75%
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ADR66036 standard; protein; 251 AA.
Human prostatic carcinoma derived protein SEQ ID 232 #1.
WO2004076614-A2.
                                                                                                                                                                                                         ID 131
                                                                                                                                                                                                                                                                                                                                                                                                             ADR66934 standard; protein; 251 AA.
Human prostatic carcinoma derived DNA SEQ ID 232 #4.
WO2004076614-A2.
                                                                                                                                                                                    ADR66277 standard; protein; 248 AA.
Human prostatic carcinoma derived protein SEQ
WO2004076614-A2.
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Indels:
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Human prostate specific antigen (PSA) variant
WO200240059-A2.
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AAW10600 standard; protein; 261 AA.
Human prepro-Trp226-glandular kallikrein-2.
WO9701630-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PA (AMBI-) AWERICAN FOUND BIOLOGICAL RES INC.
PA (MINC/) MINCHEFF M S.
PA (LOUK/) LOUKINOV D I.
PA (ZOUB/) ZOUBAK S.
PEST LOCAL SIMILATLY: 41.38$ Mismatch
Query Match:
                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR84668 standard; protein; 261 AA.
Prepro-hK2 kallikrein.
WO9530758-A1.
                                            10-SEF-ZOVE.
(HINZ/) HINZMANN B.
(DAHL/) DAHL B.
(ROSE/) ROSENTHAL A.
(HERM/) HERNANN K.
(PILA/) PILARSKY C.
t Local Similarity: 40.25$
                                                                                                                                                                                                                                                                                                                                                       40.25%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.25% 22.39%
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PA (ORIN ) ORION YHTYMAE OY.
Best Local Similarity: 40.23$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.29$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Best Local Similarity: 40.
                                                                                                                                                                                                                                        PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSEJ) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Best Local Similarity: 40.
                                      HINZ/) HINZMANN B
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   WO2004076614-A2.
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**Rhesus macaque prostate specific antigen (PSA/KLK3), SEQ ID NO:4.

**WO2003031569-A2.

17-APR-2003.

(CENZ ) CENTOCOR INC.

(CENZ ) Similarity: 42.62* Mismatches: 96

Match: 22.46* Indels: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP27546 standard; protein; 281 AA.
Human kallikrein-3 (KLK-3) EHT103 protien b variant SeqID 20.
FR2848569-A1.
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RESULT 1360
ID ADP27545 standard; protein; 297 AA.
DE Human Kallikrein-3 (KLK-3) EHT103 protien a variant SeqID 19.
PN FR2848569-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ59028 standard; protein; 261 AA.
Human PSA analogue (L155/Y154) precursor protein seguence.
WO2003047506-A2.
                                                                                                                                                                                                                                                             ADJ59026 standard; protein; 261 AA.
Human PSA analogue (Y154) precursor protein sequence
WO2003047506-A2.
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13
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Human prostatic carcinoma derived DNA SEQ ID 131 #4.
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Rat SCCE protein N-terminal fragment SEQ ID 48.
WO200262135-A2.
                                                                                                                                                                                                                                                                                                               12-JUN-2003.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Local Similarity: 40.40% Mismatches:
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Local Similarity: 40.40% Mismatches:
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Human prostate-specific antigen protein.
US2003235594-A1.
                                                                                                           AAR82703 standard; protein; 247 AA.
Human pancractic trypsin III.
25-JUL-1995.
(SANY) SANKYO CO LTD.
(LOCAL Similarity: 40 91% Miss
rry Match: Indi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity: 39.70%
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Local Similarity: 39.70%
Match: 22.48%
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Best Local Similarity: 40.00%
Query Match: 22.43%
PN JP63160582-A.
PD 04-JUL-1988.
PA (SANY) SANKXO CO LTD.
Best Local Similarity: 40.91%
Query Match:
RESULT 1355
ID AAR82703 standard; protein;
DE Human pancreatic trypsin IIIP
PN JP07184655-A.
PD 25-JUL-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity: 42.67% y Match: 22.48%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-AUG-2002.
(EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-2004.
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RESULT 1361
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RESULT 1362
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112 11

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Prostate-specific glandular kallikrein protein pphK2
                                                                                                                                                                                                                                                   AM06911 standard; protein; 261 AA.
Prostate-specific glandular kallikrein prepro-hK2.
W09634964-A2.
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Indels:
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AAW96189 standard; protein; 261 AA.
Prepro human Kallikrein 2 (preprohK2).
AAY08894 standard; protein; 238 AA. Chimeric serine protease FXT protein. EP927764-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW49085 standard, protein, 261 AA.
Wild-type human Kallikrein 2 (hK2).
WO9821365-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB21318 standard; protein; 261 AA.
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                                                                                                                               AAB21314 standard; protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BAYU) BAYLOR COLLEGE MEDICINE:
(MAYO-) MAYO FOUNDATION.
Local Similarity: 40.80%
Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID AAB21318 standard; protein; 261
DE Human KLK2.
PD WOOD0053776-A2.
PD 14-SEP-2000.
PA (MOUN ) MOUNT SINAI HOSPITAL.
Best Local Similarity: 40.80%
Query Match:
RESULT 1378
ID AAU06279 standard; protein; 261
                                                PD 07-JUL-1999.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
Best Local Similarity: 40.52%
                                                                                                                                                                                      14-SEF-2000.
(MOUN ) MOUNT SINAI HOSPITAL.
LOCAl Similarity: 40.80%
v Match:
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07-NOV-1996.
(HYBR-) HYBRITECH INC.
(MAYO-) MAYO FOUNDATION.
it Local Similarity: 40.80%
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DA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITECH INC.
Best Local Similarity: 22.19$
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PA (HYBR-) HYBRITECH INC.
Best Local Similarity: 40.80
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(YOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE Prepro human Kallikr
W09859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDAT
PA (YOUN/) YOUNG C Y F.
PA (TIND/) TINDALL D J.
PA (KLEE/) KLEE G G.
Best Local Similarity: 4
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                                                                                                                                                 Human KLK2
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Query Match:
RESULT 1374
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RESULT 1373
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RESULT 1376
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RESULT 1377
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RESULT 1375
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RESULT 1371
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AAB19818 standard; protein; 237 AA.
Prostate specific antigen elevated in benign prostatic hyperplasia.
WO200066718-A1.
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AAB19819 standard; protein; 237 AA.
Prostate specific antigen specific to benign prostatic hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADASÖS46 standard, protein, 237 AA.
Human prostate specific antigen (PSA/KLK3), SEQ ID NO:1.
WO2003031569-A2.
17-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB11041 standard, peptide, 237 AA.
Human prostate-specific antigen N-terminal fragment #2
EP1043394-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate specific antigen protein. 198101992-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PA (SEA-) SERATEC GES BIOTECHNOLOGIE MBH.
Best Local Similarity: 41.56% Misma
Query Match: 22.14% Indel
                                                                                                                                                                                                                                                    AAW83213 standard; protein; 237 AA.
Prostate-specific antigen protein hK3.
WO9846795-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW96187 standard; protein; 237 AA.
Human prostate specific antigen (PSA)
W09859073-A1.
                                                                                                                      ADB75390 standard; protein; 261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD 09-NOV-2000.

PA (HENBR-) HYBRITECH INC.

PA (BAYU ) BAYLOR COLLEGE MEDICINE.

Best Local Similarity: 41.56$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-NOV-2000.
(HYBR-) HYBRITECH INC.
(BAYU) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                   PD 22-OCT-1998.
PA RAYU ) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
Best Local Similarity: 41.56%
Human Kallikrein2 polypeptide. WO200145728-A2. 28-JUN-2001. (EPIM-) EPIMMUNE INC. Local Similarity: 40.80% ry Match:
                                                                                                                                 Prostate cancer marker protein. WO2003009814-A2.
                                                                                                                                                                                        PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 40.80%
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 12-MAR-1990.
PA (CENZ ) CENTOCOR INC.
Best Local Similarity: 41.56%
22.14%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUN) YOUNG C Y F.
PA (TIND) TINDALL D J.
PA (KLEE/) KLEE G G.
Best Local Similarity: 41.56$
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Query Match: 22.14%
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                                                                   Best Local Similarity:
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RESULT 1382
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RESULT 1379
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RESULT 1380
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RESULT 1381
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RESULT 1385
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RESULT
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Mismatches: Indels:	237 AA. ic antigen (PSA).	Mismatches: Indels:	; 237 AA. sequence. TUMAN SERVICES. Mismatches:	Indels: 37 AA. en (PSA).	Mismatches: Indels:	245 AA. :t.	Mismatches: Indels:	237 AA. cotein hK3 (PSA).	Mismatches: Indels:	237 AA. uence.	N SERVICES. Mismatches: Indels:	261 AA. riant.	Mismatches: Indels:	261 AA. kallikrein hK2v217.	Mismatches: Indels:
PA (CENZ) CENTOCOR INC. Best Local Similarity: 41.56% Obery March: 22.14%	tein; specif	(MIKO/) MIKOLAJCZYK S D. (RITT/) RITTENHOUSE H G. Local Similarity: 41.56% Y Macch: 22.14%	.5	Query Match: 22.148 RESULT 1389 ID ADF60980 standard; protein; 237 DE Human prostate specific antigen PN US2003166036-A1.	04-SELZUGJ. (MIKO/) MIKOLAJCZYK S D. (RITT/) RITTENHOUSE H G. Local Similarity: 41.56\$ Y Macch: 22.14\$	in;	PD 07-MAY-1987. PA (BLOT-) BIOTECHN RES PARTN. PA (CALB-) CALIF BIOTECHNOL INC. Best Local Similarity: 39.75% Query Match:	standard, protein; -specific antigen pr 8-A1.	PD 22-JAN-1998. PA (MAYO-) MAYO FOUNDATION. PA (HYBR-) HYBRITECH INC. Best Local Similarity: 41.56% Query Match: 22.05%	standard; protein; A mature protein seg 7506-A2. 003.	PA (USSH) US DEPT HEALTH & HUMAN SERVICES Best Local Similarity: 41.56% Misma Query Match: 1ndel	; protein; -hK2v217 va	U.A.N.Y. 1998. (HYBR-) HYBRIECH INC. (MAYO-) MAYO FOUNDATION. Local Similarity: 40.80%	ndard, protein; cific glandular	PD 22-JAN-1998. PA (MAYO-) MAYO FOUNDATION. PA (HYBR-) HYBRITECH INC. Best Local Similarity: 40.80% Query Match:
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Query Match:

ENSULT 1402

ID AAM83204 standard; protein; 244 AA.

DE Prostace-specific glandular kallikrein protein phK2.

PN WO980271994.

PA (MAYO-) MAYO FOUNDATION.

PA (MAYO-) MAYO FOUNDATION.

Best Local Similarity: 41.81 Mismatches: 96

Query Match:

RESULT 1403

ID AAM45396 standard; protein; 244 AA.

DE Prostate-specific glandular kallikrein precursor pro-hK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD 25-MAR-2004.

PA (AMTI-) ANTIGEN EXPRESS INC.

Best Local Similarity: 39.60$ Mismatches: 105

Query Match: 22.00$ Indels: 13

RESULT 1401

DE ADJ59027 standard; protein; 237 AA.

DE Human PSA analogue (Y154) mature protein sequence.

PD 12-JUN-2003.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PA (USSH ) US DEPT HEALTH & 156$ Mismatches: 96

Ouery Match: 21.95$ Indels: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uery Match: 22.00$ Indels: 11
ESULT 1398
AAU74930 standard; protein; 232 AA.
E Amino acid sequence of prostase protein fragment #1.
N WO200200867-A1.
D 03-JAN-2002.
A (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
A (SMIK ) SMITHKLINE 32.00$ Mismatches: 76
ESULT 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
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11
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E Human prostase antigen #1.

PN W0200104143-A2.

PN W0200104143-A2.

PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

PA (CORI-) CORIXA CORP.

Best Local Similarity: 43.78$ Mismatches:

Query Match: 22.00$ Indels:

RESULT 1397

ID AAU74769 standard; protein; 232 AA.

DE Protein sequence of prostase homologue #1.

PN W0200200708-A2.

PN
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Indels:
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Indels:
SGULT 1395
AAW59129 standard; protein; 232 AA.
A Homo sapiens Tub Interactor (hTI-1) protein.
1 W09812302-A1.
26-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DE Pro-hK2 kallikrein.
PN WO9530758-A1.
PD 16-NOV-1995.
PD 16-NOV-1995.
PA (MAYO-) MAYO FOUNDATION.
PA (HYBR-) HYBRITECH INC.
Best Local Similarity: 41.18% Miss Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADO38617 standard; protein; 261 AA.
Prostate Specific Antigen (PSA).
US2004058881-A1.
25-MAR-2004.
                                                                                                                                                                                         A (MILL-) MILLENNIUM PHARM INC.
set Local Similarity: 43.78%
lery Match:
22.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JAN-1998. (MAYO-) MAYO FOUNDATION.
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16-NOV-1995.
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RESULT 1414
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(ELLE/)
(MACD/)
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RESULT 1416
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(LILL/)
(CASM/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query N
RESULT
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Human kallikrein-2 (KLK-2) EHT102 protein a variant SegID 11.
FR2848569-A1.
                                                                                                                                                                                                                                                                                         ADP27538 standard; protein; 281 AA.
Human kallikrein-2 (KLK-2) EHT102 protein b variant SeqID 12.
FR2848569-A1.
18-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ59029 standard; protein; 236 AA.
Human PSA analogue (L155/Y154) mature protein sequence.
WO2003047506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PA (ULUCAL Similariuge)

Best Local Similariuge

Query Match:

Query Match:

Query Match:

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Query Match:

RESULT 1410

ID AAW83202 standard; protein; 237 AA.

DE Prostate-specific glandular kallikrein protein hK2.

DE Prostate-specific glandular kallikrein protein hK2.

DE Prostate-specific glandular kallikrein protein hK2.

PN W09846795-AI.

Orn-1998.
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Mature prostate-specific glandular kallikrein hK2.
WO9802748-A1.
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Indels:
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Indels:
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Indels:
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Local Similarity: 41.56% Mismat
/ Match: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR77098 standard; protein; 237 AA.
Prostate-pecific antigen.
WOS528498.Al.
26-OCT-1995.
                       Query Match: 21.90% In
RESULT 1404
ID AAW96188 standard; protein; 244 AA.
DE Pro human Kallikrein 2 (prohK2).
PN W09859073-A1.
                                                                                                                                                                                        AAW03130 standard; protein; 250 AA.
Prostate-specific antigen.
                                                                                                                                                                                                                                                                                                                                         Local Similarity: 41.81%
Match: 21.90%
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Match: 21.90%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z6-UCI-1255.
(UYCO ) UNIV COLUMBIA NEW YORK.
Local Similarity: 40.69%
MATCH:
                                                                                                                                                   41.81% 21.90%
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PA (HYBR-) HYBRITECH INC.
Best Local Similarity: 41.99%
Query Match:
RESULT 1412
           41.81% 21.90%
                                                                                                                                                                                                                                                      40.52%
                                                                                             JO-DEC-1796.

(MAYO-) MAYO FOUNDATION.

(YOUN/) YOUNG C Y F.

(TINDA) THNDALL D J.

(KLEE/) KLEE G G.
(HYBR-) HYBRITECH INC
Local Similarity: 41
                                                                                                                                                                                                                           11-JUL-1996.
(UYBO-) UNIV BOSTON.
Local Similarity: 4
                                                                                                                                                                                                                 WO9621042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-2004.
                                                                                      30-DEC-1998
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RESULT 1411
ID AAW45395
DE Mature pi
PN W09802748
PD 22-JAN-15
PA (MYBR-) PA
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RESULT 1406
ID ADP27538
DE Human ka
PN FR284856
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RESULT 1405
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DE
PN
PA
PA
PA
PA
Best
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ADJ83076 standard; protein; 217 AA.
Irypsin protein which is related to human NOVX protein - SEQ ID 67.
US2003170630-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI17269 standard; protein; 217 AA.
Polypeptide homologous to a human NOVX domain SeqID 805.
WO200268649-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADII7277 standard; protein; 217 AA.
Polypeptide homologous to a human NOVX domain SeqID 813
WO200268649-A2.
                                                                                                                                             11
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Indels:
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Indels:
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RESULT 1413

ID ADA50561 standard; protein; 237 AA.

DE Kallikrein KLK2, SEQ ID NO:16.

PN WO2003031559-A2.
                                                                                                                                                                                                                                                                                                                                        AAR84667 standard; protein; 237 AA.
Mature kallikrein hK2.
WO9530758-A1.
 AAW96186 standard; protein; 237 AA.
Mature human Kallikrein 2 (hK2).
WO9859073-A1.
ID AAW96186 standard, proceed by Mature human Kallikrein 2 (hK NV W09859073-A1.
PD 30-DEC-1998.
PA (MAYO-) MAYO FOUNDATION.
PA (YOUN/) YOUNG C Y F.
PA (TIND) TINDALL D J.
PA (KLEE/) KLEE G G.
Best Local Similarity: 41.99$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PN MCZOSEP-2002.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 44.44$
                                                                                                                                                                                                                                                   PD 17-APR-2003.
PA (CENZ ) CENTOCOR INC.
Best Local Similarity: 41.99%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity: 44.44%
Query Match: 21.66%
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PA (HYBR-) HYBRITECH INC.
Best Local Similarity: 41.99%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIU X.
SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BURGESS C E.
SHIMKETS R A.
GROSSE W M.
SZEKERES E S.
VERNET C A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GANGOLLI E A.
FERNANDES E R.
RIEGER D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CASMAN S J.
BOLDOG F L.
GORMAN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEPLEY D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDINGER S
GUNTHER E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MILLET I.
SCIORE P.
ELLERMAN
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21.25\$

87 13		96 11		96			96 11		96 14		97	ID NO:2892.	82 30		101	Halybin.	110
Mismatches: Indels:	AA.	Mismatches: Indels:	AA. A217V.	Mismatches: Indels:	AA.		Mismatches: Indels:	240 AA. gen.	Mismatches: Indels:	AA.	Mismatches: Indels:	SEQ	Mismatches: Indels:	AA.	Mismatches: Indels:	AA. ike protease, Ha	INST. Mismatches:
G. 44.44% 21.66%	žď ;	998. BAYLOR COLLEGE MEDICINE MAYO FOUNDATION. milarity: 21.99*	; protein; 237 ikrein 2 (hK2)	DATION. INC. 41.99% 21.66%	protein; 237 likrein 2 (hK2)	DATION. F. J.	41.99% 21.66%	•	S SYSTEM. 41.03% 21.54%	; protein; 237 hK3.	FOUNDATION. TECH INC. TLY: 41.13%	l; protein; 227 AA. and therapeutic pprotein	RP. 39.59% 21.44%	, protein; 238 hK2.	FOUNDATION. TECH INC. TLY: 40.93%	standard; protein; 279 AA. per Salmosa thrombin-like protease, A2.	2-1996.) MOGAM BIOTECHNOLOGY RES Similarity: 37.66%
MITHSON ilarity:	standard nt A217V -A1.	~	T 1419 AAW49087 standard; protein; Mutant human Kallikrein 2 (WO9821146-A2	22-MAY-1998. (MAYO-) MAYO FOUNDATION (HYBR.) HYBRITECH INC. Local Similarity: 41.9! MACCH: A.20.	1. 1720 AAW96190 standard; protein; Variant human Kallikrein 2 WO0060072.1	201		T 1421 AAW11023 standard; protein; Human prostate specific ant	MOS640/54-A1. 19-DEC-1996. (TEXA) UNIV TEXAS Local Similarity: Match:	T 1422 AAR84671 standard; protein; Mature kallikrein hK3. WO9530758-A1.	1995. MAYO HYBRI imilar	43 standard diagnostic	25-MAR-2004. (INCY-) INCYTE CORP Local Similarity: Match:	A. 1727 Mature kallikrein hK2. WO9530758-A1.	-1995.) MAYO) HYBRI Similar	26 Vj	L7.2PR-1996. (MOGA-) MOGAM BIO7 Local Similarity:
PA (S Best Lo Query M	ğ	PD 22-OCT- PA (BAYU) PA (MAYO-) Best Local S Query Match:	ID AAI	at ery	ID AAI DE Va		3t	IDS	PD 19-DEC-PA (TEXA) Best Local S Query Match:	RESULT 1422 ID AAR846 DE Mature PN W09530	ir ir	KESULT 1423 ID ABM826 DE Human PN WO2004	3 tr	ID AAI DE Mat	at ery	ID AAI OE KOI	床

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ABBOSSS standard, protein, 234 AA.
Deinagkistrodon acutus venom thrombin-like protein (234 residue variant).
CN1181421-A.
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Query Match:

RESULT 1432

ID AAW1872 standard; protein; 205 AA.

DE Protein encoded by prostate tumour clone P703 splice variant DE13.

PN W09837093-A2.

PN W09837093-A2.

PN W09837093-A2.

PN W09837093-A2.

PN W09837093-A2.

PN W09837093-A2.

Mismatches: 70

Best Local Similarity: 43.72% Indels: 7
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Query Match:

RESULT 1433

ID AAYR2005 standard; protein; 205 AA.

DE Human immunogenic prostate tumour protein sequence SEQ ID NO:176.

PN W0200004149-A2.

PN W0200004149-A2.

PN COORI-5000.

PA (CORI-) CORIA, CORP.

Best Local Similarity: 43.72$ Mismatches: 70

Best Local Similarity: 43.72$ Indels:
                                                                                                                                                                                                           ID AAMS2944 standard; protein; 260 AA.

DE Agkistrodon halys brevicaudus thrombin-likle protease, salmobin.

PN KR98002267-A.

PD 30-MAR-1998.

PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.

Best Local Similarity: 36.14* Mismatches: 106

Query Match: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ABC70966 standard; protein; 227 AA.

DE Human protein modification and maintenance molecule (PMPM)-4.

PN W02003063688-A2.

PD 07-AUG-2003.

PA (INCY-) INCYTE GENOMICS INC.

Best Local Similarity: 39.18$

Query Match: Indels: 30
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Human prostate tumour protein partial variant sequence #2.
US2002090372-A1.
                                                                                                                                                                                                                                                                                                                                                  Query Match:

RESULT 1428

ID AABSO47 standard; protein; 205 AA.

BE Human prostate cancer-related intracellular protein #1.

PN WO200071711-2.

PD 30-NOV-2000.

PA (SAAI/) SAATCIOGLU F.

Best Local Similarity: 44.22% Mismatches: 69
                                                                                                                                                 11
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DE Prostate tumour specific gene clone DE13 protein.

NO9837418-A2.

PD 27-AUG-1998.

PA (CORI-) CORIA, CORP.

Best Local Similarity: 43.72% Mismatches:

Query Match:
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PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
Best Local Similarity: 37.66* Mismatches:
Query Match:
RESULT 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches:
Indels:
                                                                                                                                              Mismatches:
Indels:
DE AAG7900 standard; protein; 233 AA.
DE Mamushi fibrinolytic enzyme, brevinase.
PN KR2001045716-A.
PD 05-JUN-2UN-2UN-2P W.
PA (LEEJ/) LEE J W.
PA (PARK/) PARK W.
Best Local Similarity: 37.93% Mismi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.22%
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(XUJJ/) XU J.
(DILL/) DILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
RESULT 1434
ID ABG94140
DE Human pro
PD US200209
PD (NUJ)
PA (XUJ))
PA (XUJ))
                                                                                                                                                                  Query Match:
RESULT 1427
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RESULT 1429
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Human P703P-DE13 protein SEQ ID NO 176.
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                                    XU J.
DILLON D C.
            JS2002022248-A1.
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RESULT 1448
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                                                                                                          FANG/
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RESULT
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RESULT
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 sequence for P703P-DE13.
                                                                                                                                                                                                                                                                                                                  T 1438
AAG9005 standard; protein; 205 AA.
Human prostate-specific amino acid sequence P703P-DE13
WO200134802-A2.
                                     AAM01120 standard; protein; 205 AA.
Human prostate-specific amino acid sequence P703P-DE13.
WO200151633-A2.
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Indels:
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Prostate tumour antigen predicted amino acid
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Prostate cancer specific antigen P703P #2.
US2002192763-A1.
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Human prostate cDNA encoded protein #6.
WO200173032-A2.
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PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.72%
Query Match:
RESULT 1441
ID ABRGENAT
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MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
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17-MAY-2001.
(CORI-) CORIXA CORP.
Local Similarity: 43.72%
20.64%
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(CORI-) CORIXA CORP.
Local Similarity: 43.72%
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(CORI-) CORIXA CORP.
Local Similarity: 43.72%
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(CORI-) CORIXA CORP.
Local Similarity: 43.72%
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SKEIKY Y A W.
HEPLER W T.
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DAY C H.
VEDVICK T S.
CARTER D.
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HARLOCKER S
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RETTER M W.
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KALOS M D.
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(FOYT/)
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RESULT 1438
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(MITC/)
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ABU92024 standard; protein; 218 AA.
Human protein modification and maintenance molecule-4 (PMMM-4).
WO2003031939-A2.
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Prostate tumour specific protein sequence SEQ ID 176.
WO200289747-A2.
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Human prostate specific protein P703P-DE13.
US2003185830-A1.
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ADG26042 standard; protein; 205 AA.
Human prostate-specific polypeptide #6.
US2003157089-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADK36957 standard; protein; 281 AA. Novel human polypeptide SeqID9039. WO200216439-A2.
                                                                                                                                                                                                                                            ABG76668 standard; protein; 205 AA. Prostate tumour protein #6. US2002081880-A1. (XUUJ/) XU J.
                                                                                                                         (LISX/) LA C. (WANG) WANG A. (SKEI/) SKEIKY YA W. (HEPL/) HEPLER W T. (HEND/) HENDERSON R. Local Similarity: 43.72%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD 28-FEB-2002.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 39.26%
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PA (DILL/) DILLON D C.
Best Local Similarity: 43.72%
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PD 14-NOV-2002.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 43.72%
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PA (CORI-) CORIXA CORP.

Best Local Similarity: 43.72%

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Query Match: 20.64%
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(CORI-) CORIXA CORP.
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Best Local Similarity:
                                                                                             VEDVICK
                                                                                                         CARTER
JIANG
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T 1455
ABM83248 standard; protein; 299 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:3497.
WO2004023973-A2.
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Indels:
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Prostate specific antigen (PSA/KLK3), SEQ ID
WO2003031569-A2.
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Indels:
   ABG75786 standard; protein; 226 AA.
Trypsin domain consensus sequence, SMART.
US2002165152-A1.
                                                                                                                                                                                                                                                              ADA05736 standard; protein; 198 AA.
Human NOV18c protein SEQ ID NO:96.
WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                 ADN62900 standard; protein; 198 AA.
 ID ABG75786 standard; protein; 226
DE Trypsin domain consensus sequence US2002165152-A1.
PD 07-NOV-2002.
PA (KAPE/) KAPELLER-LIBERMANN R.
Best Local Similarity: 42.58*
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL) MILLER C E. (RAST) RASTELLI L. (STON) STONE D J. (PENA) PENA C E A. (SHEN/) SHENOY S G. (SHEN/) SHINKETS R A. (ROTH/) SHINKETS R A. (LEAC/) LEACH M D. (LEAC/) LEACH M D. (LEAC/) LEACH M D. (BERG) BERCHS C. (EISE) SEISEN A. (GANG) GANGOLLI E A. (RIEG/) RIEGER D K. (RIEG/) RIEGER D K. (RIEG/) RIEGER D K. (SADD) SPADERNA S K. (LOCAL SIMILARITY: 36 82% FY MATCH:
                                                                                                                                                                         PD 25-MAR-2004.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 36.07%
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PA (CURA-) CURAGEN CORP.
Best Local Similarity: 36.82%
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PD 17-AFR-2003.
PA (CENZ ) CENTOCOR INC.
Best Local Similarity: 38.74%
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATTURAJAN M.
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PEYMAN J A.
KEKUDA R.
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CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMITHSON G.
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GORMAN L.
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RESULT 1456
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PA (SCRM/)
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RESULT 1459
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RESULT 1457
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(GUOX/)
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                                                                                                                           G-coupled protein receptor related polypeptide, SEQ ID No 12. WO200283841-A2.
                                                                                                                                                                                                                                 T 1450
AD193921 standard, protein, 218 AA.
Human G-coupled protein receptor-related protein #6.
US2004006205-A1.
(LILL/) LI L.
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38
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65
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AAY20641 standard; protein; 207 AA.
Hans secreted protein from cDNA clone HKAET41.
W09940183-A1.
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   Amino acid sequence of cod trypsin isozymes. WO200078332-A2.
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Human trypsin domain consensus protein #2.
WO200226802-A2.
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DE Amino acid sequence of cod trypsin iso PN W020078312-A2.
PD 28-DEC-2000.
PA (BJAR/) BJARNASON J B.
Best Local Similarity: 44.30% Mism Query March: 20.38% Inde RESULT 144.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-1997.
(MOGA-) MOGAM BIOTECHNOLOGY RES INST.
Local Similarity: 36.64% Misn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW46773 standard; protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of Salmonase.
EP814164-A2.
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Best Local Similarity: 42.58%
Query Match:
RESULT 1454
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(HUMA-) HUMAN GENOME SCI INC.
Local Similarity: 50.28*
                                                                                                                                                                 24-OCT-2002.
(CURA-) CURAGEN CORP.
Local Similarity: 37.76%
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VERNET C A.
MACDOUGALL J R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZHONG M.
MEZES P S.
FURTAK K.
PATTURAJAN M.
BURGESS C E.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                               MILLER C E.
SPYTEK K A.
ZERHUSEN B D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHIMKETS R A.
TAUPIER R J.
EDINGER S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RASTELLI L.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ZHONG H.
SMITHSON G.
CASMAN S J.
BOLDOG F L.
                                                                                                                                                                                                                                                                                                                                                                                                                  PENA C E A.
SHENOY S G.
                                                                                                                                                                                                                                                                                                                                GERLACH V.
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RESULT 1453
ID AAE2144
DE Human t
PN WO20022
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Query
RESUL
ID
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NO:15.

75 36

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AAB08510 standard; protein; 230 AA.
A recombinant protein C activator polypeptide.
WO200050612-A2.
US2003065160-A1.
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RESULT 1473
ID AAR20557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
RESULT 1471
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RESULT
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RESULT
          Human protein modification and maintenance molecule polypeptide SeqID8. 09-OCT-2003.
                                                                                                                                                                                          ABM82829 standard; protein; 215 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:3078.
WO2004023973-A2.
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                                                                                                                                                                                                                                                                                                                        77
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36
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Indels:
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Indels:
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Indels:
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Indels:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                           ADA05738 standard; protein; 181 AA.
Human NOV18d protein SEQ ID NO:98.
WO2003029424-A2.
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RESULT 1463
ID ABM82641 standard; protein; 222 AA.
DE Human diagnostic and therapeutic pp
PN WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN62902 standard; protein; 181 AA.
  ADG75684 standard; protein; 215 AA
                                                                                                                                                                                                                                                                                                                                                                                        ID ADA05738 Standaru, procession SEQ ID 10-APR-2003.

PA (CURA-) CURAGEN CORP.

Best Local Similarity: 37.39%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         // BISEN A.

3// GANGOLDI E A.

3// RIEGER D K.

D// SPADERNA S K.

1. Similarity: 37.39$
                                                                                                                                                                                                                                                        25-MAR-2004.
(INCY-) INCYTE CORP.
Local Similarity: 37.14%
                                                                       09-OCT-2005.
(INCY-) INCYTE CORP.
Local Similarity: 37.14%
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Best Local Similarity: 36.69%
Query Match: 19.70%
RESULT 1464
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SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
LEACH M D.
AGGE M L.
BERGHS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
ZHONG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATTERTON E.
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RASTELLI L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2004038223-A1.
26-FEB-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human NOV18d.
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RESULT 1462
DE Human NOV
PN US2004039
PD 25-EBB-20
PA (SMIT/) PA (SMIT/) PA (GUUJ/) PA
                                                                                                                                                                                                                                                                                                                                            Query Match:
RESULT 1461
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Local Si
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(GANG/)
(RIEG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROTH/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHIM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGEE/
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T 1470
ABB09590 standard; protein; 218 AA.
Deinagkistrodon acutus venom thrombin-like protein (218 residue variant).
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                                                                                                                                                                                                                                                                                                                                                                                                            ABB51196 standard; protein; 246 AA.
Human secreted protein encoded by gene 179 SEQ ID NO:1149.
WO200162891-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID ABM84665 standard; protein; 220 AA.

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4914.

PN WO2004023973-A2.

PD 25-MAR-2004.

PA (INCY-1 INCYTE CORP.

Best Local Similarity: 36.65% Mismatches: 82

Ouery Match: 19.60% Indels: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABO26933 standard; protein; 246 AA.
Protein associated with novel secreted protein gene 179
US6525174-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AABO8511 standard; protein; 230 AA.
Biosynthetic variant of protein C activator polypeptide.
WO200050612-A2.
                                                                                                                                                                                                                                                                                                                                                 110
      Ouery Match:
RESULT 1465.

DE A. Contortrix protein; 231 AA.

DE A. Contortrix protein C activator protein fragment.

PN W09842860-A1.

PD 01-OCT-1998.

PA (RPMS-) RPMS TECHNOLOGY LTD.

Best Local Similarity: 36.21% Mismatches: 94
94
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PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.

Best Local Similarity: 36.49% Mismatches:

March: 19.63% Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human secreted protein #179 fragment #1.
Mismatches:
                                                                                                                                                                                                                                                                                                                                                 Mismatches:
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                                                                                                                                                                                     Query Match:
RESULT 1466
ID AAW89041 standard; protein; 246 AA.
DE Polypeptide fragment encoded by gene 179.
PN W09884963-A2.
                                                                                                                                                                                                                                                                                                                                                                       Indels:
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AAR20557 standard; protein; 234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABO45453 standard; protein; 246 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 41.56*
19.68*
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Best Local Similarity: 41.56*
Ouery Match:
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PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 41.56%
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Query Match: 19.68%
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PA (F PA (F Best L Query N RESULT	P P P P P P P P P P P P P P P P P P P	Query N Query N RESULT	EO OO OO OO OO OO OO OO OO OO OO OO OO O	Query N Query N RESULT ID AT	00 P P P P P P P P P P P P P P P P P P	Best Lo Query N RESULT TD AT	3 A A A A	Best L Query N RESULT	A A A A	Best Lo Query N RESULT ID AB	DE PN	Best Lo Query N RESULT ID AI	PN	PA PA PBEST Quest RESOLETI	A DI DE P	PD 00 PA (4
105 4		109 4		109 4		109 4		65 53		101 4		100 5	ID NO:1150.	100 5		100 5
Mismatches: Indels:	AA.	Mismatches: Indels:	AA.	Mismatches: Indels:	AA.	Mismatches: Indels:	AA. rotein #1.	Mismatches: Indels:	AA. 186.	INST. Mismatches: Indels:	AA. gene 179.	Mismatches: Indels:	179 SEQ	Mismatches: Indels:	AA. 9 fragment #2.	Mismatches: Indels:
PN D54023097-A. PD 30-JAN-1992. PA (BADI) BASF AG. Best Local Similarity: 36.68% Query Match:	standard; protein; 255 in. 84-A. 988.	32.92%	ഗ	FA (FUUI) FULISAWA FRAKA CU DID. BEST LOCAL Similarity: 32.92% Query Match: 19.46% RESHIT 1476	69 standard; protein; 255 a batroxobin. 838-A1.	PA (BRIM) BRISTOL-MYERS SQUIBB CO. Best Local Similarity: 32.92% Query Match: 19.46%	AAE21441 standard; protein; 249 AA. Human trypsin domain consensus protein WG200225802-A2.	PA (MILL-) MILLENNIUM PHARM INC. Best Local Similarity: 40.32% Query Match: 19.43%	6 standard; protein; 231 bin, a snake venom prote: 267-A.	PD 40-MARA-1998. PA (MOKA-) MOKAM BIOTECHNOLOGY RES : Best Local Similarity: 34.21% Query Match: 19.36% PRENIT 1479	42 standard; protein; 228 ptide fragment encoded by 963-A2.	FD 10-DEC-1290. PA (HUMA-) HUMAN GENOME SCI INC. Best Local Similarity: 42.22% Query Match: 19.17%	ABB51197 standard; protein; 228 AA. Human secreted protein encoded by gene WO200162891-A2.	PD 30-AUG-2001. PA (HUMA-) HUMAN GENOWE SCI INC. Best Local Similarity: 42.22\$ Query Match: 19.17\$	ID AB045454 standard; protein; 228 AA. DE Novel human secreted protein #179 fragment PN US2003065160-A1.	PD 03-APR-2003. PA (HUMA-) HUMAN GENOME SCI INC. Best Local Similarity: 42.22\$ Query Match: 19.17\$

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T 1486
ABM82831 standard; protein; 233 AA.
Himan diagnostic and therapeutic pprotein SEQ ID NO:3080.
A02004023973-A2.
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8
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28
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14
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48
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                                                                        AAB11711 standard; protein; 264 AA.
Mouse serine protease BSSPS (mBSSPS) SEQ ID NO:4.
MO20001243-A1.
02-JUN-2000.
(FUSO ) FUSO PHARM IND LTD.
Local Similarity: 39.10% Mismatches:
                                                 Mismatches:
Indels:
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Indels:
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Indels:
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Indels:
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Indels:
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Fibrinogenolytic protein #3 from snake venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-2003.
(GEST ) GENSET SA.
(GEST ) GENSET SA.

18.93* Indels:
ULT 1488
ARG75785 standard, protein; 227 AA.
US2002165152-A1.
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                                                                                                                                                                                      ULT 1484
AAM52945 standard; protein; 236 AA.
Flaboxobin, a snake venom protease.
KR98002267-A.
30-MAR-1998.
(MOKA-) MOKAM BIOTECHNOLOGY RES INST.
Local Similarity: 36.25$
Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ULT 1489
ADES6223 standard; protein; 253 AA.
ADES6223 standard; protein; 253 AA.
Human Protein P00746, SEQ ID NO 4094.
WO2003016475-A2.
27-FEB-2003.
(GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
St Local Similarity: 38.49$ Misme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE39993 standard; protein; 253 AA.
Human adipsin protein #2.
US2003092620-A1.
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17 1490
AAP70758 standard; protein; 269 AA.
196200276-A.
06-JAN-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 1491
AAE39992 standard; protein; 253 AA.
Human adipsin protein #1.
US6525174-B1.
25-FEB-2003.
(HUMA-) HUMAN GENOME SCI INC.
È Local Similarity: 42.22%
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(INCY-) INCYTE CORP.
Local Similarity: 36.78*
18.97*
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(SANY ) SANKYO CO LTD.
Local Similarity: 38.55*
Match: 18.78*
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Mismatches: Indels:

37.41%

85 14

Mismatches: Indels:

40.19%

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RESULT 1500
ID ADE8221 standard; protein; 263 AA.
ID ADE8221 standard; protein; 263 AA.
DE Rat Protein AAB31922, SEQ ID NO 4092.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARE ) BAYER AG.
Best Local Similarity: 37.41$ Misma
   (HERM/) HERMANN K.
(PILA/) PILARSKY C
Local Similarity:
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RESULT
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Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580.
WO2004030615-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABM02830 standard; protein; 212 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:3079.
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM82644 standard; protein; 212 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2893.
25-MAR-2004.
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ADR66037 standard, protein; 213 AA.
Human prostatic carcinoma derived protein SEQ ID 233 #1
WO2004076614-A2.
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Human prostatic carcinoma derived DNA SEQ ID 233 #4.
WO2004076614-A2.
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56
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14
                                                                                                         ID AAB11710 standard; protein; 264 AA.

DE Human serine protease BSSP5 (hBSSP5) SEQ ID NO:2.

WO200031243-A1.

PD 02-JUN-2000.

PA (FUSO ) FUSO PHARM IND LTD.

Bast Local Similarity: 36.84* Mismatches:

Query Match:

IB.71* Indels:
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Human GENSET polypeptide clone name vCTRL-1.
WO2003014151-A2.
20-FEB-2003.
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Consensus sequence of trypsin-like domain.
WO2003031463-A2.
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(MILL-) MILLENNIUM PHARM INC.
Local Similarity: 39.05%
18.68%
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(GEST ) GENSET SA.
Local Similarity: 36.84%
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PD 25-WAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 36.33*
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(INCY-) INCYTE CORP.
Local Similarity: 36.33%
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15-APR-2004
(GETH) GENENTECH INC.
Local Similarity: 36.84%
PN US2003092620-A1.
PD 15-MAY-2003.
PA (GEST ) GENSET SA.
Best Local Similarity: 38.49%
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(DAHL/) DAHL E.
(ROSE), ROSENTHAL A.
(HERM/) HERMANN K.
(PILA/) PILARSKY C.
L LOCAL SIMILARITY: 400.
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(HINZ/) HINZMANN B.
(DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
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ID ADR6699
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PN W0200407
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PA (BHZL/)
PA (BAHL/)
PA (ROSE/)
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RESULT 1493
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-C-f-cgn2 1/05F0 spool py/0310015385/runat 05032005_173552_17285/app_query.fasta_1.1287
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-LOOPEXT=0 -UNITS=Eits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=Eits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=1500 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -AALIGN=15
-MODE-LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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; ORGANISM: Human
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

WUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Ni, et al.
TITLE OF INVENTION: Human Serine Protease and Serine FILE REFERENCE: PR391
CURRENT APPLICATION NUMBER: US/09/244,111
CURRENT FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 60/073,961
EARLIER PILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATCHIN Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                     Gaps:
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811.00
64.11%
64.11%
                                                                                                                                       TYPE: PRT
CRGANISM: Homo sapiens
US-09-244-111-6
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                             LENGTH: 162
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736 TGTGGGGGAGTCCTTCAAGGTCTGGTGTCTGGGGGTCTGTGGGGCCCTGTGGACAAGAT 795
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CCCTTTTCCCCCAGACTTTGGAAGTGACCCACCATGGGGCTCAGCATCTTTTTGCTCCTG 147
                                                                    -----TGTGTTCTTGGGCTCAGCCAGCCACCCAAGATTTTCAATGGCACT 198
                                                                                                                                            GAGTGTGGGCGTAACTCACAGCCGTGGCAGGGGGCTGTTTGAGGGCACCAGCCTGCGC 258
                                                                                                                                                                                                                   259 TGCGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGGGGCTCACTGCAGCGGCAGC 318
                                                                                                                                                                                                                                                                                           319 AGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCTCGACTGGACCGAGCAGATC 378
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18 LeuGlyGlyAlaTrpAlaGlyHisSerArgAlaGlnGluAspLysValLeuGlyGlyHis 37
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Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                    6 ProArgAlaAlaLysThrTrp-----
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Patent No. 6203979
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
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ZIP: 94304
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US-09-008-271A-7
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                                                                                           198 CysAlaGlySerSerLysGlyAlaAspThrCysGlnGlyAspSerGlyGlyProLeuVal
                                                          676 TGTGCAGGCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGGCCCCCTGGTG
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09070526
Patent No. 6100059
GENERAL INFORMATION:
APPLICANT: SOUTHAN, CHRISTOPHER
APPLICANT: CLINKENBEARD, HELEN
APPLICANT: BURGESS, NICOLA
TITLE OF INVENTION: No. 6100059e1 Compounds
NUMBER OF SEQUENCES: 4
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FastSEQ for Windows Version 2.0
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APPLICATION NUMBER: GB 9711952.3
FILING DATE: 9-JUN-1997
APPLICATION NUMBER: EP 97309646.4
FILING DATE: 1-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESITA, PAUL F
REGISTATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-30353
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,526
FILING DATE: 30-APR-1998
CLASSIFICATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
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INFORMATION FOR SEQ ID NO: 2:
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TYPE: amino acid
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TELEFAX: 610-407-0701
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57.98%
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ADDRESSEE: RATNER & F
STREET: P.O. BOX 980
CITY: VALLEY FORGE
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OPERATING SYSTEM:
SOFTWARE: FastSEQ
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Query Match:
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COUNTRY: US
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237 AspLysProGlyValTyrThrAsnIleCysArgTyrLeuAspTrpIleLysLysIleIle 256
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                                                                           676 TGTGCAGGCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTG
                                                        616 ATCGTCTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGGGGAGAATCACGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
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Conservative:
Mismatches:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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622.50
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48.99%
30.13%
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amino acid
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TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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STATE: CA
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Query Match:
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CysGlyGlyValLeuValGlyGlyAsnTrpValLeuThrAlaAlaHisCysLysLysPro 77
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESEQ for Windows Version 2.0
SOFTWARE: ISASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: «Unknown>
FILING DATE: «Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: 91,201
RELECOMMUNICATION INFORMATION:
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124
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLLGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLNNOT27
CLONE: 1798496
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                             TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 260 amino acids
                                                                                                                                                                                                                                                                                                        TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM
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57.69$
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Query Match:
DB:
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622.50
60.32%
48.99%
30.13%
; ORGANISM: Mus sp.; FEATURE: ; OTHER INFORMATION: At; CTHER INFORMATION: tc US-09-618-259-8
                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-205-258-427
                                                           Alignment Scores:
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                                         ATCTTTTTGCTCCTGTGTGTT-----CTTGGGCTCAGCCAGGCAGCCACCCGAAG 183
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ProCysGlyLysProGluLysProGlyValTyrThrLysIleCysArgTyrThrThrTrp
                                                   184 ATTITCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGCTGTTTGAG
                                                                                                                   GCCACCAGCCTGCGGGGGGGGGTCCTTATTGACCACAGGGGGTCCTCACAGCGGCT
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APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
FILE REFERENCE: D6020CIP2
CURRENT APPLICATION WUMBER: US/09/618,259
CURRENT FILING DATE: 2000-07-18
PRIOR FILING DATE: 1998-08-21
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 8
LENGTH: 260
                    US-10-015-385A-193 (1-1091) x US-09-025-059-3 (1-260)
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Patent No. 6642013
GENERAL INFORMATION:
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232 ProCysGlyLysProGluLysProGlyValTyrThrLysIleCysArgTyrThrThrTrp
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HisCysLysLysGlnLysTyrSerValArgLeuGlyAspHisSerLeuGlnSerArgAsp
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Amino acid sequence of mouse neuropsin homologous to TADG-14; accession no. D30785
                                                                                   260
121
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93
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                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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; Patent No. 6525174
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APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
                 TITLE OF INVENTION: 207 Human Secreted Protein FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT PILING DATE: 1998-06-04
EARLIER PILING DATE: 1998-06-04
EARLIER PELING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PELICATION NUMBER: 60/048,896
EARLIER PELICATION NUMBER: 60/048,876
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PPLICATION NUMBER: 60/048,964
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APPLICATION NUMBER: 60/048,895
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APPLICATION NUMBER: 60/048,900
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APPLICATION NUMBER: 60/048,970
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APPLICATION NUMBER: 60/048,875
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APPLICATION NUMBER: 60/048,917
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,962
FILING DATE: 1997-06-06
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PPLICATION NUMBER: 60/048,971
LING DATE: 1997-06-06
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PLICATION NUMBER: 60/048,899
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PLICATION NUMBER: 60/048,893
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LING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,883
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PPLICATION NUMBER: 60/048,884
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| CysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeu 102
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                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                         EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER APPLICATION NUMBER: 60/092,923
EARLIER PILING DATE: 1997-12-18
EARLIER PILING DATE: 1997-12-18
EARLIER PELING DATE: 1997-12-18
EARLIER PELING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
SOFTWARE: PARENTIN NUMBER: 60/094,657
SOFTWARE: PARENTIN PARE: 1998-07-30
SOFTWARE: PARENTIN VOY: 2.0
                 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,877
60/048,963
               90-90-1661
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62.25%
48.19%
29.94%
APPLICATION NUMBER:
                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-09-205-258-427
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Best Local Similarity:
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Pred. No.:
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                                                                                                    367 ACCGAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCC--- 423
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55 IleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLys 74
                                                   778 GGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGAC
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OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
OTHER INFORMATION: with homo sapien serine protease catalytic domain
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Matches:
Conservative:
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APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
TITLE OF INVENTION: Zymogen Activation System
FILE REPERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386, 642
CURRENT APPLICATION NUMBER: US/09/386, 642
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Artificial Sequence
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602.50
60.35%
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Percent Similarity:
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                     837
                                        CTCAGCATCTTTTTGCTCCTGTGTGTTTCTTGGGCTCAGCCAGGCAGCCACACAGAGATT 186
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|LeuGlnLeuIleLeuLeuAlaLeuAlaThrGlyLeuValGlyGlyGluThr---ArgIle
                     778 GGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGAC
                                                                                                                                                                                                                                     APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guedler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
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Mismatches:
Indels:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastERG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
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Matches:
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                                                                                                           242 TrpileGlnGluThrMetLysAsnAsn 250
                                                                                      838 TGGATCCGGATGATCATGAGGAACAAC 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF-0481 US
                                                                                                                                                                                     Sequence 1, Application US/09025059
Patent No. 6075136
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REPREBICE/DOCKET NUMBER: PF-04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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618.50
62.25%
48.19%
29.94%
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ADDRESSEE: Incyte Ph
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Best Local Similarity:
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CLONE: 2723646
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IMMEDIATE SOURCE:
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US-09-025-059-1
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Matches: Conservative: Mismatches: Indels:

Length:

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Description of Artificial Sequence: Fusion with homo sapien serine protease catalytic
                                                      1.62e-39
598.50
63.79%
49.14%
28.97%
) OTHER INFORMATION:
) OTHER INFORMATION:
US-09-386-642-14
                                                                                        Similarity:
                                                                           Percent Similarity;
Best Local Similarity
Query Match:
DB:
                                              Alignment Scores:
Pred. No.:
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US-08-944-483-24
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PheGlnGlyGlnGlnLeuLeuCysGlyGlyValLeuValGlyGlyAsnTrpValLeuThr
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                                                                  AAGATTTTCAATGGCACTGAGTGT - - - GGGCGTAACTCACAGCCGTGGCAGGTGGGGCTG
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LysileValGlyGlyTyrAsnCysLeuGluProHisSerGlnProTrpGlnAlaAlaLeu
                                                                                                           TTTGAGGCCACCAGCCTGCGGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACA
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APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
     Mismatches:
Indels:
Gaps:
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Patent No. 6420157
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
     51.10%
29.16%
     Similarity:
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US-09-386-642-14
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Patent No. 6232456
GENERAL INFORMATION:
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: ERIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WOLDIKE, Helle Fabricius
APPLICANT: KJELDSEN, Thomas Borgium
TITLE OF INVENTION: A Process For Producing Trypsin
TITLE OF INVENTION: (Trypsinogen)
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 59453280 No. 5945328th America, Inc.
541 CACGICTCAGGCTGGGGCAICACCAACCACGCACGGAACCCAIICCCGGAICIGCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        778 GGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGAC
                                                           481 ACCAGCAGCGTTCAACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGC
                                                                                                                                                                                                                          501 TGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGCCATGGTGTATCCCGGGAGAATC
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FastSEQ for Windows Version 2.0
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NAME: Rozek, Carcl
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 4500.204-US
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-9555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,267A
FILING DATE: 22-OCT-1997
CLASSIFICATION: 435
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Patent No. 5945128
GENERAL INFORMATION:
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MEDIUM TYPE: Diskette
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                                      TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
UNMER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 TTCAATGGCACTGAGTGTGGGGCGTAACTCACAGCCGTGGCAGGTGGGGGCTGTTTGAGGGC 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 CysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeu 100
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                             ZIP: 60064.3500
COMPUTER REAABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                            ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
    KENT D.
STEVEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
-LENGTH: 248 amino acids
TYPE: amino acid
STRANDEDNESS: single
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597.50
62.25%
47.79%
28.92%
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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    STEWART, 1
STROUPE, 8
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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ORGANISM: Human
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION:
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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Search completed: March 5, 2005, 23:08:24 Job time : 54 secs

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trypsin (EC 3.4.21.4) I precursor, pancreatic - chicken N.Alternate names: trypsinogen I C.Species: Gallus gallus (chicken) (chores: Gallus gallus (chicken) (chores: 28-oct-1996 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004 (choresion: 555067; 57345; 555065; 572346; 571155 R;Wang, K.; Gan, L.; Lee, I.; Hood, L. Biochem. J. 307, 471-479, 1995 A;Title: Isolation and characterization of the chicken trypsinogen gene family. A;Reference number: S55065; MUID:95251611; PMID:7733885
                         --CAGGCAGCCACA 177
                                                                              178 CCGAAGATTTTCAATGGCACTGAGTGTGGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTG 237
                                                                                                                                   238 TITGAGGCACCAGCCTGCGCGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACA 297
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                                        :::|||||||::||||
4 LeuPheLeuIleLeuSerCysLeuGlyAlaAlaValAlaPheProGlyGlyAlaAspAsp 23
                                                                                                         43
                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-248 <WAN1>
A;Residues: 1-248 <WAN1>
A;Cross-references: UNIPROT:Q90627; UNIPROT:Q90628; EMBL:U15156; NID:g603904
A;Experimental source: clone 1-P38
A;Rycession: S72345
A;Molecule type: DNA
                                                                                                                                                                                                                                              358 CTCGACTGGACCGAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCCATCCCGGCTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                            GINCYSLeuAsnAlaProileLeuSerAspGlnGluCysGlnGluAlaTyrProGlyAsp
                                                                                                 24 AspLysileValGlyGlyTyrThrCysProGluHisSerValProTyrGlnValSerLeu
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                         133 ATCTTTTGCTCCTGTGTGTTCTTGGGCTCAGC---
US-10-015-385A-193 (1-1091) x S55066 (1-248)
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                                                                                                                                                                CACGTCTCAGGCTGGGGCATCACCAACCACGCACGGAACCCATTCCCGGATCTGCTCCAG
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232 ProCysGlyLysProGluLysProGlyValTyrThrLysIleCysArgTyrThrTrp
               GlnProGluGlnGluIleGlnValAlaGlnSerIleGlnHisProCysTyrAsnAsnSer
                                                    124 TCG---ACGAGCCACGAGCACGACCTCCGGCTGCGGCTGCGCCTGCCCCTTCCGCGTA
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3 64 TGGACCGAGCAGATCCGGCACAGCGCGTTCTCTGTGACCCATCCCGGCTACCTGGGAGCC
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A; Residues: 1-248 cWAN2>
A; Experimental source: clone 1-P38
A; Experimental source: clone 1-P38
A; Molecule type: mRNA
A; Residues: 1-9, 'V, '11-12, 'T', 14-102, 'A', 104-214, 'I', 216-248 cWAN3>
A; Cross-references: EMBL:U15155; NID:g603902; PIDN:AAA79912.1; PID:g603903
A; Experimental source: clone P1
A; Accession: S72346
A; Molecule type: DN
A; Residues: 1-9, 'V, '11-12, 'T', 14-102, 'A', 104-214, 'I', 216-248 cWAN4>
A; Residues: 1-9, 'V, '11-12, 'T', 14-102, 'A', 104-214, 'I', 216-248 cWAN4>
A; Residues: 1-9, 'V, 'II-12, 'T', '14-102, 'A', '104-214, 'I', '216-248 cWAN4>
A; Residues: 1-9, 'V, 'II-12, 'T', '14-102, 'A', '104-214, 'I', '216-248 cWAN4>
A; Residues: 1-9, 'V, 'II-12, 'T', '14-102, 'A', '104-214, 'I', '216-248 cWAN4>
A; Residues: 1-9, 'V, 'II-12, 'T', 'II-12, 'A', 'II-12,
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A/Cross-references: U.H.; Neurath, H.; Walsh, K.A.

Biochemistry 12, 3146-313, 1973

A/Title: Determination of the amino acid sequence of porcine trypsin by sequenator analys A/Accession: A90368; MUID:73258692; PMID:4738933

A/Title: Determination of the amino acid sequence of porcine trypsin by sequenator analys A/Accession: A90368

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N;Contains: trypsinogen
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A90641, A90369, A00947
R;Charles, M; Rovery, M.; Guidoni, A.; Desnuelle, P.
Biochim. Biophys. Acta 69, 115-129, 1963
A;Title: Su le trypsinogene et la trypsine de porc.
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361 GACTGGACCGAGCAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGA 420

us-10-015-385a-193.n2p.rpr.spdi

197 TTOANTEGACTOAGGTUTAGGCCTAAACTCAAGGCGTGCACAGGTGGGTCTAAGGCGCTAAGGCGTAAGGCGCTAAGGCGCTAAGGCGCTAAGGCGCGCGC	Alignment Scores: 3.61e-29 Length: 253
6 GludiyAanGludiphelieAanBlaAlayellellelThTHisProAssPheAanGludiphelieAanGlaAyellellelThTHisProAssPheAanGludiphelieAanGarcaccccccccccccccccccccccccccccccccc	Db 3 PheLeuLeuCysValleuLeuGlyAlaAlaAlaAlaPheAspAspAspIysIle 21

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A;Cross-references: UNIPROT:P07146; GB:X04574; NID:g54918; PIDN:CAA28243.1; PID:g54919 C;Superfamily: trypsin; trypsin homology
C;Superfamily: trypsin; trypsin homology
C;Reywords: calcium binding; hydrolase; protein digestion; serine proteinase
F;1-23/Domain: signal sequence #status predicted <SIG>F;24-246/Product: trypsin #status predicted <MAT>F;24-239/Domain: trypsin homology <TRX>F;24-239/Domain: trypsin homology <TRX>F;0-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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AspLeuLeuGlnCysValAspAlaProValLeuProGlnAlaAspCysGluAlaSerTyr 175
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TyrThrGlnValCysLysPheThrLysTrpIleAsnAspThrMetLysLysHis 252
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Liypsin (EC 3.4.21.4) precursor - mouse
Liypsin (EC 3.4.21.4) precursor - mouse
Liypsin (EC 3.4.21.4) precursor - mouse)
C;psecies: Mus musculus (house mouse)
C;pate: 30-Jun-1988 #text_change 0;
C;Accession: B2528
R;Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res: 14, 8307-8330, 1986
A;Title: Sequence organisation and transcriptional regulation of 1
A;Reference number: A93646; MUID:87066713; PMID:3641189
A;Recession: B2528
A;Molecule type: mRNA
A;Residues: 1-246 <STE>
                                                                                                                     ATGGGGCTCAGCATCTTTTGCTCCTGTGTGTTCTTGGGCTCAGC
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   Matches:
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C:Species: Bos primigenius taurus (cattle)
C:Species: Bos primigenius taurus (cattle)
C:Species: Bos primigenius taurus (cattle)
C:Species: Bos primigenius taurus
C:Species: Bos primigenius taurus
C;Accession: 813813
R;1e Huercu, I:; Wicker, C.; Guilloteau, P.; Toullec, R.; Puigserver, A.
Exidement 193, 767-773, 1990
A;Title: Isolation and nucleotide sequence of cDNA clone for bovine pancreatic anionic transpaces on Si3813
A;Reference number: S13813; MUID: 91065383; PMID: 1701147
A;Residues: 1-247
A;Molecule type: mRNA
A;Cross-references: UNIPROT: 029463; EMBL:X54703; NID: 9829; PIDN: CAA38513.1; PID: 9830
C;Superfamily: trypsin; trypsin homology
C;Superfamily: trypsin homology
C;Superfamil: trypsin homology
C;Superfamil: trypsin homology cTRY>
F;63,107,200/Active site: His, Asp, Ser #status predicted
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                                   CACGICICAGGCIGGGCCAICACCAACCACCCACGGAACCCAITCCCCGGAICTGCTCCAG
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ACCAGCAGCGTTCAACCCCTGCCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGC
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221 TrplleLysGlnThrlleAlaSerAsn 229
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A; Note: the sequence agrees with that shown
R; Bode, w; Schwager, P.
J. Mol. Biol. 98, 693-717, 1975
A; Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom resolution
A; Note: the sequence agrees with that shown
R; Bode, w; Schwager, P.
J. Mol. Biol. 98, 693-717, 1975
A; Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom resolution
A; Reference number: A9254; WIDD: 76072097; PMID: 512
A; Contents: annotation; X-ray crystallography; binding sites for calcium, substrate, and
C; Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.
C; Comment: Atroacatalytic cleavage after Lys-6 leads to beta-trypsin by releasing a termis specudotrypsin, trypsin homology
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin promology agestion; serine proteinase; zymogen
F; 1-229/Product: trypsin opeptide #status experimental <APT>
F; -7.222/Domain: activation peptide #status experimental <APT>
F; -7.131, 132-229/Product: alpha-trypsin #status experimental
F; -7.131, 132-229/Product: His, Asp, Ser #status experimental
F; -7.132/Cleavage site: Lys-16 autolytic) #status experimental
F; -7.132/Cleavage site: Lys-Ser (autolytic) #status experimental
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                                      trypsin (EC 3.4.21.4) precursor - bovine
N;Contains: trypsinogen
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: A90164; A00946; S08774
R;Mikes, O.; Holeysovsky, V.; Tomasek, V.; Sorm, F.
Biochem. Biophys. Res. Commun. 24, 346-352, 1966
A;Title: Covalent structure of Bovine trypsinogen. The position of the remain A;Reference number: A90164; MUD:67168848; PMID:5967094
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                                                                                                                                                                                                                                                                                                                                                                                                                  <MIK>
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B, Hilos. Trans R. Soc. Lond. B257, 77-87, 1970
A; Reference number: A93755
A; Contents: annotation; revisions
B; Titani, K.; Exicsson, L.H.; Neurath, H.; Walsh, K.A.
B; Titani, K.; Exicsson, L.H.; Neurath, H.; Walsh, K.A.
A; Title: Amino acid sequence of dogfish trypsin.
A; Reference number: A00950; MUID: 75146445; PMID: 1092332
A; Contents: annotation; revisions
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anionic

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trypsin (EC 3.4.21.4) precursor, cationic - dog
N;Alternate names: cationic trypsinogen
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: B26273
R;Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. S, 2669-2676, 1985
A;Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA sequer
A;Reference number: A26273; MUID:86284628; PMID:3841794
A;Accession: B26273
A;Molecule type: mRNA
A;Residues: 1-246 <PIN>
A;Cross-references: UNIPROT:P06871; GB:M11590; NID:g164096; PIDN:AAA30900.1; PID:g164097
C;Superfamily: trypsin; trypsin homology
C;Reywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
F;24-246/Product: trypsin, cationic #status predicted <NZ>
F;24-236/Domain: trypsin homology <TRX>
F;24-236/Product: trypsin, cationic #status predicted <NZ>
F;24-236/Domain: trypsin homology <TRX>
F;24-246/Froduct: trypsin homology <TRX>
F;24-246/Froduct: trypsin homology <TRX>
F;24-236/Domain: trypsin homology <TRX>
F;24-236/Domain: trypsin homology <TRX>
F;24-236/Froduct: trypsin homology <TRX>
F;24-236/Froduct: trypsin homology <TRX>
F;24-236/Froduct: trypsin homology <TRX>
F;24-246/Froduct: trypsin homology <TRX>
F;24-246/Froduct: trypsin homology <TRX>
F;24-246/Froduct: tryp
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121 AlaArgValAlaThrIleSerLeuProArgAlaCysAlaAlaProGlyThrGlnCysLeu 140
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A;Accession: A26273
A;Molecule type: mANA
A;Molecule type: mANA
A;Residues: 1-247 «PIN»
A;Cross-references: UNIPROT:P06872; GB:MII589; NID:gl64094; PIDN:AAA30899.1; PID:gl64095
A;Cross-references: UNIPROT:P06872; GB:MII589; NID:gl64094; PIDN:AAA30899.1; PID:gl64095
C;Superfamily: trypsin; trypsin; pancreas; protein digestion; serine proteinase; zymogen
F1-15/Domain: signal sequence #status predicted «APT»
F16-23/Domain: signal sequence #status predicted «APT»
F14-247/Product: trypsin, anionic #status predicted «APT»
F14-237/Domain: signal sequence *RS/Diguilfide bonds: #status predicted
F13-233,139-206,171-185/Diguilfide bonds: #status predicted
F13-160,48-64,132-233,139-206,171-185/Diguilfide bonds: #status predicted
F131,107,200/Active site: His, Asp, Ser #status predicted
F175,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trypsin (EC 3.4.21.4) precursor, anionic - dog
NyAlternate names: cationic trypsingen
C;Species Canis lupus familiaris (dog)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: A26273
C;Accession: A26273
Mol. Cell. Biol. 5, 2669-2676, 1985
Mol. Cell. Biol. 5, 2669-2676, 1985
A;Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA seque
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #te
C;Accession 375547
R;Fletcher, T.S.; Alhadeff, M.; Craik, C.S.; Largman,
Biochemistry 26, 3081-3086, 1987
                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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|ValSerTrpIleGlnGlnThrIleAlaAlaAsn 246
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F;63,107,200/Active site: His, Asp, F;75,77,80,85/Binding site: calcium
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A,Title: Isolation and characterization of a cDNA encoding rat cationic trypsinogen. A,Reference number: A27547; MUID:87271609; PMID:3607011
A,Accession: A27547
A,Accession: A27547
A,MOJecule type: mRNA
A,Residues: 1-247 <FLIS
A,COSS-references: UNIPROT:P08426; GB:M16624; NID:9206498; PIDN:AA41985.1; PID:9206499
C,Superfamily: trypsin homology
C,Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
F;25-240/Domain: trypsin homology <TRY>
F;25-240/Domain: trypsin homology <TRY>
F;31-161,49-65,133-234,140-207,172-186/Disulfide bonds: #status predicted
F;64,108,201/Active site: His, Asp, Ser #status predicted
F;64,08,801/86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                             1.79e-28
544.50
60.32%
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26.36%
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Best Local Similarity:
Query Match:
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trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)
C;Species: Salmo salar (Atlantic salmon)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S66657; S31779
RMale, R.; Lorens, J.B.; Smalas, A.O.; Torrissen, K.R.
Eur. J. Biochem. 232, 677-685, 1995
A;Title: Molecular cloning and characterization of anionic and cationic variants of tryps
A;Reference number: S66657; MuID:96035908; PMID:7556223
A;Accession: S66657
A;Accession: S66657
A;Residues: 1-238 «AMA.
A;Residues: 1-238 «AMA.
A;Residues: 1-238 «AMA.
A;Coss-references: UNIPROT:P35033; EMBL:X70074; NID:g64387; PIDN:CAA49679.1; PID:g64388
C;Superfamily: trypsin; trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-7/Domain: signal sequence (fragment) #status predicted «SIG»
F;8-15/Domain: signal sequence (fragment)
F;8-15/Domain: crypsin III #status predicted «APT»
F;6-238/Product: trypsin/ovv. *TRY».
C;231/Product: trypsin/ovv. *TRY».
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;16-231/Domain: trypšin homology <TRY>
F;22-152,40-56,124-225,131-198,163-177,188-212/Disulfide bonds: #status predicted
F;55,99,192/Active site: His, Asp, Ser #status predicted
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|TrpGlyTyr-----GlyCysAlaLeuProAspAsnProGlyValTyrThrLysValCys 233
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588
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                                                                                                                                                                GATCTGCTCCAGTGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGCCATGGTGTGTAT
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Conservative:
Mismatches:
Indels:
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                                                                                     trypsin (EC 3.4.21.4) I precursor - rat

NyAlternate names: trypsingen I
C'Species: Rattus norvegicus (Norway rat)
C'Species: Rattus norvegicus (Norway rat)
C'Bate: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004
C'Accession: B22657; A00948
R'Craik, C.S.: Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984
A;Title: Structure of two related rat pancreatic trypsin genes.
A;Reference number: A22657; MUID: 85054880; PMID: 6094547
A;Recession: B22657
A;Molecule type: DNA
A;Recission: B22657
A;Molecule type: DNA
A;Residues: 1-246 < CRAS
A;Cross-references: UNIPROT: P00762; GB: J00778; NID: 9206507; PIDN: AAA98518.1; PID: 9206508
A;Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17
B;MacDonald, R.J.; Starty, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982
A;Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of A;Reference number: A00948; MUID: 82265624; PMID: 6896710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aintrons: 14/1; 67/2; 152/1; 197/3
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin; predicted <SIG>
F; 1-15/Domain: activation peptide #status predicted <APT>
F; 24-36/Product: trypsin I #status predicted <APT>
F; 24-39/Domain: trypsin nomology <TRX>
F; 30-160, 48-64,132-233, 139-206, 171-185/Disulfide bonds: #status predicted
F; 63,107,200/Active site: His, Asp, Ser #status predicted
F; 77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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21 AspAspLys1leValGlyGlyTyrThrCysProGluHisSerValProTyrGlnValSer
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76
7
       TyrValAsnTrpIleGlnGlnThrValAlaAlaAsn 247
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Mismatches:
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543.00
63.56%
44.53%
26.28%
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A; Residues: 1-246 < MAC>
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Best Local Similarity:
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| ValLeuGluGlyGlyGlyGlnPheIleAspAlaGluLysIleIleArgHisProGluTyr 100
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                 175 ACACCGAAGATTTTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGG
                                         AGAATCACGAGCAACATGGTGTGTGCAGGCGCGTCCCG---GGGCAGGATGCCTGCCAG
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LeuSerTrpIleGlnGluThrMetAlaAsnAsn 247
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C, Species: Ratture norvegicus (Norway rat)
C, Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C, Accession: S05494
R; Luetcke, H.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.F.
Nucleic Acids Res. 17, 6736, 1989
A; Title: A fourth trypsinogen (P23) in the rat pancreas induced by CCK.
A; Reference number: S05494; MUID: 89386010; PMID: 2780302
A; Reference number: S05494; MUID: 89386010; PMID: 2780302
A; Rocession: S05494
A; Molecule trype: mRNA
A; Residues: 1-247 < LUEA
A; Residues: 1-247 < LUEA
A; Residues: 1-247 < LUEA
C; Superfamily: trypsin, trypsin, homology
C; Keywords: calcium binding; hydrolase; protein digestion; serine proteinase; zymogen
F; 1-15, Domain: aignal sequence #status predicted < APT>
F; 24-247/Product: trypsin IV #status predicted < APT>
F; 24-247/Product: trypsin homology < TRY>
F; 24-240/Domain: attivation peptide #status predicted < APT>
F; 24-240/Domain: trypsin homology < TRY>
F; 24-240/Domain: trypsi
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0FRY3_CHICK
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Compugen Ltd
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STRAIN-CSTBL/GJ; TISSUE=Tongue;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
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MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
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Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasakin N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matumnoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system=384-format
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male tongue cDNA, RIKEN full-length enriched
11brary, clone:221008B01 product:similar to KALLIKKEIN 12 (EC
3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (KLK-L5) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/61; TISSUE=Tongue;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                                                                                                        234 AA
PRT;
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                              musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                  Name=Klk12;
Mus musculu
       841
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                                                                                                                                                     09CV76
                                                                                                  RESULT 2

OGCV76

OGCV
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219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 CCGTGGCAGGTGGGGCTGTTTGAGGGCACCAGCCTGCGCTGCGGGGGTGTCCTTATTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

--- SIMILANITY: Belongs to peptidase family S1.

EMBL, AK002217; BAB26143.1; ---
HSSP, P00760; LEZX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 CACAGGTGGGTCCTCACAGCGGCTCACTGCAGCGGCAGCAGGTACTGGGTGCGCCTGGGG
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                                                                                                                                                                                                                      MEDOPES'S COLOURS.

MEDOPES'S COLOURS.

MEDOPES'S COLOURS.

GO; GO:0004263; F: Chymotrypain activity; IEA.
GO; GO:0004293; F: Chypsin activity; IEA.
GO; GO:0006295; F: Crypsin activity; IEA.
GO; GO:0006508; P: Protecolysis and peptidolysis; IEA.
INTERPRO! IPRO01314; Peptidase S1.
INTERPRO: IPRO01314; Peptidase S1.
INTERPRO: IPRO01314; Peptidase S1.
INTERPRO: IPRO01303; Peptidase S1.
PRONITS; PRO0122; CHYMOTRYPSIN.
SMART; SM00022; CHYMOTRYPSIN.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
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166
27
41
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Matches:
Conservative:
Mismatches:
Indels:
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952.50
82.13%
70.64%
46.10%
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819
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060259, Q9HCB3; Q9UIL9; Q9UQ47;

15-JUL-1999 (Rel. 38, Last sequence update)

15-JUL-1999 (Rel. 38, Last sequence update)

25-JUL-1999 (Rel. 34, Last sequence update)

25-JUL-1999 (Rel. 34, Last sequence update)

POUTO-2004 (Rel. 45, Last sequence update)

POUTO-2004 (Rel. 34, Last sequence update)

POUTO-2004 (Rel. 34, Last sequence update)

POUTO-2004 (Rel. 34, Last sequence update)

POUTO-2004 (Rel. 38, Last sequence update)
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"Cloning of tumor-associated differentially expressed gene-14, a novel
serine protease overexpressed by ovarian carcinoma.";
Cancer Res. 59:4435-4439(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE-99203457; PubMed=10102990;
Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
"A novel form of human neuropsin, a brain-related serine protease, is
qenerated by alternative splicing and is expressed preferentially in
human adult brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Clark H.F., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98372070; Pubmed-9714609; DOI=10.1016/S0378-1119(98)00232-7; Yoshida S., Taniguchi M., Hirata A., Shiosaka S.; "Sequence analysis and expression of human neuropsin cDNA and gene."; Gene 213:9-16(1998).
GATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGAGTCCTTCAAGGTCTG
                                                                                                                                                                           GTGTCCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCTAT
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [4] SEQUENCE FROM N.A. (ISOPORM 1).
SEQUENCE FROM N.A. (ISOPORM 1).
Gan L., Gelinas R., Gown A.M., Moss P., Smith R., Wang K.;
Wolecular cloning and characterization of a novel serine prote "Wolecular cloning and characterization of a novel serine prote ovasin, a potential molecular marker for ovarian carcinomas.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                            820 ATTIGCAAGTAIGIGGACTGGAICCGGAIGAICAIGAGGAACAAC 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99413504; PubMed=10485494;
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KLK8 HUMAN

KLK8 HUMAN

TIS-JUL-

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,

Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,

Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,

Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,

Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,

Olsen A.S., Carrano A.V.;

Sequence analysis of chromosome 19q13.4.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wisand D., Woods K., Xie M.-H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P., Gray A.;
The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mann; 0203413; F.serine-type peptidase activity; TAS. GO; GO:0008236; F.serine-type peptidase activity; TAS. GO; GO:0007399; P:neurogenesis; TAS. InterPro; IPR001031; Peptidase S1. InterPro; IPR001254; Peptidase S1. InterPro; IPR001314; Peptidase S1A. Pfam; PR00089; TYPB$*in, 1. PR10815; PR00722; CHYMOTRYPSIN. PROSITE; PS50240; TRYPEIN DOM; 1. PROSITE; PS00134; TRYPEIN HIS; I. PROSITE; PS001134; TRYPEIN HIS; I. Alternative splicing; GlyCoprotein; Hydrolase; Serine protease; Alternative splicing; GlyCoprotein; Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isoid=060259-2; Sequence=VSP 005401;
TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in pancreas while isoform 2 is expressed in adult brain and hippocampus Both forms are also found in fetal brain and placenta. Not detected in kidney, spleen, liver and lung. SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=O60259-1; Sequence=Displayed;
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                                                                                                                                                                                                    Genome Res. 13:2265-2270(2003).
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EMBL; AB012761; BAA28676.1; -.
EMBL; AB010780; BAA88684.1; -.
EMBL; AB008390; BAA82665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; APOSS982; ADDS6080.1;
EMBL; APOSS42; AADZ5879.1;
EMBL; APO95743; AADZ9579.1;
EMBL; APO95743; AADZ9574.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP243527; AAG33361.1;
EMBL; AX359036; AAG83356.1;
EMBL; AC01473; AAG23254.1;
HSSP; P00760; 1F77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew; HGNC:6369; KLK8.
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Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Rianner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Sacres M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A., Gubbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Hale S., Garcia A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

""Generation and initial analysis of more than 15,000 full-length human
                                                  736 TGTGGGGGAGTCCTTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGGCCCTGTGGACAAGAT 795
                 218 CysAspGlyAlaLeuGlnGlyIleThrSerTrpGlySer---AspProCysGlyArgSer
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
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125
26
                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Kallikreln 8, isoform 1 preproprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sci. U.S.A. 99:16899-16903(2002)
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V; EF5934EB96295660
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Matches:
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SMART; SMO0202; TYP, SPS. 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN LHS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN SRR; 1.
Hydrolae; Procease; Serine procease.
SEQUENCE 260 AA; 28090 MW; EF5934EB96
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58.08%
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                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                               Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
By similarity.
By similarity.
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By similarity.
By similarity.
By similarity.
A -> AACGELDIATITY.
A -> AACGELDIATITY.
WENSTEPPAA (11 isoform 2).
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|IlePheProGlnLysLysCysGluAspAlaTyrProGlyGlnIleThrAspGlyMetVal
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EF439E5B8C83E660 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
                           similarity.
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By similar
Neuropsin.
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632.50
58.08%
48.08%
30.61%
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Best Local Similarity:
Query Match:
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Signal; Zymogen
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15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
protease 1).
Name-KLk8; Synonyms-Bspl, Nrpn, Prss19;
Rattus norvegicus (Rat).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia: Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
  96
13
  Mismatches:
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                      Indels:
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                                      Gaps:
                                                                             US-10-015-385A-193 (1-1091) x Q8IW69 (1-260)
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6 ProArgAlaAlaLysThrTrp
  48.08%
30.47%
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[1]
  Best Local Similarity:
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NRPN RAT
AC 088780;
DT 15-JUL-199
DT 25-OCT-200
DE Neuropsin
DE protease 1
DE Name=Klk8;
GN Name=Klk8;
CC Eukaryota;
CC Eukaryota;
CC Mammalia;
CX NCBI_TAXIB_RN [1]
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ProfrpglnfhrAlaLeuPheGlnGlyGluArgLeuValCysGlyGlyValLeuValGly
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similarity).
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Pfam, PF00089; Trypsin, 1.
SMART; SM00029; Trypsin, 1.
PROSITE; PS50240; TryPsin DOM; 1.
PROSITE; PS50134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Glycoptcein; Hydrolase; Serine protease; Signal; Zymogen.
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By similarity.
Neuropsin.
Charge relay system (By sim: Charge relay system (By sim: Charge relay system (By sim: Charge relay system (By sim: By similarity.
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Matches:
Conservative:
Mismatches:
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InterPro; IPR001254; Peptidase SI.
InterPro; IPR001314; Peptidase SIA.
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ005641; CAA06643.1; -.
HSSP; Q61955; INPM.
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Best Local Similarity:
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Pred. No.:
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                             65 AspArgTrpValLeuThrAlaAlaHisCysLysLysAspLysTyrSerValArgLeuGly
                                                                                                                                                                        GAACACACCCTCAGCCAGCTCCACTGGACCGAGCAGATCCGGCACAGCGGCTTCTCTGTG
                                                                                                                                                    400 ACCCATCCCGGCTACCTGGGAGCCTCG---ACGAGCCACGAGCACGACCTCCGGCTGCTG
                                                                                                                                                                                                                           CGGCTGCGCCTGCCCGTCCGCGTAACCAGCGTTCAACCCCTGCCCTGCCCAATGAC
                                                                                                                                                                                                                                                                                                       577 AACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BALB/c; TISSUE-Hippocampus;
MEDLINE-95548817; PubMed=762137;
Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
"Expression and activity-dependent changes of a novel limbic-serine
procease gene in the hippocampus.";
UNEUROSCI. 15:5088-5097(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Czech II; TISSUE-Mammary gland;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8)
Mame=KIK8, Synonyms=Nrpn, Prss19;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         817 TATATTTGCAAGTATGTGGACTGGATCCGGATGATCATG 855
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244 LysIleCysArgTyrThrAsnTrpIleLysLysThrMet 256
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jozdan H., Moore T., Max S.I., Wang J., Hsialeh F.,
Diatchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,
Rabal S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan F.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Roberzation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
ENZYME REGULATION: Strongly inhibited by diisopropyl
fluorophosphate, leupeptin and (4-amidinophenyl)methanesulfonyl 1-
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J. Biol. Chem. 274-4220-4224 (1999).
-!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
hippocampal plasticity. Has a strong proteolytic activity against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/C; TISSUE=Brain; MEDI=10.1074/jbc.273.18.11189; MEDLINE=9822502; Pubmed=9556608; DOI=10.1074/jbc.273.18.11189; Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K., Shiosaka T., Midorikawa K., Kamachi T., Kawabe A., Shiosaka S.; "Characterization of recombinant and brain neuropsin, a plasticity-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
Shiosaka S., Hakoshima T.,
"Crystal structure of neuropsin, a hippocampal protease involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   system
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-!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISSUE=Hippocampus;
MEDLINE=99134351; PubMed=9933620; DOI=10.1074/jbc.274.7.4220;
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TISSUE SPECIFICITY: Expressed specifically in the limbic mouse brain and is localized at highest concentration in neurons of the hippocampal CAI-3 subfields.

MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              related serine protease.";
J. Biol. Chem. 273:11189-11196(1998).
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MGD; MGI:892018; KIK8.
InterPro; IPR009003; Pept Ser Cys.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1.
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PDB; INPM; X-ray; A/B=33-256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
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33 IleLeuGludiyArgGluCysIleProHisSerGlnProTrpGlnAlaAlaLeuPheGln

ATTITCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCGCTTTGAG

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CACTGCAGCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACACAGCCTCAGCCTCGAC 363

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124 TCG----ACGAGCCACGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTA

152 600 9

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Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
                                                                                                                                                                    similarity).
similarity).
similarity).
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Matches:
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SIGNAL 1 28
PROPEP 29 32
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541 CACGTCTCAGGCTGGGGCATCACCACCCCCCCGGAACCCATTCCCGGATCTGCTCCAG

181 ACCAGCAGCGTTCAACCCCTGCCCCAATGACTGTGCAACGGCTGGCACCGAGTGC

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                                         ||| ::: ||| ||| ||| CysalagluvalLysileTyrSerGlnAsnLysCysGluArgAlaTyrProGlyLysIle
                                                                                                                                                                                     GGGGCCCCCTGGTGTGTGGGGGAGTCCTTCAAGGTCTGGGTGTCCTGGGGGTCTGTGGGG
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232 ProCysGlyLysProGluLysProGlyValTyrThrLysIleCysArgTyrThrThr
TGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGCCATGGTGTATCCCCGGGAGAATC
                                                                                                                                                   CCCTGTGGGACAAGATGGCATCCCTGGAGTCTACACCTATATTTGCAAGTATGTGGACTGG
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MEDLINE=98438738; PubMed=9765601; DOI=10.1016/S0167-4781(98)00116-X;
Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;
"cDNA cloning and expression of a novel serine protease, TLSP.";
biochim. Biophys. Acta 1399:225-228(1998).
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16-COT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
25-CCT-2004 (Rel. 40, Last annotation update)
25-CCT-2004 (Re
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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ATCTTTTGCTCCTGTGTGTT-----CTTGGGCTCAGCCAGGCAGCACCACAAG 183

US-10-015-385A-193 (1-1091) x NRPN_MOUSE (1-260)

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PROGRESSION REPORT AND LONG CONTROL NO. 1 (1500 PM) LONG CONTROL NO. 1 (15
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalan D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.S., Sohners R.M., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Robertain and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                               ISOId=Q9UBX7-2; Sequence=VSP 005402; TISSUE SPECIFICITY: Expressed In brain, skin and prostate. Isoform 1 is expressed preferentially in brain; isoform 2 in prostate. SIMICARITY: Belongs to the peptidase SI family. Kallikrein
                                                                                                                                                                                                 and mouse cDNA sequences.";

Proc. Natl. Acad. SG1. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Possible multifunctional protease. Efficiently cleaves
bz-Phe-Arg-4-methylcoumaryl-7-amide, a kallikrein substrate, and
wakly cleaves other substrates for kallikrein and trypsin.
-!- SUBCELULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
By similarity.
N-linked (GlCNAc. . .) (Potential).
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PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB012917; BAA33404.1; ALT_INIT.
EMBL; AB013730; BAA88713.1; --
EMBL; AF164623; BAA88713.1; --
EMBL; AF164623; AAD47815.1; --
EMBL; AF243527; AAG33364.1; --
EMBL; AF243527; AAG33364.1; --
EMBL; AF243527; AAG33257.1; --
EMBL; AC011473; AAG23257.1; --
EMBL; BC022068; AAH22068.1; --
HSSP; P007060; LEZX.
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MIM; 604434; -.
GO; GO:0008236; F:serine-type peptidase activity; TAS.
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InterPro; IPR001254; Peptidase SI.
InterPro; IPR001314; Peptidase SIA.
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PRINTS; PR00722; CHYMOTRYPSIN.
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Genew; HGNC:6359; KLK11.
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N-linked (GlcNAc. ..) (Potential).
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N-linked (GlcNAc. ..) (Potential).
M -> MQRIRWILNDWKSSGRGIJAAKEPGARSSPLQAM
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Matches:
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Mismatches:
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                                                                                                                                                                                                     MEDINE=21094033; PubMed=11177570; DOI=10.1089/104454900750058080; Olsson A.Y., Persson A.M., Valconen-Andre C., Lundwall A.; "Glandular Kallikreins of the cotton-top tamarin: molecular cloning the encoding the tissue kallikrein."; DNA Cell Biol. 19:721-727(2000).
                                                                   Saguinus oedipus (Cotton-top tamarin).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Callitrichidae, Saguinus.
NCBI_TaxID=9490;
                                                                                                                                                                                                                                                                                                                                                       GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004263; F:trypatidase activity; IEA.
GO; GO:0004285; F:trypatin activity; IEA.
GO; GO:0004285; F:trypain activity; IEA.
GO; GO:0004285; F:trypain activity; IEA.
InterPro; IPR001284; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR00303; Pept Ser Cys.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYSIN.
SMART; SMO0222; Tryp SFC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN MW; A040914ABC8FECRD CRC64; SEQUENCE 255 AA; 28078 MW; A040914ABC8FECRD
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Mismatches:
Indels:
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Matches:
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611.00
62.34%
49.37%
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489
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166 ValSerIleIleGlyHisLysGluCysGluArgAlaTyrProGlyAsnIleThrAspThr 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           787 GGACAAGATGGCATCCTGGAGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGG 846
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                          66 ProHisTyrVallleLeuLeuGlyGluHisAsnLeuGluLysThrAspGlyCysGluGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 AlaValThrArgLySProGlyValTyrThrLysValCysLysTyrPheAspTrpIleHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams M., Mural R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:2447533; Klk15.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
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Last annotation update)
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EMBL; AY152434; AAN78422.1; -.
HSSP; P00760; 1EZX.
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1-MAR-2003 (TrEMBLrel. 23,
1-MAR-2004 (TrEMBLrel. 26,
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01-MAR-2003
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Q8CGR4;
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AAC-----CCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGTCTCCCATGCC 630
                                                                                             :::
158 SerGlnValSerLeuProAspThrLeuHisCysAlaAsnIleSerIleIleSerAspAla 177
                                                                                                                                                        631 ACCIGCCATGGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAGGCGGCGTC 690
                                                                                                                                                                                747
                                                                                                                                                                                                                                                                        198 GlyArgGlyAlaGluSerCysGluGlyAspSerGlyGlyProLeuValCysGlyGlyIle 217
                                                                                                                                                                                                                                                                                                                                           CTICAAGGICIGGIGICCIGGGGGICTGIGGGGCCCTGIGGACAAGAIGGCAICCCIGGA 807
                                                                                                                                                                                                                                                                                                                                                                   TITITGCTCCTGTGTTCTTGGGCTCAGCCAGGCAGCCACCGAAGATTTTCAATGGC 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---CCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGAGTC
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

PubMed=15203212; DOI=10.1016/j.ygeno.2004.01.009;

Olsson A.Y., Lilja H., Lundwall A.;

"Taxon-specific evolution of glandular kallikrein genes and identification of a progenitor of prostate-specific antigen.";

Genomics 84:147-156(2004).

-I MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
glandular kallikrein 11.
; 247B29D3F0DEF8F1 CRC64;
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115
37
90
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Matches:
Conservative:
Mismatches:
Indels:
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250 Gi
27630 MW;
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610.00
61.79%
46.75%
29.53%
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Best Local Similarity:
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250 A
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Pred. No.:
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DB:
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Q63ZF2;
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83 SerAsnTyrCysLeuSerHisLeuSerArgTyrlleValHisLeuGlyGlnHisAsnLeu 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 TACCTGGGAGCC-----TCGACGAGCCACGAGCACGACCTCCGGCTGCGGCTGCGC 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 ITCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 IleLysGlyPheGluCysLysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 CysLeulysProTrpValSerLeuThrSerProThrHisValSerProAspLeuSerSer
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                                                                                                                                                                                                                                   Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                      databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR00903; Pept_Ser_Cys.
Pfam; PR00099; Trypsin; 1.
PRINTS; SM00020; Trypsin; 1.
PROSITE; PS00240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
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121
35
38
88
88
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                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Variant form hippostasin/KLK11.
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                -i-SIMILARITY: Belongs to peptidase family EMBL; AB078780; BAC54105.1; -. HSSP; P00760; 1EZX.
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SEQUENCE 275 AA; 30165 MW;
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                                                                  PRELIMINARY;
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                                                                                                                                                                                                                          Homo sapiens (Human)
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           TISSUE=Prostate;
                                                                                         Q8IXD7;
01-MAR-2003
01-MAR-2003
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                                                                                                                                                                                                     Name=KLK11;
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                                                                Q8IXD7
                         RESULT 11
Q8IXD7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 ATCTITITGCTCCTGTGTGTTCTTGGGCTCAGCCAGCCACCACA-----CCGAAGATT 186
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|SerGlyTrpGlyLeuLeuSer---AspAsnAsnProGlyAlaThrGlySerGlnLysSer
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Matches:
Conservative:
Mismatches:
Indels:
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001034; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Cys.
Pfam; PF000089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_SER; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1-254)
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608.00
60.87%
49.01%
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757 CTGGTGTCCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACC 816
-i- SIMILARITY: Belongs to peptidase family S1.

EMBL; BC069518; AAH69518.1; -

EMBL; BC069480; AAH69480.1; -.

HSSP; P00761; 1AKS.

GO; C00004263; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.
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                                                                                                                                                                                                                                                         UNKKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-015-385A-193 (1-1091) x Q6ISI0 (1-255)
                                                                                                                      UnterPro; IPR001254; Peptidaee S1.
InterPro; IPR001314; Peptidaee S1.
InterPro; IPR00103; Pept Ser_Cys.
Pfam, PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM0020; Tryp SPc; 1.
PR0SITE; PS0240; TryPSIN DOM; 1.
PR0SITE; PS00134; TRYPSIN HIS; UNKNOW Hydrolase; Protease; Serine protease.
SEQUENCE 255 AA; 28016 MW; 1581BT
                                                                                                                                                                                                                                                                              protease.
                                                                                                                                                                                                                                                                                                                                                     7.67e-30
599.00
59.38%
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Pred. No.:
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MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

M. Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. Buctow K.H., Scheefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M. J., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Jones S.J., Marra M.A.,

A Marra M.A.,

A Jones S.J., Marra M.A.,

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                                                                                                                                                                                                                                                                                                                                                        GCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGAGTCCTTCAAGGTCTGGTG 762
                                                                                                                                                                                                                                                                                                                                                                            TCCTGGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGGAGTCTACACCCTATATT 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerTrpGlyGln---AspProCysAlalleThrArgLysProGlyValTyrThrLysVal 261
                                                                                                                                GCTGGCACCGAGGCTCAGGCTGGGGCATCACCAACCACCACGGAACCCATTC
                                                                                                                                                                                                                                                                                                                  TyrProGlyAsnileThrAspThrMetValCysAlaSerValGlnGluGlyGlyLysAsp
                                                         CTGCCCGTCCGCGTAACCAGCAGCGTTCAACCCCTGCCCCTGCCCAATGACTGTGCAACC
                                                                                CCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGTCTCCCATGCCACCTGCCATGGTGTG
                                                                                                                                                                                                                                                                                  TATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAGGC----GGCGTCCCGGGGCAGGAT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE=PCR rescued clones;
Director MGC Project;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC 864
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SEQUENCE FROM N.A.
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|21 ValArgProAlaValLeuProThrArgCysProHisProGlyGluAlaCysValValSer 140
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                                                                                                                                                                                                      250 AGCCTGCGCTGCGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACACAGGGGCTCACTGC
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|GlyTrpGlyLeuValSerHisAsnGluProGlyThrAlaGlySerProArgSerGlnVal
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1581B784D4A39C4F CRC64
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18
                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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Isoid=09H2R5-4; Sequence=VSP 005404; In the thyroid gland. Also TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also expressed in the prostate, salivary, and adrenal glands and in the colon testis and kidney. SIMILARITY: Belongs to the peptidase SI family. Kallikrein subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pubmed=14799258; Die=10.1186/gb-2004-5-2-18; Pubmed=14799258; Die=10.1186/gb-2004-5-2-18; Hillman R.T., Green R.E., Brenner S.E.; Handapreciated role for RNA surveillance."; Genome Biol. 5:RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH060.1-RESEARCH0
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Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=11010966; DOI=10.1074/jbc.M005431200;

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Molacular cloning of the human kallikrein 15 gene (KLKIS). Uprequlation in prostate cancer.";

J. Biol. Chem. 276:53-61(2001).
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Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Peeper B., Wang K., R., R., R., R., R., Lei H., McCuaig J.,
"Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaro org. Melacaca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY
                                                                                                    817 TATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC 864
                                                                                                                                      240 LysValCysHisTyrLeuGluTrpIleArgGluThrMetLysArgAsn 255
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"A novel serine proteinase-like sequence from human brain.";
Biochim. Biophys. Acta 1218;225-228(1994).
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                                                                                                                                                                                                                                                                                       KLKF HUMAN STANDARD; PRT; 256 AA. O9H2R5; Q15358; Q9H2R3; Q9H2R4; Q9H2R6; Q9HBG9; 16-OCT-2001 (Rel. 40, Created) L16-OCT-2001 (Rel. 40, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) KAllikrein 15 precursor (EC 3.4.21.-) (ACO protease).
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SEQUENCE FROM N.A.
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 ITCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 ACCAGCCTGCGCGGGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGCGGCTCAC
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Charge relay system (By similarity).
Charge relay system (By similarity).
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
Missing (in isoform 4).
Frid=VSP 005404.
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Kallikrein 15.
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GO; GO:0005576; C:extracellular, NAS.
GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
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V -> G (in isoform 3).

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Missing (in isoform 3).

/FTId=VSP_005407.
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  entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                   X75363; CAA53145.1; ALT_SEQ.
P00760; 1EZX.
                                                                                         EMBL; AF242195; AAG09470.1; -.
EMBL; AF242195; AAG09471.1; -.
EMBL; AF242195; AAG09472.1; -.
EMBL; AF243527; AAG33354.1; -.
EMBL; X75363; CAA53145.1; ALT_SBC; P00760; 1EZX.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ of Submitted (JUL-1998) to the EMBL/GenBank/DDBJ of Submit. Strans. Belongs to peptidase family S1 HSSP; P00760; 1EZX.
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MGD; MGI:1929977; 2310015108Rik.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR009003; Pept_Ser_Gys.
Pfam; PR00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00202; TRYPSIN.
PROSITE; PS50240; TRYPSIN_DOM; 1.
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Hydrolase; Protease; Serine pi
SEQUENCE 249 AA; 27604 MW;
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01-MAY-2000 (TrEMBLrel. 13,
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Best Local Similarity:
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STRAIN-C57BL/6J; TISSUE=Tongue;

X MEDINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;

A RDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;

A Konno H., Atiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Amamenco R., Matsunatoch H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawii J., A Okazaki Y., Murammatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771(2000).
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hippostasin prostate type (Mus musculus adult male tongue cDNA, RIKEN
Hippostasin prostate type (Mus musculus adult male tongue
telul-length enriched library, clone:2310015108 product:procease,
serine, 20, full insert sequence) (Mus musculus adult male tongue
cDNA, RIKEN till-length enriched library, clone:2310040F07
product:procease, serine, 20, full insert sequence).
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MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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STRAIN=C57BL/6J; TISSUB=Tongue;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKENY FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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STRAIN=C57BL/6J; TISSUE=Tongue;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
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STRAIN=C57BL/6J; TISSUE=Tongue;
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Nature 420:563-573(2002).
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Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayateu N., Hiramoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konn H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Salto H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AAGATTTTCAATGGCACTGAGTGTGGGCGTAACTCACAGGCGGTGGCAGGTGGGGCTGTTT
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Matches:
Conservative:
Mismatches:
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PRINTS; PR00722; CHYMOTRYPSIN.
SMARY; SM0020; Tryp_SPS; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN HIS; UNKNOWN 1.
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InterPro; IPR001314; Peptidase S1A.
InterPro; IPR009003; Pept_Ser_Cys.
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ADD39786 standard; protein; 248 AA.
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PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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PA (GETH ) GENENTECH INC.

BEST LOCAL Similarity: 100.00%

69.47%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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Best Local Similarity: 100
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TD ADD70709 standard;
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RESULT 15
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RESULT 16
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RESULT 14
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GenCore version 5.1.6

March 5, 2005, 23:40:21; Search time 183 Seconds (without alignments)
4611.536 Million cell updates/sec
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SUMMARIES

Description
                                                                                                3967864
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Human PRO1303 (UNQ669) amino acid sequence SEQ ID NO:194.
09-WAR-2000.
(GETH ) GENENTECH INC.
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2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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WO200053750-A1.
14-SEP-2000.
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Human KLK-L5 protein #4.
WW020053776-A2.
14-SEP-2000.
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PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
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Best Local Similarity: 100.00%
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Protein of the invention #54
WOZ00078961-Al.
28-DEC-2000.
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
Query Match: 69.47%
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PD 07-201.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 100.00$
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
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RESULT 4

1D AAV4933 standard; p
DE Human PRO1303 (UNQ66
PN W0200012708-A2.
PD 09-MAR-2000.
PA (GETH ) GENETH IN
Best Local Similarity: 1
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Perfect score:
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RESULT 5
ID AAM23994
DE Human ESTP W WO200154PP D 02-AUG-21PA
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RESULT 2
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RESULT 6
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ABO33635 standard; protein; 248 AA.
Novel human secreted and transmembrane protein PRO1303
US2003073130-A1.
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Novel human secreted and transmembrane protein
US2003073129-A1.
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US2003083462-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
Local Similarity: 100.00$ Mismatches:
// MAtch: Indels:
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DE Human secreted/transmembrane protein PRO1303.
DE 20303096954-A1.
PD 22-0303096954-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
                                                                                                                                                            Human secreted/transmembrane protein PRO1303 US2003044841-A1.
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Human secreted/transmembrane protein PRO1303
US2003096955-A1.
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                                                                                                                                             ABO44488 standard; protein; 248 AA.
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Human PRO polypeptide #54.
US2003064925-A1.
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248 AA. : protein PRO1303.	Mismatches: Indels:	248 AA. : protein PRO1303.	Mismatches: Indels:	248 AA. protein PRO1303.	Mismatches: Indels:	248 AA. : protein PRO1303.	Mismatches: Indels:	248 AA. : protein PRO1303.	Mismatches: Indels:	65 standard; protein; 248 AA. secreted/transmembrane protein PRO1303.	Mismatches: Indels:	248 AA. : protein PRO1303.	Mismatches: Indels:	248 AA. protein PRO1303.	Mismatches: Indels:	248 AA. protein PRO1303.	Mismatches: Indels: 248 AA.
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	PD 15-MAY-2003. PA (GETH ) GENENTECH INC. Best Local Similarity: 100,00% Ouery Match: 69.47%	KESULI 1/ ID ADD40263 standard; protein; 2 DE Human secreted/transmembrane PN US2003082627-A1.	7,7	4 standard; ecreted/trar 69179-81	# # 17	KESULI 19 ID ADE20096 standard; DE Human secreted/trar PN US2003092883-A1.	PD 15-MAY-2003. PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match:	KESULT 20 ID ADE50007 standard; protein; i DE Human secreted/transmembrane PN US2003082626-Al.	PD 01-MAY-2003, PA (GETH ) GENENTECH 1 Best Local Similarity: Query Match:	RESULT 21  ID ADE21565 standard; DE Human secreted/trai	OS-MAY-2003. (GETH ) GENENTECH st Local Similarity:	RESULT 22 ID ADF29990 standard, protein; 248 AA. DE Human secreted/transmembrane protein	PD 30-002-2003. PA (GETH ) GENENTECH Best Local Similarity: Query Match:	RESOLI 4.2 ADF55883 standard; protein; 248 AA. DE Human secreted/transmembrane protein PROL30. PN US2003204054-Al.	T-2003. [ ) GENENTECH . Similarity: .h:	RESULT 24 ID ADH99387 standard; protein; 248 AA. IDE Human secreted/transmembrane protein PN US2003065142-A1.	PD 03-APR-2003. PA (GETH ) GENENTECH I Best Local Similarity: Query Match: TREULT 25 TO ANR96567 standard:

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Human secreted/transmembrane protein FR01303.

BE Human secreted/transmembrane protein FR01303.

NUS200319993-AJ.

PD 23-OCT-2003.

PA (GETH) GENEWTECH INC.

Best Local Similarity: 100.00\$ Mismatches:

GUSTY ARCH: 69.47\$ Indels:

RESULY 28

ID ADF29513 standard; protein; 248 AA.

PA (GETH) GENEWTECH INC.

PA (GETH) GENEWTECH INC.

PA (GETH) GENEWTECH INC.

Best Local Similarity: 100.00\$ Mismatches:

QUETY MACH: 69.47\$ Indels:

RESULY 29

ID ADE37044 standard; protein; 248 AA.

DE Human secreted/transmembrane protein FR01303.

PN US2003195334-AA.

PN USCO03195334-AA.

Best Local Similarity: 100.00\$ Mismatches:

QUETY MACH: 69.47\$ Indels:

RESULY 28

PN USCO03195334-AA.

Best Local Similarity: 100.00\$ Mismatches:

QUETY MACH: 69.47\$ Indels: Mismatches: Indels: Mismatches: Indels: ADH04513 standard; protein; 248 AA.

DE Human secreted/transmembrane protein PRO1303.

PN US2004005626-A1.

PD 08-JAN-2004.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00* Mismatches:

Query Match: 69.47* Indels: RESULT 31

ID ADH04036 standard; protein; 248 AA.

ID ADH04036 standard; protein; 248 AA.

DE Human secreted/transmembrane protein PR01303.

PR US2003220471-A1.

PD 27-NOV-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00\$ Mismatches:

Onery Match: 69.47\$ Indels: ADH03559 standard; protein; 248 AA.

DB Human secreted/transmembrane protein PR01303.

DB US2003224478-A1.

PD 04-DEC-2003.

PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.

Query Match:

GOGY ATTRICT:

GOGY ATT Mismatches: ADH61514 standard; protein; 248 AA. Human secreted/transmembrane protein PRO1303 DE Human secreted/transmembrane protein PRO1303.
PN US2003195347-A1.
PD 16-0CT-2003.
PA (ERTH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: DE Human secreted/transmembrane protein PRO1303.
DE Human secreted/transmembrane protein PRO1303.
PD 13-0CT-2003.
PA (GETH ) GENENTECH INC.
PA (GETH ) GENENTECH INC.
Query Match:
RESULT 27
INGELES Mismatches: Indels: ADH03082 standard; protein; 248 AA. Human secreted/transmembrane protein PRO1303. US2003216562-A1. Indels: PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
Query Match: 69.47% 69.47% Query Match: RESULT 34 ID ADH61514 DE Human 8e Query Match: RESULT 32 Query Match: RESULT 30 Query Match: RESULT 26

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Mismatches: Indels:	AA. endocrine cancer.	Mismatches: Indels:	48 AA. protein PRO1303.	Mismatches: Indels:	AA.	Mismatches: Indels:	AA.	Mismatches: Indels:	AA.	Mismatches: Indels:	AA. endocrine cancer.	Mismatches: Indels:	AA. ID NO:2150.	Mismatches: Indels:	AA.	Mismatches: Indels:	AA. (18817).
INC. 100.00% 69.47%	protein, 248 , marker of	I HOSPITAL. 100.00% 69.47%		INC. 100.00% 69.47%	protein; 248 sin.	INC. 100.00% 69.47%	protein; 254 in #3.	HOSPITAL. 100.00% 65.83%	protein; 254 ptide #11.	100.00% 65.83%	rotein; 254 marker of	I HOSPITAL. 100.00% 65.83%	protein; 254 sequence SEQ	INC. 100.00% 65.83%	protein; 184 in #1.	I HOSPITAL. 100.00% 51.54%	protein; 248 ike protein 5
14130-A1. 2004. GENENTECH imilarity:	ADN10927 standard; Human kallikrein 12 WO2004029285-A2.	(MOUN ) MOUNT SINAI Local Similarity: Match:	ur 36 ADL94713 standard; protein; 2 Human secreted/transmembrane US2004073015-Al	15-APR-2004. (GETH ) GENENTECH I LOCAL SIMILARITY: MATCH:	T 37 ADT94373 standard; pr. Human PRO1303 protein AU2003259607-A1.	2003. GENENTECH imilarity:	ir 38 AAB21303 standard; protein; Human KLK-L5 protein #3. WO200053776-A2.	14-SEP-2000. (MOUN ) MOUNT SINAI Local Similarity: Match:	6676 standard; n novel polype 0244340-A2.	06-JUN-2002. (HYSE-) HYSEQ INC. Local Similarity: Match:	0926 standard; n kallikrein 1: 04029285-A2.	08-APR-2004. (MOUN ) MOUNT SINAI Local Similarity: Match:	4 standard; RO protein 39956-A2.	2004. GENENTECH imilarity:	1. % AAB21301 standard; protein; Human KLK-L5 protein #1. WO200053776-A2.	14-SEP-2000. (MOUN ) MOUNT SINAI Local Similarity: "Match:	
PN US20040 PD 22-JAN- PA (GETH ) Best Local S Query Match: PRESHIFT 35		PA (MOUN) Best Local S Query Match:	RESULT ID AL DE H	PD 11 PA (( Best Lo	ļģ.	PD 27-NOV-PA (GETH ) Best Local S Query Match:	ID AAB2 DE Huma	# # # # # # # # # # # # # # # # # # #	ID DE NA	it i		PD 08-APR- PA (MOUN) Best Local S Query Match:	ID AL DE HILL	PD 13-MAY-PA (GETH) Best Local S Query Match:	5	PD 14-SEP- PA (MOUN) Best Local S Query Match:	ID A

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AAB08953 standard; protein; 30 AA.
Human secreted protein sequence encoded by gene 22 SEQ ID NO:110.
WO200017222-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADR72141 standard; peptide; 16 AA.
Common protein epitope tag, PET, for human kallikrein 4.
US20041380-A1.
16-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:

RESULT 50

ID AAU76373 standard; protein; 70 AA.

DE Human Marcov Model trypsin consensus protein sequence.

PD 24-JAN-2002.
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Human novel polypeptide sequence, SEQ ID NO:1470.
WO2003029271-A2.
                                                                                                                                                                                                                                                                                                                                                                      MESULI 40

B. Human kallikrein 12, marker of endocrine cancer.

DB. Human kallikrein 12, marker of endocrine cancer.

PN W02004029285-A2.

PD 08-APR-2004.

PA (MOUN) MOUNT SINAI HOSPITAL.

Best Local Similarity: 100.00% Mismatches:

Query Match: 18.21% Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duery Match:

RESULT 51

ID ABP09500 standard; protein; 107 AA.

DE Human ORRY protein sequence SEQ ID NO:18982.

PN WO200192523-A2.

PD 06-DEC-2001.

PA (CURA-) CURAGEN CORP.

Best Local Similarity: 100.00$ Mismatches:
                                                                                              AAY28642 standard; protein; 162 AA.
Human secreted protein from cDNA clone HKAFV61.
WO9940183-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE Sequence of tissue plasminogen (TPA) analogue.

NG9709906-A.

PD 02-UUL-1987.

PA (WPJO) UPJOHN CO.

PA (MARO/) MAROTTI K R.

Best Local Similarity: 100.00$ Mismatches:

Query Match: 3.92$ Indels:
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Indels:
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Human KLK-LS protein #2.
WO200053776-A2.
14-SBP-2000.
                                                                                                                                                                                                                                  ID AAB21302 standard; processing the Human KLK-LS protein #2.

PN W020053776-A2.

PD 14-SEP-2000.

PA (MOUN ) MOUNT SINAI HOSPITAL.

Best Local Similarity: 100.00%
                                                                                            ID AAY28642 standard; process, and be human secreted protein from cDNA PN W09940183-A1. PD 12-AUG-1999. PA (HUMA-) HUMAN GENOME SCI INC. Best Local Similarity: 100.00$
PN MCAC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID AAU76373 Btauwaaa, gebool BE Human Marcov Model trypsin corporation W0200206455-A2.
PD 24-JAN-2002.
PA (FARB ) BAYER AG.
Best Local Similarity: 100.00%
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PA (ENGR-) ENGENEOS INC.
Best Local Similarity: 100.00%
4.48%
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RESULT 47

ID ADR72141

DE Common DP

BN US200418

PN 16-SEP-20

PA (ENGE-) 1
                                                             Query Match:
RESULT 44
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RESULT 45
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RESULT 48
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AD3833076 standard; protein; 217 AA.
Trypsin protein which is related to human NOVX protein - SEQ ID 67.
US2003170630-A1.
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Indels:
                  Mismatches:
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Indels:
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                                                              ABO00751 standard; protein; 217 AA.
Polypeptide encoded by novel human contig #2.
WO2003023013-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE21442 standard; protein; 226 AA.
Human trypsin domain consensus protein #2.
WO200226802-A2.
                                  Indels:
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US2002165152-A1.
                                                                                                                                                                                         ADI21707 standard; protein; 217 AA. Novel human polypeptide #186. WO2003025148-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BOLD) BOLDOG F L.
(GONG) GORMAN L.
(GANG) GANGOLLI E A.
(FERN) FERNANDES E R.
(RIEG) RIEGER D K.
(EDIN) EDINGER S R.
(GONT) GUNTHER E.
(MILL) MILLET I.
(SCIO) SCIORE P.
(ELLE) ELLERWAN K.
(MACD) MACDOUGALL J R.
(SMIT) SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protease PRTS-7 protein.
WO200183775-A2.
08-NOV-2001.
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(KAPE/) KAPELLER-LIBERMANN R.
Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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PA (HYSE-) HYSEQ INC.
Best Local Similarity: 100.00%
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                Best Local Similarity: 100.00%
Query Match: 3.64%
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ZERHUSEN B D.
PATTURAJAN M.
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TCHERNEV V T.
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 (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                       HYSEQ INC.
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RESULT 63
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(SPYT/)
(ZERH/)
(PATT/)
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(CASM/)
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RESULT 66
                                                 RESULT 62
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RESULT
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Consensus sequence of trypsin serine protease-like protein domain.
WO200173074-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADI17269 standard; protein; 217 AA.
Polypeptide homologous to a human NOVX domain SeqID 805.
WG200258649-A2.
06-SER-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI17277 standard; protein; 217 AA.
Polypeptide homologous to a human NOVX domain SegID 813
WO200268649-A2.
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Human serine protease #5 encoded by clone HHFBJ67.
WO200068247-A2.
                                                                                   Chain 2 of modified tissue plasminogen activator EP253582-A.
                                  Mismatches:
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                                                                                AAP81986 standard; protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU77550 standard; protein; 199 AA.
                                                                                                                                                                                                                                                                                                                                 ABG30791 standard; protein; 187 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Membrane-type serine protease #1.
WO200212461-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 27-DEC-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00%
RESULT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC.
Local Similarity: 100.00%
Match: 3.64%
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Local Similarity: 100.00%
Match: 3.64%
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Best Local Similarity: 100.00%
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20-JAN-1998.
(NOVO ) NOVO IND AS.
Local Similarity: 100.00$
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(CURA-) CURAGEN CORP.
Local Similarity: 100.00%
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 100.00%
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US2002119925-A1.
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                                                 3.64%
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(TANO-) TANOX INC.
Local Similarity:
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Local Similarity:
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W09942133-A1.
                                                                                                                                                                                                                                                         16-NOV-2000
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                                               Query Match:
RESULT 53
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RESULT 55
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RESULT 58
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RESULT 56
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RESULT 59
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Query M RESULT

Mismatches:

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Mismatches:

Indels:

Mismatches: Indels:

Mismatches: Indels:

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Human transmembrane serine protease (MTSP) polypeptide #3.
US2004001801-A1.
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Mouse serine protease BSSP2 (mBSSP2), SEQ ID NO:2.
WO200031272-A1.
                                                                                                                                                                                                                                                                                                                                                   Human membrane-type serine protease (MTSP) 4 WO200157194-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE21441 standard; protein; 249 AA.
Human trypsin domain consensus protein #1.
WO200226802-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ46899 standard; protein; 235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA50474 standard; protein; 238 AA. Human protease SEQ ID NO:72. WO2003040393-A2.
                                                                                                                                                                                                                                                                                                                                       AAE06932 standard; protein; 235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; 235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR07241 standard; protein; 245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cell surface protease #3 WO200295007-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-APR-2002.
(MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD 15-MAY 2003.
PA (DECO-) DECODE GENETICS EHP.
Best Local Similarity: 100.00%
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PA (CORV-) CORVAS INT INC.
Best Local Similarity: 100.00%
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(CORV-) CORVAS INT INC.
Local Similarity: 100.00$
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Best Local Similarity: 100.00%
Ouery Match:
3.64%
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Best Local Similarity: 100.00%
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Best Local Similarity: 100.00
                                                                                                                                                                  (EDIN/) EDINGER S R.
(MILL/) MILLET I.
(SCIO/) SCIORE P.
(ELLE/) ELLERMAN K.
(MACD/) MACDOUGALL J R.
(SMIT/) SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.64%
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                                                                 CASMAN S J.
BOLDOG F L.
GORMAN L.
GANGOLLI E A.
FERNANDES E R.
RIEGER D K.
   GROSSE W M.
SZEKERES E S.
VERNET C A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADI10375 standard;
                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                t-PA(Del296-302).
WO9010649-A.
20-SEP-1990.
                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001.
                                                  (LILL/)
(CASM/)
(BOLD/)
(GORM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
RESULT 81
                                                                                                                                                                                                                                                                                                        Match:
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                                                                                                                                   (RIEG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match:
                      SZEK/)
VERN/)
                                                                                                                     GANG/
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RESULT 82
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RESULT
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                                                                                                                                                                                                                                                                                                         Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADI17268 standard; protein; 230 AA.
Polypeptide homologous to a human NOVX domain SeqID 804.
W0200158649-A2.
06-SEP-2002.
(CURA-) CURAGEN CORP.
Local Similarity: 100.00% Mismatches: 0
Y Match: 3.64% Indels: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE AD17276 standard; protein; 230 AA.

DE Polypeptide homologous to a human NOVX domain SeqID 812.

PN W0200268649-A2.

PD 06-SEP-2002.

PA (CURA-) CURAGEN CORP.

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.64% Indels: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP03097 standard; protein; 228 AA.
Human insulin resistance-related adipsin protein.
JP2004041208-A.
12-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypsin-like serine protease protein - SEQ ID 66.
US2003170630-A1.
                   Mismatches:
Indels:
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Indels:
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                                                              DE Trypsin domain consensus sequence, PFAM.

DE Trypsin domain consensus sequence, PFAM.

PN US2002165152-A1.

PD 07-NOV-2002.

PA (KAPE/) KAPELLER-LIBERMANN R.

Best Local Similarity: 100.00% Mismat Query Match: 3.64% Indels
                                                                                                                                                                                                                                                                                                                                                      Antipsoriatic protein sequence #262.
WO2004028479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 228 AA.
                                                                                                                                                                                                     protein; 228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADJ83075 standard; protein; 230 AA.
                                                                                                                                                                                                                                                                                                                                       protein; 228 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP23853 standard, protein, 220
PRO polypeptide SEQ ID NO:1031
WO2004041170-A2.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 100.00%
Query Match: 3.64%
                                                                                                                                                                                                                                                15-MAY-2003.
(GEST ) GENSET SA.
Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-2004.
(SANY ) SANKYO CO LTD.
Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WOCKULAY-2004.
21-MAY-2004.
(GETH) GENENTECH INC.
Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                       PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00$
                                                                                                                                                                                                                   Human adipsin protein #3.
US2003092620-Al.
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TCHERNEV V T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
LEPLEY D M.
BURGESS C E.
SHIMKETS R A.
                                                                                                                                                                                                   AAE39994 standard;
                                                                                                                                                                                                                                                                                                                                       ADN04134 standard;
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RESULT 69
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RESULT 71
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RESULT 70
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RESULT 73
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RESULT
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RESULT
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Mismatches:

Indels:

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Mismatches:

Indels:

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Mismatches:

Indels:

Mismatches: Indels:

### Similarity: 100.000	JOCAL SIMILALICY; Y Match: LT 100 AAE25043 standard; Human kringle 2 se;	ָבֶּר [ָ]	ID AAE24195 standard; protein; DE Human K2S heterologous prote PN WO200240696-A2.	Match:	PD 23-MAY-2002. PA (BOEH ) BOEHRINGER INGELHEIM Best Local Similarity: 100.00%		IDS AAE24189 standard; protein; DR Human native K2S heterologo:	Query Match: 3.64% RESULT 98	(OKLA-) OKLAHOMA M	PN WO200032759-A1. PD 08-JUN-2000.	ID AAY99592 standard; protein; DE Vampire bat salivary plasmir	Best Local Similarity: 100.00% Query Match: 3.64% preum on	W09957251-A2. 11-NOV-1999. (OKLA-) OKLAHOMA	AESOLI 79 ID AAVSO873 standard; protein; DE Vampire bat saliva plasminog	Best Local Similarity: 100.00% Query Match: 3.64%	Z/-FEB-ZUUS. (GEHO ) GEN HOSPITA (FARB ) BAYER AG.	DE Human Protein P00746, SEQ ID PN WO2003016475-A2.	3 standard; protein	st Local Si		ID AAE3992 standard; protein; DE Human adipsin protein #1. DN 11590030920-41	ř.	PA (GEST) GENSET SA. Best Local Similarity: 100.00%	DE Human adipsin protein #2. PV US2003092620-A1.	RESULT 93 ID AAE39993 standard; protein;	Best Local Similarity: 100.00% Query Match: 3.64%	FN WOZOUSO 140353-AZ.  PD 15-MAY-200DF GENETICS EHF.	ID ADA50481 standard; protein; DE Human protease SEQ ID NO:79.	ery Match: SULT 92	UNIV ARKAN
100.00\$ Mismatches:  3.64\$ Indels: protein; 250 AA. HOSPITAL ASSOC. 100.00\$ Mismatches: 3.64\$ Mismatches: 100.00\$ Mismatches: 3.64\$ Mismatches:																				1										
protein; 250 AA.  Hospital Assoc. Hospital Hospital Hos	יהושטף היוארובים									-																				
100.00\$ Mismatches:  protein; 250 AA.  HOSPITAL ASSOC.  100.80\$ Mismatches:  3.64\$ Indels:  protein; 250 AA.  HOSPITAL ASSOC.  100.00\$ Mismatches:  100.00\$ Mismatches:  100.00\$ Mismatches:  protein; 250 AA.  SYSTEM.  protein; 252 AA.  SYSTEM.  100.00\$ Mismatches:  protein; 252 AA.  3.64\$ Indels:  protein; 253 AA.  3.64\$ Indels:  protein; 253 AA.  100.00\$ Mismatches:  3.64\$ Indels:  protein; 253 AA.		00		, 0	c			o 0	c			00			00			0	0			00			0	0				00
100.00% 3.64% THOSPITA INCSYSTER INCSYSTER INCSYSTER INCOVERTA INC		SENTRUM. Mismatches: Trdels:			Micmatches			mismacues. Indels:	Migmat Shoo.			Mismatches: Indels:			Mismatches: Indels:				Mismatches:			; he		CD (20	Indels:	ASSOC.	ASSOC. NST. TNC.		clone phg3	
rity:  ldard; l lSRAEL rity: lSRAEL rity: lSRAEL rity: lAdard; l lO enco ldard; l lda	100.00% 3.64% protein;	EBSFORSCHUNGSZENTRUM (y: 100.00% M	protein; ted prote	3.64%	SYSTEM.		protein;	3.64%	SYSTEM.		protein;	100.00% 3.64%	SYSTEM.		100.00%	SYSTEM			SYSTEM.		protein;	100.00% 3.64%	CHN INC.		3.64%	HOSPITAL	HOSPITAL CANCER I		protein; product f	3.64%
Best Local Similarity: 18 Best Local Similarity: 18 BEST IN 83.  ID AAR05772 standard; ID Human adipsin gene ID AAR07239 standard; ID AAR07249 standard; ID AAR07249 standard; ID AAR07244 standard; ID Human Gene ID	Local Similarit Match: T 91 AAB98506 standa	24-DEC-1998. (DEKR-) DEUT KR Local Similarit	AAY08025 standa Mouse protease- DE19736198-C1.	ocal Similaric Match: 90	0-SEP-1990. TEXA ) UNIV TEXAS	t-PA(R299->E). WO9010649-A.	7243 standard;	Sımılarıty: :	) UNIV TEXAS		7244 standard;				imilarity:	EXAS	7240 standard; (R304->E).	Match: JT 86	(TEXA) UNIV TEXAS	C-PA(R304->S). WO9010649-A.	AAR07239 standard;	Local Match	MOSUULS4U-A. 22-FEB-1990. (CALB-) CALIF BIOTEC	1 standa dipsin/D	Ma B	(BE	N COR	W09	AAR05772 standard; Human adipsin gene	sımılarıty: :

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AAE25043 standard; protein; 268 AA.
Human kringle 2 serine protease protein fragment (residues 260-527).
WO200240650-A2.
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PA (GEHO) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.64% Indels: 0
RESULT 96
Nay597251-AZ.
PD Vampire bat saliva plasminogen activator protein fragment.
PN W09957251-AZ.
PD 11-NOV-1999.
PA (OKLA-) OKLAHOWA MEDICAL RES FOUND.
Best Local Similarity: 100.00% Mismatches: 0
RESULT 97
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Human K2S heterologous protein fragment (260-527) mutant #2.
WC200240696-A2.
33-MAY-2002.
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Human native K2S heterologous protein fragment (260-527).
WO200240696-A2.
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Vampire bat salivary plasminogen activator DSPA.
WO200032759-A1.
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PN US2003092620-A1.

PD 15-MAY-2003.

Best Local Similarity: 100.00$ Misma Query Match: 3.64$ Indel RESULT 95

BESULT 95

RESULT 96

RE
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St Local Similarity: 100.00% Mismi
ery Match: Inde
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB Human adipsin protein; 253 AA.

DB Human adipsin protein #2.

PN US2003092620-A1.

PD 15-MAY-2003.

PA (GEST ) GENSET SA.

Best Local Similarity: 100.00% Mism Justy Match: 3.64% Index                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-2002.
(BOEH ) BOERHINGER INGELHEIM INT GMBH.
st Local Similarity: 100.00% Mism ery Match: 3.64% Inde
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ADA50481 standard; protein; 253 AA.
Human protease SEQ ID NO:79.
WO2003040393-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE39992 standard; protein; 253 AA.
                                                                                                                                                         15-NAZ-2003.
(DECO-) DECODE GENETICS EHF.
st Local Similarity: 100.00$
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ULT 93
AAE39993 standard;
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SULT 98
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SULT 100
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SULT 94
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RESULT 110
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Human Kringle 2 serine protease protein fragment (residues 220-527).
WO200240650-A2.
                                                                          AAE24194 standard; protein; 272 AA.
Human K2S heterologous protein fragment (260-527) mutant #1.
W020240696-A2.
                                                                                                                                                                                                                                                                                                                                                                             AAE24196 standard; protein; 274 AA.
Human K2S heterologous protein fragment (260-527) mutant #3.
WO200240696-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE24193 standard; protein; 314 AA.
Human KZS heterologous protein fragment (220-527) mutant #3.
WO200240695-AZ.
23-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human K2S heterologous protein fragment (220-527) mutant #2.
W0200240696-A2.
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                                      0.0
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Mouse serine protease BSSP2 (mBSSP2), SEQ ID NO:4.
WO200031272-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB11697 standard; protein; 311 AA.
Mouse serine protease BSSP2 (mBSSP2), SEQ ID NO:6.
WO200031272-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE24191 standard; protein; 312 AA.
Human K2S heterologous protein fragment (220-527)
WO200240696-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE24188 standard; protein; 308 AA.
Human native K2S heterologous protein fragment
WO200240696-A2.
PD 23-MAY-2002.
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Best Local Similarity: 100.00% Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
Local Similarity: 100.00% Mismatches:
Match: 3.64% Indels:
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(BOEH ) BOEHRINGER INGELHEIM INT GMBH.
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(FUSO) FUSO PHARM IND LTD.
Local Similarity: 100.00%
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Human tissue plasminogen activator (tPA) analogue comprising the B domain of Protein A linked to a catalytic fragment of tPA. WO8705934-A.
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Human kringle 2 serine protease protein fragment (residues 197-527).
WO200240650-A2.
23-MAY-2002.
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Human K2S heterologous protein fragment (197-527) mutant #2.
WO200240696-A2.
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Human K2S heterologous protein fragment (197-527) mutant #1.
WO200240696-A2.
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Human K2S heterologous protein fragment (193-527) mutant #2.
WO200240696-A2.
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Human K2S protein fragment (residues 197-527) mutant #2.
WO200240650-A2.
23-MAY-2002.
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                                                                                     AAB03159 standard; protein; 321 AA.
Mouse trypsin family serine protease Tespec PRO-3.
WO200026352-A1.
                                                                                                         DE Mouse trypsin family serine protease Tespec PRC PN W020002532-A1.
PD 11-MAY-2000
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC. Best Local Similarity: 100.00%
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ADP29456 standard; protein; 324 AA.
Human secreted protein SEQ ID #223.
WO2004035732-A2.
29-APR-2004.
(FIVE-) FIVE PRIME THERAPEUTICS INC.
(FIVE-) AMISTREPLATED SIMILARITY: 100.00$
(BOEH ) BOEHRINGER INGELHEIM INT GMBH.
Local Similarity: 100.00% Mism
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PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
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PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
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PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.

Best Local Similarity: 100.00% Misr
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PA (CREA/) CREA R.
Best Local Similarity:
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st SUZ	ID AAE24187 Standard; protein; 343 AA.  DE Human K2S heterologous protein fragment (191-527) mutant #2.  PN WO200240696-A2.  PD 23-MAY-2002	at ery	AESOLI 112 AB224186 standard; protein; 343 AA. DE Human K2S heterologous protein fragment (191-527) mutant #1. PN W0200240696-A2. DD 23-AMX-2003	PA (BOEH) BOSHRINGER INGELHEIM INT GMBH.  Best Local Similarity: 100.00% Mismatches: 0 Query Match: 3.64% Indels: 0 PRESITY 130	l standard; protein; 343 P 2S protein fragment (resid 0650-A2. 2002.	(BOEH) BOERKINGER INGELHEIM st Local Similarity: 100.00% sry Match: SULT 131	0 standard; protein; 343 / 2S protein fragment (resion650-A2. 2002.	SOEHRINGER nilarity:	4 a 6 L	(FUJI ) FUJISAWA PHARM CO LTD. st Local Similarity: 100.00\$ sry Match: 3.64\$ SULT 133	ID AAPJATAS BEGINGARG; Procein; 343 AA. DE Sequence of coding region in plasmid pthTTrp. PN EP302456-A. PD 08-FEB-1989. PD 108-FEB-1989. PD 108-FEB-1989.	it Local Similarity: 100.00%  ry Match: 3.64% SULT 1344 ctandard: proteir	tPA-8. JP05076361-A. 30-MAR-1993. (TAXE ) TAKEDA CHEM IND LTD. st Local Similarity: 100.00\$	1 standard; protein; 348 AA 361-A.	(TAKE ) TAKEDA CHEM IND LTD. (TAKE ) TAKEDA CHEM IND LTD. St Local Similarity: 100.00%  Bry Match: SULT 136	ID AAP70641 standard; protein; 354 AA.  DB Modified tissue plasminogen activator.  DD AU8661804 A.  PD 05-MAR-1987.  PA (ELIL ) LILLY & CO ELI.  Best Local Similarity: 100.00% Mismatches: 0
PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH. Best Local Similarity: 100.00% Mismatches: 0 Query Match: 3.64% Indels: 0	RESULT 119 ID AAE25039 standard; protein; 335 AA. DE Human K2S protein fragment (residues 193-527) mutant #2. DN MOJONOJAKEALAS	a t	5.0%% Standard, protein; 335 AA. S protein fragment (residues 197-527) mut	ا با	SULT 121 AAR24200 standard, protein, 337 AA. Human K28 heterologous protein fragment (197-527) WO200240696-A2.	PD 23-MAY-2002. PA (BOEH ) BOEHRINGER INGELHEIM INT GMEH. Best Local Similarity: 100.00% Mismatches: 0 Query March: 3.64% Indels: 0	JT 122 AAE24201 standard; Human K2S heterolog WO200240696-A2.	PD 23-MAY-2002. PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH. BEST Local Similarity: 100.00% Mismatches: 0 Ouery Match: 3.64% Indels: 0	123 E24199 standard; protein; 337 AA. man K2S heterologous protein fragment 200240696-A2.	PD 23-MAY-2002. PA GDEH ) BOEHRINGER INGELHEIM INT GMBH. Best Local Similarity: 100.00* Mismatches: 0 Query Match: 3.64* Indels: 0	RESULT 124 ID AAE25049 standard; protein; 337 AA. DE Human K2S protein fragment (residues 197-527) mutant #4. PN W0200240650-A2.	# PF	8 standard; protein; 337 AA. 2S protein fragment (residues 197-527) mut 0650-A2. 2002. BECHRINGER INGELHEIM INT GMBH. imllarity: 100.00% Mismatches:	/ Match: Jr 126 AAE24184 standard; protein; 339 AAHuman K2S heterologous protein fra	FN WCZOCZ4028-AZ. PD 23-MAY-2002. PA (BOBH) BOEHRINGER INGELHEIM INT GMBH. Best Local Similarity: 100.00% Mismatches: 0 Query Match: 3.64% Indels: 0	8 standard; 2S protein 1 0650-A2. 2002. BOEHRINGER

RESULT 146 ID AAR35407 standard; protein;	ery ery	-527).	Tesidues 174-527).	(IAKE ) st Local S: sry Match: SULT 149 AAR3540(	PN JP05076361-A. PD 30-MAR-1993. PA (TAKE) TAKEDA CHEM IND LTD. Best Local Similarity: 100.00\$ Query Match: 3.64\$ RESULT 150 ID AAR35411 standard; protein; DE LPA-17.	###	PD 30-MAR-1993. PA (TAKE) TAKEDA CHEM IND LTD Best Local Similarity: 100.00% Query Match: 3.64% RESULT 15.2 ID AAR35414 standard; protein; DE LPA-6. PN JP05076361A.	i i i i i i i i i i i i i i i i i i i	SU-TAKE 1993.  (TAKE) TAKEDA  It Local Similarit  sty March:  1017 154  AAR35410 stande  tPA-1166  JOCOSTO361-A.  30-MAR-1993.	# 75 E
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Query Match:
RESULT 165
ID AAW28535 standard; protein; 356 AA.
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PD 19-AUG-1997.
PA (ELIL ) LILLY & CO ELI.
Best Local Similarity: 100.00%
                        JS5658788-A.
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Human recombinant tissue-type plasminogen activator (r-PA).
CN1429909-A.
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Thrombolytically active protein K1K2P, based on human t-PA.
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Tissue plasminogen activator derivative, mt-PA6-E.
US5595736-A.
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PA (SHAN-) SHANGHAI XINSHENGYUAN MEDICINE RES CO LT.

Best Local Similarity: 100.00$ Mismatches:
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Best Local Similarity: 100.00$ M
Best Local Similarity: 100.00$ M
RESULT 164
ID AAW28537 standard; protein; 356 AA.
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AAR35405 standard; protein; 355 AA.
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AAR35412 standard; protein; 355 AA.
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AAR35402 standard; protein; 355 AA.
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(BOEF ) BOEHRINGER MANNHEIM GMBH.
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JP05076361-A.
30-MAR-1993.
(TAKE ) TAKEDA CHEM IND LTD.
8t Local Similarity: 100.00$
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30-MAR-1993.
(TAKE) TAKEDA CHEM IND LTD.
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(ELIL) LILLY & CO ELI.
Local Similarity: 100.00%
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JP05076361-A.
                                   EPA-18.
JP05076361-A.
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Query Match:
RESULT 162
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RESULT 159
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RESULT 156
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RESULT 157
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[GARSYQ] - [Plasminogen 443-541] - [t-PA 262-527] hybrid.
WQ9204450-A.
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                                                                                                                                Tissue plasminogen activator derivative, mt-PA6-D. US5595736-A.
                                                                                                                                                                                                                                                           AAW14432 standard; protein; 356 AA.
Tissue plasminogen activator derivative, mt-PA9.
US5595736-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE25034 standard; protein; 377 AA.
OmpA-K2S fusion protein.
WO200240650-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                        Mutant tissue plasminogen activator
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PN W09854199-A1.

PD 03-DEC-1998.

PA (HUMA-) HUMAN GENOME SCI INC.

PA LOCAL Similarity: 100.00% NO.
                                                                                                                        AAW14430 standard; protein; 356 AA.
                                                                                                                                                                                                                                                                                                                                                                                         T 168
ADF32668 standard; protein; 356 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR05123 standard; protein; 358 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW87770 standard; protein; 372 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB11399 standard; protein; 378 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PA (AIRF-) AIR FORCE GEN HOSPITAL.
Best Local Similarity: 100.00%
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3.64%
                     PN USDOCCOLORD 19-AUG-1997.
PA (BLIL) LILLY & CO ELI.
Best Local Similarity: 100.00%
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PD 21-JAN-1997.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
Query Match: 3.64%
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PA (ELIL ) LILLY & CO ELL.

Best Local Similarity: 3.64%

Query Match: 3.64%
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(MERI ) MERCK & CO INC.
(SCHD ) SCHERING AG.
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mt-PA6-D.
US5658788-A.
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EP352119-A.
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RESULT 171
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JP63230084-A.
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EP383417-A.
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RESULT 190
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RESULT 188
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Best
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E. carotovora PelB-rPA fusion protein encoded by pET20b(+)-rPA.
EP1054063-A2.
22-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR41796 standard; protein; 383 AA.
CD4/Tissue-type plasminogen activator (tPA) fusion protein.
WO9318162-Al.
E. coli expression plasmid pET20b(+)-rPA encoded protein.
EP1048732-A1.
02-NOV-2000.
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Local Similarity: 100.00% Mismatches:
y Match: 3.64% Indels:
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Sequence of coding region in plasmid pmTTk.
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Expression plasmid pET20b(+)-rPA protein.
21-FPB-2001.
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Modified tissue plasminogen activator.
US5244806-A.
14-SEP-1993.
                                                                                                            AAB74200 standard; protein; 378 AA.
PelBa-rPA fusion protein.
EP1077262-A1.
21-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 383 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CD4/tPA fusion protein.
US5961973-A.
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Human CD4-tPA fusion protein.
US6287561-B1.
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(CREA-) CREAGEN INC.
Local Similarity: 100.00%
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PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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(CREA/) CREA R.
Local Similarity:
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Query Match:
RESULT 179
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RESULT 181
ID AAR41023
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RESULT 176
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RESULT 182
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RESULT 177
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RESULT 174
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RESULT 178
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AAPB2587 standard; protein; 390 AA. Modified tissue plasminogen activator lacking F and G region and kringle region 2 and Q-96, I-98 and S-119 substd for N, T and M resp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and G region and kringle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 187
ID AAP70021 standard; protein; 393 AA.
DE Sequence of tissue plasminogen activator (tPA) deriv. with AAs 45-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 186
AAP82588 standard; protein; 390 AA.
AAP82ise standard; protein; 390 AA.
AAP8258 at sissue plasminogen activator lacking F and G
region 1 and G-183 and S-186 substd for S and T resp.
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Indels:
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ID AAP94418 standard; protein; 389 AA.

ID Sequence of coding region in plasmid pmSTTK.

BY EP104256-A.

PN 08-FEB-1989.

PA (FUJI) FUJISAWA PHARM CO LTD.

Best Local Similarity: 100.00% Mismatche:
                                                                                                                                                                                                                                                                          1D AAU75907 standard, protein; 389 AA.
DE Human epidermis-specific serine protease #2.
PN W0200200702-A2.
PD 03-AN-2002.
PA (FARB ) BAYER AG.
Best Local Similarity: 100.00% Mismatches
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Recombinant plasminogen-activator.
EP242835-A.
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Modified Bat-PA(H).
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GE9242836-A.

28-0CT-1987.

(BOEF ) BOEHRINGER MANNHEIM GMBH.

Local Similarity: 100.00%
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PA (BORF) BOEHRINGER MANNHEIM GMBH.
RATIV) MATTES R.
BEST LOCAL Similarity: 100.00$
PN EP302456-A.
PD 08-FEB-1989.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Bëst Local Similarity: 100.00%
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PD 26-SEP-1988.
PA (EISA) EISAI CO LTD.
Best Local Similarity: 100.00%
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PD 26-SEP-1988.
PA (EISA) EISAI CO LTD.
Best Local Similarity: 100.00%
3.64%
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PD 22-AUG-1990.
PA (SCHD) SCHERING AG.
Best Local Similarity: 100.00$
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(SCHD ) SCHERING AG.
Local Similarity: 100.00%
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ABW84894 standard; protein; 422 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:5143.
WO2004023973-A2.
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Sequence of coding region in plasmid pTQ1PA delta trp.
EP302456-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP94412 standard, protein; 437 AA.
Sequence of coding region in plasmid pSTQktrp.
EP302456-A.
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Indels:
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Delta(92-179) and delta(466-470) tPA variant
WO9113149-A.
                                                                                                                                                                                                                                        Indels:
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                                                                                                                                              418 AA.
                                                                                                                                                                                                                                                                    ADJ38447 standard; protein; 418 AA.
Human novel protein NOV10b.
US2003212256-A1.
                   ABG76907 standard; protein; 418 AA.
                                                                                                                                                           Human NOV11 protein SEQ ID NO:32 WO200294870-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUJISAWA PHARM CO LTD.
                                                                                                                                           ABR57427 standard; protein;
                                  Human spinesin-like protein.
WO200233087-A2.
25-APR-2002.
                                                                                                                                                                                        28-NOV-200z.
(CURA-) CURAGEN CORP.
Local Similarity: 100.00%
                                                              25-APR-20Uz.
(CURA-) CURAGEN CORP.
Local Similarity: 100.00$
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Best Local Similarity: 100.00%
Query Match:
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GERLACH V.
MACDOUGALL J R.
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(KEKU/) KEKUDA R.
(SPYT/) SPYTEK K A.
(GANG/) GANGOLLI E A.
(FERN/) FERNANDES E R.
(GORM/) GORMAN L.
                                                                                                                                                                                                                                                                                                                                                                               MALYANKAR U M.
SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATTURAJAN M
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BURGESS C E.
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PEYMAN J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PADIGARU M.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELLERMAN SHIMKETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-1989.
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RESULT 204
                                                                                                                                                                                                                                                                                                                                                                                                               (MILL/)
(PEYM/)
(STON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TAUP/)
(BURG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GUNT/)
(ELLE/)
(SHIM/)
(PADI/)
                                                                                                                                                                                                                                                                                                                                                                               (MALY/)
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                                                                                                                                                                                                                                                                                                                                                    GERL/)
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   RESULT 200
                                                                                                               Query N
RESULT
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Human secreted protein sequence encoded by gene 22 SEQ ID NO:69.

MO200017222-A1.

30.MAR-2000.
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD37850 standard; protein; 413 AA. Human secreted protein #33. WO200290526-A2. 14-NOV-2002. (HTMA-) HUMAN GENOME SCI INC. bt Local Similarity: 100.00$ Missry March: 3.64$ Ind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC74423 standard; protein; 413 AA.
Human secreted protein - SEQ ID 1056.
WO2003038063-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC74063 standard, protein; 413 AA.
Human secreted protein - SEQ ID 696,
WO2003038063-A2.
                                                                                                                                                                                                                                                                                                                                                                                                               ADAS7353 standard; protein; 413 AA. Human secreted protein #99. WO2002102994-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD38017 standard; protein; 413 AA. Human secreted protein #200. W0200290526-A2.
                                AAG78109 standard; protein; 395 AA.
                                                                                                                                                         AAR25190 standard; protein; 396 AA.
                                                                                                                                                                                                                                                                                 ADAS6816 standard; protein; 413 AA.
Human secreted protein #99.
WO2002102994-A2.
27-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                           ID ADA57353 Standard, F-1.

DE Human secreted protein #99.

PN W02002102994-A2.

PD 27-DEC-2002.

PA (HTMA-) HTMAN GENOME SCI INC.

Best Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID AABO8912 standard; protein; 414
DE Human secreted protein sequence
PN W020017222-A1.
PD 30-MAR-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00%
Query Match:
                                               Human thrombolytic enzyme NTA.
CN1287174-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-NOV-2002.
(HUMA-) HUMAN GENOME SCI INC.
Local Similarity: 100.00$
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PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                             PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 100.00%
Query Match: 3.64%
                                                                                                                                                                                       PD 01-JUL-1992.
PA (ELIL ) LILLY & CO ELI.
Best Local Similarity: 100.00%
Query Match: 3.64%
                                                                                                          100.00%
                                                                           14-MAR-2001.
(DOUD/) DOU D.
Local Similarity:
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RESULT 194
                                                                                                                            Match:
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RESULT 195
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RESULT 197
Query Match:
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RESULT 198
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RESULT 199
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                 RESULT 191
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Human hepsin/plasma transmembrane serine protease-like protein.
                                                                                                                  AAR08150 standard; protein; 446 AA.
Non-glycosylated tPA deriv. lacking finger- and EGF-domains.
EP400545-A.
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[GARSYQ]-[Plasminogen 347-541]-[t-PA 262-527] hybrid.
WO9204450-A.
                                                                                                                                                                                                                                                                                                                                     AAB11699 standard; protein; 457 AA.
Human serine protease BSSP2 (hBSSP2), SEQ ID NO:10.
02-00031272-A1.
02-UN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of novel human protease #51.
WO200200860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP94416 standard; protein; 472 AA.

DE Sequence of coding region in plasmid pmTQK112.

PN EP302456-A.

PD 08-FEB-1989.

PA (FUJI) FUJISAWA PHARM CO LTD.

Best Local Similarity: 100.00% Mismatches:

Query Match: Indels:
                                     Mismatches:
Indels:
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Indels:
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Human novel protein NOV10a.
US2003212256-A1.
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                                                                                                                                                                                   PD 05-DEC-1990.
PA (BOEF) BOSHRINGER MANNHEIM GMBH.
Best Local Similarity: 100.00$
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PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00%
3.64%
                                                                                                                                                                                                                                                                                                                                                                                                                                PD 02-UUN-2-U-V.
AA (FUSO) FUSO PHARM IND LTD.
Best Local Similarity: 100.00%
Phory Match: 3.64%
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PA (BEEC ) BEECHAM GROUP PLC.
Best Local Similarity: 100.00$
        PA (FUSO ) FUSO PHARM IND LTD.
Best Local Similarity: 100.00%
Query Match: 3.64%
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MACDOUGALL J R.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAUPIER R J.
BURGESS C E.
ZERHUSEN B D.
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SHIMKETS R 1
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PEYMAN J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATTURAJAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUGE-) SUGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STONE D J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GUNTHER E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200233087-A2.
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(BURG/)
(ZERH/)
                                                              Query Match:
RESULT 216
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RESULT 218
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(MALY/)
(SMIT/)
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(ELLE/)
(SHIM/)
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RESULT 220
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GUOX/)
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RESULT
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t-PA variant d92-179, N184D, I210R, G211A, K212R, V213R, T252R, F305H.
W09002798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR09261 standard; protein; 439 AA.
t-PA variant d92-179, I210R, G211A, K212R, V213R, T252R, F305H.
W09002798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR09259 standard; protein; 439 AA.
t-PA variant d92-179, 1210R, G211A, K212R, V213R, F305H.
W09002798-A.
                                                                                                                                                                                                                                                                                                                                                              AAP94409 standard; protein; 438 AA.
Sequence of coding region in plasmid pTOkPA delta trp.
EP302456-A.
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Mouse serine protease BSSP2 (mBSSP2), SEQ ID NO:8.
WO200031272-A1.
02-UDN-2000.
                                                              Mismatches:
                                                                                                                                        AAP94413 standard; protein; 437 AA.
Sequence of coding region in plasmid psTQitrp
Sequence of Coding region in plasmid psTQitrp
08-FEB-1989.
(FUJI ) FUJISAWA PHARM CO LTD.
Local Similarity: 100.00% Mismatches:
y Match: 108-808.
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Delta 2-89 tissue plasminogen activator.
US5376547-A.
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Modified tissue plasminogen activator.
AU8661804-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR09258 standard; protein; 439 AA.
t-PA variant d92-179, F305H.
WO9002798-A.
PD 08-FEB-1989.

PA (FUJI) FULISAWA PHARM CO LTD.

Best Local Similarity: 100.00$

Query Match: 3.64$

RESULT 207

ID AAP94413 standard; protein; 437 A

DE Sequence of coding region in plas

PN EP302456-A.

PA (FUJI) FUJISAWA PHARM CO LTD.

Best Local Similarity: 100.00$

Query Match: 3.64$

RESULT 208

ID AAP94409 standard; protein; 438 A

DE Sequence of coding region in plas

PN EP30456-A.

PD 08-FEB-1989.
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(AMHP ) AMERICAN HOME PROD CORP.
Local Similarity. 100.00%
Match: 3.64%
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08-FEB99.

(FUJI) FUJISAWA PHARM CO LTD.

Local Similarity: 100.00$

3.64$
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(GETH ) GENENTECH INC.
Local Similarity: 100.00$
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PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00$
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PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 100.00%
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A (GETH) GENENTECH INC.

Best Local Similarity: 100.00%

Annaw Match: 3.64%
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RESULT 211
ID AAR09261
DE t-PA vari
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Query Match:
RESULT 209
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Query Match:
RESULT 210
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RESULT 212
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RESULT 215
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Query Match
RESULT 214
ID AAP706
DE MOdifi
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Environmentally sourced protease protein SeqID 140.
WO2004033668-A2.
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Indels:
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Indels:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID ARR03004 standard; protein; 476 AA.

DE Tissue plasminogen activator (t-PA) deriv.

PN E9152710-A.

PD 31-JAN-1990.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

Best Local Similarity: 100.00$
                                                                                                                                                                                                                                                                AAP70642 standard; protein; 473 AA.
Modified tissue plasminogen activator.
AU8661804-A.
                                                                                                                   Novel human protein; 472 AA. W02003102159-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD05463 standard; protein; 476 AA. Desmodus rotundus urokinase protein.WO2003037363-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
RESULT 228
ID AAR05122 standard; protein; 477 AA.
DE Bat-PA(H).
PN EP32119-A.
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                                                                                                                                                                                                                                                                                                                                                                                                   protein; 475 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR06458 standard; protein; 477 AA.
PA (KEKU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (GANCOLLI E A.
PA (FERN/) FERNANDES E R.
PA (GORN/) GORMAN L.
Best Local Similarity: 100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                               PN W02004033668-A2.
PD 22-APR-2004.
PA (DIVE-) DIVERSA CORP.
Best Local Similarity: 100.00$
Query March:
3.64$
ID AAR03004 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD 22-AUG-1990.
PA (SCHD) SCHERING AG.
Best Local Similarity: 100.00%
Query Match: 3.64%
                                                                                                                                                                                                                                                                                                                PD 05-MAR-1987.

PA (ELLL) LILLY & CO ELI.

Best Local Similarity: 100.00%

3.64%
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Local Similarity: 100.00%
/ Match:
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PA (SCHD) SCHERING AG.
Best Local Similarity: 100.00%
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                                                                                                                                                                                                               Local Similarity: 100.00%
Match: 3.64%
                                                                                                    3.64%
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PA (MERI) MERCK & CO INC.
PA (SEPI) SCHERING AG.
Best Local Similarity: 100.0
                                                                                                                                                                                                 CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                  ADM99257 standard;
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EP383417-A.
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EP383417-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAY-2003
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RESULT 227
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RESULT 229
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RESULT 224
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RESULT 230
                                                                                                      Query Match:
RESULT 223
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RESULT 225
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ADQ19247 standard; protein; 482 AA.
Human myocardial infarction-associated gene derived protein, SEQ ID 910.
WQ2004058052-A2.
                   ပ်
AAPB1036 standard; protein; 479 AA. Modified tissue plasminogen activator lacking F and G region and with 183 and S-186 substd for S and T resp. JP632230084-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AABO8950 standard; protein; 480 AA.
Human secreted protein sequence encoded by gene 22 SEQ ID NO:107.
WO200017222-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR09248 standard; protein; 483 AA.
t-Pa variant d1-44, 1210R, G211A, K212R, V213R, F305H.
22-MAR-1990.
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Polypeptide with plasminogen activator activity
JP61139386-A.
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR09250 standard; protein; 483 AA.
t-PA variant d1-44, V213K, F305H.
W09002798-A.
                                                                                                                                                                                                                                                                                                             AAR22714 standard; protein; 480 AA.
t-PA variant MB1005.
US5100666-A.
                                                                                                                                                                      ¥
                                                                                                                                                                  AAR05571 standard; protein; 479 AA. Glycosylated plasminogen activator. JP02049586-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TOYJ ) TOYO SODA MFG CO LTD.
(SAGA) SAGAMI CHEM RES CENTRE.
(CENG ) CENTRAL GLASS CO LTD.
(HODO ) HODDGAYA CHEM IND CO LTD.
Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PN WO200017222-A1.

D 30-MAR-2000.

PA (HUMA-) HUMAN GENOME SCI INC.

Best Local Similarity: 100.00%
                                                                                                                                                                                                                                         PA (KANF ) KANEGAFUCHI CHEM KK.
Best Local Similarity: 100.00*
Query Match: 3.64*
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PA (APPL-) APPLERA CORP.
Best Local Similarity: 100.00$
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
                                                                  PD 26-SEP-1988.
PD 26-SEP-1988.
PA (BISA) EISAI CO LTD.
Best Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                                                         PD 31-MAR-1592.
PA (MONS ) MONSANTO CO.
Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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RESULT 238
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RESULT 234
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RESULT
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Indels:	in; 483 AA. (deltal-44,N67,K210,E275,I	Mismatches: Indels:	AA. -44,N103,S184,E275)	Mismatches: Indels:	AA. -44,N103,K210,E275)	Mismatches: Indels:	3 AA. 1-44,N67,S184,E275)	Mismatches: Indels:	AA. -44,N67,R252,E275)	Mismatches: Indels:	AA. -44,N103,E275,I277)	Mismatches: Indels:	AA. -44,N103,S184,E27	Mismatches: Indels:	, N67, K210, E27	Mismatches: Indels:	N67,R252,E27 ismatches: ndels:
3.64%	d; protein; 403 variant (deltal-	H INC. 7: 100.00% 3.64%	483 ltal	H INC. 100.00% 3.64%	AAK/0883 standard; protein; 483 A Human tissue PA variant (deltal-4 USSS8732-A.		യർ	H INC. 100.00\$	483 [ta]		483 lta1		483 lta1	INC. 100.00% 3.64%	483 Lta1		protein; 483 riant (deltal INC. 100.00\$
Match: T 249	AAR70855 standard; protein; Human tissue PA variant (de. US5385732-A. 31-7AN-1995,	PA (GETH) GENENTECH Best Local Similarity: Query Match: RESULT 250	AAR70879 standard, protein, Human tissue PA variant (de. US5385732-A.	PD 31-JAN-1995. PA (GETH ) GENENTECH Best Local Similarity: Query Match: RESULT 251	AAK70883 standar Human tissue PA USS385732-A.	11-JAN-1995. (GETH ) GENENTEC Local Similarity Match: T 252	ID AAR70845 standard; protein; 4 DE Human tissue PA variant (delt PN US538572-A.	PA (GETH ) GENENTECH Best Local Similarity: Query Match: RESULT 253	AAK/0848 standard; protein; Human tissue PA variant (de) USS385732-A.	PA (GETH) GENENTECH Best Local Similarity: Query Match:	AAK/0884 Standard; protein; Usesses732-A. 31-Jan-1995	PA (GETH) GENERATECH Best Local Similarity: Query Match: RESULT 255	AAR70886 standard; protein; Human tissue PA variant (de. US5385732-A. 31-JAN-1995.	PA (GETH ) GENENTECH Best Local Similarity: Query Match: RESULT 256	AAR70849 standard; protein; Human tissue PA variant (de; US5385732-A. 31.,TAN-1995	PA (GETH) GENENTECH Best Local Similarity: Query Match: RESULT 257	ID ARK70894 standard; protein; BE Human tissue PA variant (de) PN US5385732-A. PD 31-JAN-1995. PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match:
Query Matc	· DE C	PA PA Best Query RESUI	DE DE	PD PA Best Query RESUI	DE DE	PU PA Best Query RESUI	DI DE C	PA PA Best Query RESUI	DE	PA (GETH Best Locat Query Matc	0 P V C	P.P. P.B. Best Query	ID DE PN PD	PA Best Query RESUL	UI DE DE C	PA PA Best Query RESUL	ID DE DE PN PD PD PA PA Best
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00	Р305Н.		Р305Н.		V213R, T252R, F305H												. (777)
Mismatches: 0 Indels: 0	K212R, V213K,	Mismatches: 0 Indels: 0	r. K212Q, V213K,	Mismatches: 0 Indels: 0	3211A, K212R,	Mismatches: 0 Indels: 0	ڼ	Mismatches: 0 Indels: 0	į.	Mismatches: 0 Indels: 0	i	Mismatches: 0 Indels: 0	ь. Р305Н.	Mismatches: 0 Indels: 0	ن	Mismatches: 0 Indels: 0	., 1,N67,D184,E275,I277) Mismatches: 0
	n; 483 AA., , G211A, B	*0	ein; 483 AA OR, G211H, 1	* 00 *	protein; 483 AA, N184D, I210R, 0	INC. 100.00% 3.64%	protein; 483 AA , F305H.	INC. 100.00% 3.64%	protein; 483 AA, , T252R, F305H.	INC. 100.00% 3.64%	protein; 483 AA F305H.	INC. 100.00% 3.64%	protein; 483 AA. , V213K, T252R, F	INC. 100.00% 3.64%	protein; 483 AA , I210K, F305H.	INC. 100.00% 3.64%	protein; 483 AA. iant (deltal-44,N6` NC. 100.00\$ Misr
100.00% 3.64%	protein; , I210R, C	INC. 100.0 3.64	prot I21	INC. 100. 3.64	prot N18	INC. 100 3.6	Pro	3. 3.	pr	10 10	P3	3.01	ā,	ŽΗM	Ω.	ž i e	FE GA
Local Similarity: 100.00% Match: 3.64%	ESULT 240 D AAR09249 standard; protei E t-PA variant d1-44, I210R N WO9002798-A.	22-MAR-1990. (GETH ) GENENTECH INC. Local Similarity: 100.00%	7 241 AAR09254 standard; protein; t-PA variant d1-44, I210R, C	PN W09002798-A. PD 22-MAR-1990. PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00\$ Query March: 3.64\$	7 standard; riant d1-44	VTECH city:	T 243 AAR09247 standard; pro t-PA variant d1-44, F3 WASAA3788.h	: ENTECH arity:	1 standard; riant d1-44	NTECH rity:	3 standard; riant Y67N, 98-a	TECH city:	2 standard; riant d1-44 98-A.	R-1990. ) GENENTECH Similarity: h:	RESULT 247 ID AAR09253 standard; p DE t-PA variant d1-44, PN WO900278-1	NTECH rity:	1 standard; issue PA var 32-A. 1995. GENENTECH I

AAR70882 standard; protein; 483 AA. Human tissue PA variant (deltal-44,N103,R252,E275). US5385732-A.

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AAR70881 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,NI03,R210,A211,R212,R213,E275).
US5385732-A.
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Human tissue PA variant (deltal-44,N103,K213,E275,1277).
US5385732-A.
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AAR70852 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N67,K213,E275,1277).
US5385732-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR79144 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N67,S184,E275,I277).
US5385732-A.
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     AAR70878 standard, protein, 483 AA.
Human tissue PA variant (deltal-44,N103,D184,E275).
US5385732-A.
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Human tissue PA variant (deltal-44,N67,K213,E275).
US5385732-A.
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Human tissue PA variant (deltal-44,N67,E275,I277)
US5385732-A.
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Indels:
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Human tissue PA variant (delta1-44,N103,B275)
USS385732-A.
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Indels:
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Indels:
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Indels:
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AAR70843 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N67,E275)
USS385732-A.
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                                                                                                                                                                                             31-JAN-1995.
(GETH ) GENENTECH INC.
Local Similarity: 100.00%
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PD 41-JAN-1995.
PA (GETH ) CENENTECH INC.
Best Local Similarity: 100.00%
3.64%
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31-JAN-1995.
(GETH ) GENENTECH INC.
Local Similarity: 100.00%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
3.64%
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(GETH) GENENTECH INC.
Local Similarity: 100.00%
                                                        USJ-JAN-1995.
(GETH ) GENENTECH INC.
Local Similarity: 100.00$
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Best Local Similarity: 100.00%
Query Match: 3.64%
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RESULT 263
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RESULT 261
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RESULT 267
RESULT 258
ID AAR708
DE Human
PN US5385
PD 31-JAN
PA (GETH
                                                                                                Best Lo
Query M
RESULT
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AAR70888 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N103,R210,A211,R212,R213,E275,I277).
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Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275,I277)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR70847 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N67,R210,A211,R212,R213,E275).
US5385732-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR70890 standard, protein; 483 AA.
Human tissue PA variant (deltal-44,N103,K210,E275,I277).
US5385732-A.
                                                                                                                                                                                                                      AAR70889 standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N103,R252,E275,O277).
US5385732-A.
                                                                      האה / טוט standard; protein; 483 AA.
Human tissue PA variant (deltal-44,N103,D184,E275,I277).
US5385732-A.
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Human tissue PA variant (deltal-44,N103,K213,E275).
US5385732-A.
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AAR70844 standard; protein; 483 AA.
Human tissue PA variant (delta1-44,N67,D184,E275)
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PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
3.64$
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PD 31.JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
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PA (GETH ) GENENTECH INC.

BEST LOGAL Similarity: 100.00%
3.64%
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PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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Local Similarity: 100.00%
Match: 3.64%
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PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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Best Local Similarity: 100
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RESULT 275
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RESULT 268
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RESULT 276
ID ABM83:
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RESULT 273
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WO2003102159-A2
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RESULT 293
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Human diagnostic and therapeutic pprotein SEQ ID NO:3392. WO2004023973-A2.
                                                                                                      ABM83142 standard; protein; 508 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:3391.
WO2004023973-A2.
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Novel human protein NOV4i.
WO2003102159-A2.
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Novel human protein NOV4h.
WO2003102159-A2.
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PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 100.00$
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(CURA-) CURAGEN CORP.
Local Similarity: 100.00%
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PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00$
                                         (INCY-) INCYTE CORP.
Local Similarity: 100.00%
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(CURA-) CURAGEN CORP.
Local Similarity: 100.00%
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(CURA-) CURAGEN CORP.
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(CURA-) CURAGEN CORP.
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RESULT 281
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ABM80985 standard; protein; 516 AA.
Tumour-associated antigenic target (ТАТ) polypeptide PRO81669, SEQ:2539.
WO2004030615-A2.
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AAP70257 standard; protein; 516 AA.
Sequence of human tissue plasminogen activator (TPA) and leader.
EP231883-A.
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Sequence of des 1-44E275 t-PA mutant.
WO8909266-A.
                                                                     protein; 513 AA.
                                                                                                                                                                                                           ADH41521 standard; protein; 513 AA.
                                                                                                                                                                                                                                                                                                                                                  AAP60614 standard, protein, 516 AA.
Plasmid pDAP3 encoded sequence.
JP61139386-A.
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(NIPS) NIPPON SODA CO.
(CENG) CENTRAL GLASS CO LTD.
(TOYJ) TOYO SODA MFG CO LTD.
(NISC) NISSAN CHEM IND LTD.
(NISC) NISSAN CHEMICAL INDS KK.
LOCAL Similarity: 100.00%
I JOACAL 3.64%
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Antipsoriatic protein sequence #90.
WO2004028479-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-1986.
(TOXJ) TOYO SODA MFG CO LTD.
(SAGA) SAGAMI CHEM RES CENTRE.
(CENG) CENTRAL GLASS CO LTD.
(HODO) HODOGAYA CHEM IND CO LTD.
Local Similarity: 100.00%
                                                                                                                   11-DEC-2003.
(CURA-) CURAGEN CORP.
Local Similarity: 100.00%
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Query Match: 3.64%
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PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00%
              Best Local Similarity: 100.00$
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Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
                                                                                    Novel human protein NOV4e.
WO2003102159-A2.
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WO2003102159-A2.
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(CURA-) CURAGEN CORP.
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                                                                   ADH41509 standard;
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Mismatches:

Indels:

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PA (AMHP) AMERICAN HOME PROD CORP.
Best Local Similarity: 100.00%
Ouery Match:
3.64%
                                                                                                                        AAR09235 standard; protein; 520
t-PA deletion variant d297-303.
WO9002798-A.
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Best Local Similarity: 100.00%
Query Match:
3.64%
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Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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Best Local Similarity: 10 Court Match:
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RESULT 303
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t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by KPIAEK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR74681 standard; protein; 518 AA.
t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by TSRNR).
CN1082111-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR74686 standard; protein; 518 AA.
t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by DSSRW).
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t-PA mutein (N1170, N1840, delta 296-302, 44-50 replaced by DPHEAT)
CN1082111-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR74679 standard; protein; 518 AA.
t-PA mutein (N1170, N1840, delta 296-302, 44-50 replaced by TIANR).
CN1082111-A.
                                                                                                                                                                                                                                                                                                                                                                                          AAR74684 standard; protein; 518 AA.
t-PA mutein (N1170, N1840, delta 296-302, 44-50 replaced by DFVDQ)
t-PA mutein (N1170, N1840, delta 296-302, 44-50 replaced by DFVDQ)
t-PA mutein (N1170, N1840, delta 296-302, 44-50 replaced by DFVDQ)
16-FEB-1994
(BIOE-) BIOENGINEERING INST ACAD MILITARY.
Local Similarity: 100.00% Mismatches: 0
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Local Similarity: 100.00% Mismatches:
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Local Similarity: 100,00% Mismatches:
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PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.

Best Local Similarity: 100.00% Mismatches:

1.64 Indels:
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PN 16-FEB-1994.
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
Best Local Similarity: 100.00% Mismatch 3.64% Indels:
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Delta 55-62 tissue plasminogen activator.
US3376547-A.
27-DEC-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t-PA deletion variant d297-304.
                                                                                                                                                      AAR09237 standard; protein; 518 AA. t-PA deletion variant d297-305. WO9002798-A.
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                                                                                                                                                                                                                                WOYULE. 22-MAR-1990.
(GETH) GENENTECH INC.
Local Similarity: 100.00%
      PD 05-0CT-1989.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DE t-PA mutter PN CN108211. PN CN108211. PD 16-FEB-1. PA (BIOE-) Best Local Siquery Match: RESULT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
RESULT 301
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RESULT 300
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RESULT 296
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RESULT 297
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AAR74678 standard; protein; 521 AA.
t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by ESKPEAEE).
CN1082111-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR74682 standard; protein; 521 AA.
t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by ERHTSVQT)
CN1082111-A.
                                                              ID AAR74689 standard; protein; 520 AA.

E t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by QRLASQA).

PD CA.082111-A.

PD 16-PEB-1994.

PA (BIOB-) BIOENGINEBRING INST ACAD MILITARY.

Best Local Similarity: 100.00% Mismatches: 0

Query Macch: 3.64% Indels:
                                                                                                                                                                                                                      EESULT 305

ID AAR74688 standard; protein; 520 AA.

ID AAR74688 standard; protein; 520 AA.

DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by DNCRRPG).

PN CN1082111-A.

PD 16-FEB-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tissue type plasminogen activator (h-tPA) mutant polypeptide.
CN1397564-A.
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Best Local Similarity: 100.00% Mismatches:
Ouery Match: 3.64% Indels:
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Indels:
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PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.
Best Local Similarity: 100.00$ Mismatch
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(BIOE-) BIOENGINEERING INST ACAD MILITARY.
                       Indels:
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AARO242 standard; protein; 521 AA.
L-PA deletion variant d300-305.
WO9002798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR09234 standard; protein; 521 AA.
t-PA deletion variant d297-302.
WO9002798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP50400 standard; protein; 521 AA.
TPA-(13-527).
JP60041697-A.
                                                                                                                                                                                                                                                                                                                                                                                                                              ADL00357 standard; protein; 520 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PA (ASAH ) ASAHI CHEM IND CO LTD.
Best Local Similarity: 100.00%
Ouery Match: 3.64%
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ID AAP82584 standard; protein; 524 AA.

DE Modified tissue plasminogen activator lacking the G region and with G-183 Modified tissue plasminogen activator lacking the G region and with G-183 DE and S-186 substd for S and T resp.

PD 26-SEP-1988.

PA (EISA ) EISAI CO LTD.

Mismatches: 0

Query Match: 3.64% Indels: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP85585 standard; protein; 524 AA.
Modified tissue plasminogen activator lacking F and G region and with S-
119 substd for M.
UP63230084-A.
                                                 AAR74683 standard; protein; 522 AA.
t-PA mutein (N1170, N1840, delta 296-302, 44-50 replaced by YAYSQLRDQ).
CN1082111-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR99136 standard, protein, 524 AA.
Mutant human tissue plasminogen activator for fibrin clot lysis.
USS501853-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR99138 standard; protein; 524 AA.
Mutant human tissue plasminogen activator for fibrin clot lysis.
                                                                                                                            16-FEB-1994.
(BIOE-) BIOENGINEERING INST ACAD MILITARY.
The similarity: 100.00% Mismatches:
 (BIOE-) BIOENGINEERING INST ACAD MILITARY.
Local Similarity: 100.00% Mismatches:
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t-PA deletion variant d297-299.
WO9002798-A.
                                                                                                                                                                                                         T 322
AR09232 standard; protein; 523 AA.
L-PA deletion variant d297-300.
WO9002798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR09239 standard; protein; 524 AA.

-Ph deletion variant d300-302.

WO9002798-A.

22-MAR-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                             PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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PA (EISA) EISAI CO LTD.
Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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Query Match: 3.64%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
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                                    Query Match:
RESULT 321
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RESULT 323
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RESULT 327
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RESULT 329
ID AAR991
DE Mutant
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RESULT 326
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RESULT
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RESULT
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t-PA mutein (N1170, N1840, delta 296-302, 44-50 replaced by QPLQTYPSS).
16-FEB-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
Delta (466-470) tPA variant with K416A, H417A and E418A substns.
NO9113149-A.
OS-SEP-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR13919 standard; protein; 522 AA.
Delta (466-470) tPA variant with B426A, R427A, K429A and E430A
substitutions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR13917 standard; peptide; 522 AA.
Delta (466-470) tPA variant with K296A, H297A, R298A and R299A
substitutions.
                                                                                                                                                                                                                                                                                                                                                    AAR13921 standard; protein; 522 AA.
Delta (466-470) tPA variant with H432A and R434A substns.
W09113149-A.
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Delta (466-470) tPA variant with R339A and R342A substns.
W09113149-A.
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Delta (466-470) tPA variant with Y67N substitution.
W09113149-A.
 Mismatches:
Indels:
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                                              AAR09241 standard; protein; 522 AA.
t-PA deletion variant d300-304.
WO9002798-A.
                                                                                                                                                                                                         Æ
                                                                                                                                                                                                    AAR09233 standard; protein; 522
t-PA deletion variant d297-301.
WO9002798-A.
                                                                     DE t-PA deletion variance.
PN W09002799-A.
PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00%
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(GETH ) GENENTECH INC.
Local Similarity: 100.00%
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PA (GETH) CENENTECH INC.
Best Local Similarity: 100.00$
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
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PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00%
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Local Similarity: 100.00%
Match: 3.64%
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(GETH ) GENENTECH INC.
Local Similarity: 100.00%
Local Similarity: 100.00% Match: 3.64%
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05-SEP-1991.
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RESULT 318
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RESULT 313
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RESULT 314
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RESULT 315
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Query Match
RESULT 319
                   Query Matc
RESULT 312
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Mismatches:
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t-PA deletion variant d304-305.
WO9002798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR09244 standard; protein; 525 AA. t-PA deletion variant d297, d300. W09002798-A.
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t-PA deletion variant d297.
WO9002798-A.
                                                                                                                                                                            Query Match: 3.64* II
RESULT 339
ID AARDO245 standard; protein; 525 AA.
DB t-PA deletion variant d297, d305.
PN W09002798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR09229 standard; protein; 526 AA.
t-PA deletion variant d305.
WO9002798-A.
                                                                                                                                                                                                                                                                                                                                                    AAR09238 standard; protein; 525 AA.
t-PA deletion variant d300-301.
W09002798-A.
                                                                    AAR09230 standard; protein; 525 AA.
t-PA deletion variant d297-298.
WO9002798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
                                                                                                                          PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
                  100.00$
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(GETH ) GENENTECH INC.
PA (MONS ) MONSANTO CO.
Best Local Similarity: 1
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RESULT 345
                                   Query Match:
RESULT 338
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RESULT 341
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RESULT 344
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RESULT
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Mutant human tissue plasminogen activator for fibrin clot lysis.
USS501853-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            лакуулзз standard; protein; 524 AA.
Mutant human tissue plasminogen activator for fibrin clot lysis.
USS501853-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR99132 standard; protein; 524 AA.
Mutant human tissue plasminogen activator for fibrin clot lysis.
USS501853-A.
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Mutant human tissue plasminogen activator for fibrin clot lysis.
                                                                                                                                                fibrin clot lysis.
                                                                                                                                                                                                                                                                                        AAR99137 standard; protein; 524 AA.
Mutant human tissue plasminogen activator for fibrin clot lysis.
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Tissue plasminogen activator (t-PA) variant MB1018.
EP311589-A.
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                                                                                                                                AAR99134 standard; protein; 524 AA.
Mutant human tissue plasminogen activator for
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Tissue plasminogen activator mutant 2K2.
WO8907146-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PN CSC-11996.
PD GEMAR.1996.
PA (BEHW ) BEHRINGWERKE AG.
PA (CHIR ) CHIRON CORP.
BEST LOCAL SIMILARITY: 3.64%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00$
                                                                                                                                                                                                                                                                                                                                       PD C5-WAR.1996.
PA (BEHW) BEHRINGWERKE AG.
PA (CHIR ) CHIRON CORP.
Best Local Similarity: 100.00%
                PD 26-MAR-1996.
PA (BEHW) BEHRINGWERKE AG.
PA (CHIR ) CHIRON CORP.
Best Local Similarity: 3.64%
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(BEHW) BEHRINGWERKE AG.
(CHIR) CHIRON CORP.
LOCAL Similarity: 100.00%
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PA BEHW BERRINGWERKE AG.
PA (CHIR ) CHIRON CORP.
Best Local Similarity: 100.00$
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(CHIR) CHIRON CORP.
Local Similarity: 100.00%
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(CHIR ) CHIRON CORP.
Local Similarity: 100.00%
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26-MAR-1996.
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           US5501853-A.
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RESULT 337
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Query Match:
RESULT 331
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RESULT 336
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RESULT 335
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RESULT 332
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RESULT 330
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RESULT 363
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RESULT 364
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RESULT 356
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RESULT 361
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RESULT
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RESULT
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Thrombolytic proteins 1-9-1-11 having t-PA activity and R275 is deleted
or replaced and containing a modified N-linked glycosylation site.
W08704722-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP71748 standard, protein, 527 AA.
Tissue plasminogen activator substituted at positions 117 and 119.
EP238304-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP71749 standard; protein; 527 AA.
Tissue plasminogen activator substituted at positions 117 and 118.
EP238304-A.
23-58P-1987.
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Gln(117)-substituted tissue plasminogen activator.
 Mismatches:
Indels:
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Indels:
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DE t-PA deletion variant d301.

PN W09002798-A.

PD 22-MAR-1990.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00* M?

Query Match: 3.64* II
                                                                                                                                                                                                                                                                                                                                                                                                                               L-PA deletion variant d303.
WO9002798-A.
22-MAR-1990.
                                               AAR09223 standard; protein; 526 AA. t-PA deletion variant d299. W09002798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR09228 standard; protein; 526 AA. t-PA deletion variant d304. WO9002798-A.
                                                                                                                                                                                                                                                                                                             AAR09226 standard; protein; 526 AA.
     Guery Match:
RESULT 317

ID AAR09223 standard; protein; 52

ID E-PA deletion variant d299.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PN MOSTONIA
PD 13-AUG-1987.
PA (GEMY) GENETICS INST INC.
PA (LARS/) LARSEN G R.
Best Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOZUMAR-1990.
22-MAR-1990.
(GETH ) GENENTECH INC.
Local Similarity: 100.00$
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PD 23-SEP-1987.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00$
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
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D 23-SEP-1987.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3.64%
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Best Local Similarity: 100.00%
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RESULT 348
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RESULT 350
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RESULT 351
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RESULT 353
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RESULT 355
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RESULT 352
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RESULT 354
ID AAP717
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RESULT
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J 357
AAP70168 standard; protein; 527 AA.
Sequence of wild-type human tissue plasminogen activator (t-PA) from HeLa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombolytic protein with secondary structure of human tissue plasminogen
                                                                       ID AAP71750 standard; protein; 527 AA.

DE Tissue plasminogen activator substituted at positions 117 and 275.

DR E238304-A.

DA 23-SEP-1997.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR06236 standard; protein; 527 AA. Novel tissue plasmid pTPA102.
Novel tissue plasminogen activator (tPA) encoding plasmid pTPA102.
EP379890-A.
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Sequence of tissue plasminogen activator (tPA)
WO8911531-A.
                     Mismatches:
Indels:
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Indels:
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Plasminogen activator.
EP365468-A.
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AAR05806 standard, protein, 527 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 362
AR05489 standard; protein; 527 AA.
tPA024 precursor protein.
EP373896-A.
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tPA024 precursor protein.
EP373896-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 20-JUN-1990.
PD 20-JUN-1990.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
PA (YAWA) NIPPON STEEL CORP.
Best Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUN 1990.
(YAWA ) YAMANOUCHI PHARM CO LTD.
(YAWA ) NIPPON STEEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD 25-APR-1990.

PD 25-APR-1990.

RA (CIBA) CIBA GEIGY AG.

PA (UCPG-) UCP GEN-PHARMA AG.

Best Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                         PD 30-NOV-1999.
PD 30-NOV-1999.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00%
Query Match: 3.64%
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10-JUN-1987.
(CIBA ) CIBA GEIGY AG.
Local Similarity: 100.00%
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PA (FUJI) FUJISAWA PHARM CO I
Best Local Similarity: 100.00%
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JP02145184-A.
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*	Mismatches: Indels:	. 527 AA. R298A, R299A.	Mismatches: Indels:	527 AA.	Mismatches: Indels:	527 AA. K429A, E430A.	Mismatches Indels:	527 AA. K212Q, V213K, F305H	Mismatches: Indels:	527 AA.	Mismatches Indels:	527 AA. E418A.	Mismatches Indels:	; 527 AA. K212R, V213R, F305H	Mismatches Indels:	527 AA.	Mismatches Indels:
	INC. 100.00% 3.64%	rotein; H297A,	INC. 100.00% 3.64%	protein;	INC. 100.00% 3.64%	protein; R427A,	INC. 100.00% 3.64%	orotein; G211H,	INC. 100.00% 3.64%	protein; H287A.	INC. 100.00% 3.64%	protein; H417A,	INC. 100.00% 3.64%	protein, G211A,	INC. 100.00% 3.64%	protein; , H332A.	INC. 100.00%
t-PA variant R267A. W09002798-A.	ECH ty:	standard; ant K296A -A.	990. GENENTECH milarity:	standard; iant E303A 8-b	-MAR-1990. ETH ) GENENTECH cal Similarity:	367 R09277 standard; PA variant E426A	-MAR-1990. ETH ) GENENTECH ]	dard; I210R	PN WOSULZ/98-A. D 22-MAR-1990. PA (CETH ) GENENTECH I Best Local Similarity: Query Match:	7 standard; riant D283A,	PN W09002798-A. DD 22-MAR-1990. PA (GETH) GENENTECH I Best Local Similarity: Query Match:	6 standard; riant K416A, 98-A.	PD 22-MAR-1990. PA (GETH ) GENENTECH I Best Local Similarity: Query Match:	6 standard; riant I210R 98-A.	NTECH rity:	0 standard; riant H331A, 98-A.	PD 22-MAR-1990. PA (GETH) GENENTECH 1 Best Local Similarity:

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Indels:
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Indels:
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Indels:
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RESULT 376
ID AAR09272 standard; protein; 527 AA.
DE t-PA variant B347A, E348A, E349A, K351A.
PN W09002798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 379
ID AAR09273 standard; protein; 527 AA.
ID AAR09273 standard; protein; 527 AA.
DE L-PA variant D364A, D365A, D366A.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GFH ) GENENTECH INC.
Best Local Similarity: 100.00$ Missind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duery March:
RESULT 381
ID AAR05280 standard; protein; 527 AA.
DE t-PA variant H445A, R449A.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$ Mis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duery Match:
RESULT 377

ID AAR05281 standard; protein; 527 AA.

DE t-PA variant R449A, D453A.

PN W09002798-A.

PD 22-WAR-1990.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00$ Mis
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Query Match:
RESULT 380
ID AAR09262 standard; protein; 527 AA.
DE t-PA variant Y67N, F305H.
PN WO9002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mir
DE t-PA variant R339A, R342A.

PN W09002798-A.

PD 22-MAR-1990.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00$ Mism

Cuery Match: 3.64$ India

DE AR809275 standard; protein; 527 AA.

DE t-PA variant E410A.

PN W09002798-A.

PN W09002798-A.

PN GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
                                                                                                                                                                                                               Query Match:
RESULT 375
ID AAR09279 Standard; protein; 527 AA.
DE L-PA variant E408A.
PN W09002798-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1D AAR09215 standard; protein; 527 AA.
DE t-PA variant F305 H, T, N, K, R, Q.
PN W09002798-A.
D 22-MAR-1990.
PA (GETH ) GENEWTECH INC.
Best Local Similarity: 100.00$

M Query Match:
3.64$
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Query Match: 3.64% LI
RESULT 382
ID AAR09278 standard; protein; 527 AA.
DE t-PA variant H432A, R434A.
                                                                                                                                                                                                                                                                                                                                                                                ID AAR09272 Stainer, E348A, E3.
DE t-PA variant E347A, E348A, E3.
PN W09002798-A.
PD 22-MAR-1990.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
RESULT 378
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imilarity: 1 3 1 standard, p riv. (II). 4-A. 1991. RANEGAFUCHI	Query Match:  RESULT 392  ID AAR13914 standard; protein;  DE T-PA deriv. (V).  PN EP445464-A.  PD 11-SEP-1991.  PA (KANF ) KANEGAFUCHI KAGAKU PBest Local Similarity: 100.00%  Query Match:  RESULT 393	ID ARK13912 standard; protein; DE T-PA deriv. (III). PN EP44564-A. PD 11-SEP-1991. PA (KANF) KANEGAFUCHI KAGAKU BEST LOCAL Similarity: 100.00\$ Query Match: RESULT 394 ID AAR13910 standard; protein; DE T-PA deriv. (I).	PN EP445464-A. PD 11-SEP-1991  PA (KANF) KANEGAFUCHI KACAKU F Best Local Similarity: 100.00\$ Query Match: 3.64\$  RESULT 395  ID AAR13913 standard; protein; DE T-PA deriv. (IV). PN EP445464-A. PD 11-SEP-1991.		ID AAR21599 standard; protein; DE tPA variant - N117Q, D236A, PN WO9202612-A. PD 20-FEB-1992. PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00\$ Query Match: ID AAR21600 standard; protein; DE TPA variant - E94A, D95A, T1) PN WO9202612-A.	PD 20-FEB-1992. PA (GETH) GENENTECH INC. Best Local Similarity: 100.00\$ Query Match: 3.64\$ RESULT 399 ID ARR21598 standard; protein; DE tPA variant - T103N, D236A, PN W09202612-A. PD 20-FEB-1992. PA (GETH) GENENTECH INC. Best Local Similarity: 100.00\$
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INC. 100.00\$ Mismatches: 3.64\$ Indels: ; protein; 527 AA.	NC. 100.00% Mismatches: 3.64% Indels: protein; 527 AA. R462A.	100.00% Mismatches: 3.64% Indels: Protein; 527 AA. activator derivative #2. I KAGAKU KOGYO KK. 100.00% Mismatches:	3.64% Indels: protein, 527 AA, activator derivative #1. I KAGAKU KOGYO KK. 100.00% Mismatches: 3.64% Indels:	4 × 4 ×	smat dele ive	UCHI KAGAKU KOGYO KK.  H. Mismatches: 3.64* Indels: rd; protein; 527 AA. gen activator derivative #3. UCHI KAGAKU KOGYO KK.
PN WO9002798-A.  PD 22-MAR-1990.  PA (GETH) GENENTECH INC.  Best Local Similarity: 100.00%  Query Match: 333  ID AAR09279 standard; protein;  DE L-PA variant R440A.  PN WO9002798-A.	Carmar.1990.  (GETH) GENENTECH: Local Similarity: . Match: .T 384 ARR09282 standard; t-PA variant D460A, W09002798-A. 22-MAR-1990. (GETH) GENENTECH:	milarity: standard; lasminogen -A. KANEGAFUCH YAHARA H. milarity:	Query Match:  RESULT 386  ID AAR11342 standard; protein; 527 AA.  DE Tissue plasminogen activator derivat PN EP420502-A.  PD 03-APR-1991.  PA (KANP ) KANEGAPUCHI KAGAKU KOGYO KK.  PA (YAHA/) YAHARA H.  PA (YAHA/) YAHARA H.  PA (YAHA/) YAHARA H.  Query Match:  3.64* In	SULT 387 AAR11346 standard; Tissue plasminogen EP420502-A. (XANF) KANEGAFUCHI (YANF) YAHARA H. It Local Similarity: STY Match: SULT 388 WAR11347 standard; Frisue nlasminogen	PN EP420502-A. PD 03-APR-1991. PD 03-APR-1991. PA (KANP) KANEGAFUCHI KAGAKU KOGYO KK. PA (YAHA/) YAHARA H. Best Local Similarity: 100.00% Mi Query Match: 3.64% In RESULT 389 ID AAR11801 standard; protein; 527 AA. DE Tissue plasminogen activator derivat PD 03-APR-1991.	(KANF ) KANEGAR (YAHA) YAHARA it Local Similarit ENT MATCH: SULT 390 ARN11345 Standa ARN11345 Standa Zissue plasminc EP420502-A. 03-APR-1991. (KANF ) KANEGAR

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527 AA. KOGYO KK. Mismatches: Indels: 527 AA.	KOGYO KK. Mismatches: Indels: 527 AA.	KOGYO KK. Mismatches: Indels: 527 AA.	KOGYO KK. Mismatches: Indels: 527 AA.	KOGYO KK. Mismatches: Indels: 527 AA.	Mismatches: Indels: 527 AA. D238A, K240A.	Mismatches: Indels: ; 527 AA.	Mismatches: Indels: 527 AA. D238A, K240A.	Mismatches:
RESULT 391  ID AAR13911 standard, protein, DE T-PA deriv. (II).  PN EP44546-4.  PD 11-SEP-1991.  PA (KANF ) KANEGAFUCHI KAGAKU P Best Local Similarity: 100.00% Query Match: 3.64% RESULT 392  ID AAR13914 standard, protein, PN EP445464-A.	11-SEP-1991.  (KANF ) KANEGAFUCHI KAGAKU St. Local Similarity: 100.00% Antrop. 3.64% SULT 393  AAR13912 standard; protein; T-PA deriv. (III).	11-SEP-1991.  (KANF) KANEGAPUCHI KAGAKU st Local Similarity: 100.00% sry March: 3.64% SULT 394 AAR11910 standard; protein; T-PA deriv. (I).	GGAFUCHI KAGAKU rity: 100.00% 3.64% ndard; protein;	11-SEP-1991.  KANF ) KANEGAPUCHI KAGAKU st Local Similarity: 100.00% ary Match: 3.64% SULT 396 AAR21594 standard; protein; tPA variant - D95A.	3 B T	12. INENTECH INC. IARITY: 100.00% 1. Arity: 3.64% Itandard; protein It - E94A, D95A,	COFFEL 1992. COFFEL 1992. SUCCAL Similarity: STM MATCH: MATCH: AR21598 standard; CFA Variant - T103 W09202612-A. 20-FEB-1992.	PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00%

RESULT 409

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Indels:	527 AA.	Mismatches: Indels: 27 AA	•	527 AA. Mismatches: Indels:	27 AA. 6A, D238A, K240A.	Mismatches: Indels:	527 AA. Mismatches:	10013:		527 AA. Mismatches.	Indels:	Mismatches: Indels: 527 AA.	
3.64%	protein;	INC. 100.00% 3.64% protein: 5	INC. 100.00\$	protein; INC. 100.00% 3.64%	Ωı .	INC. 100.00% 3.64%	rm.	3.54% protein; tPA.	100.00\$ 3.64\$	protein; tPA.	3.64% protein; tPA.	100.00% 3.64% protein; tPA.	ъ.
Match:	ESULT 400  D AR21593 standard;  DE TPA variant - E94A.  N W09202612-A.	NTECH rity: ndard:	ariant - E94A 2612-A. B-1992. ) GENENTECH Similarity:	ESULT 402  D AAR21595 standard; E tPA variant - D95G N W09202612-A. D 20-FEB-1992. A (GETH ) GENENTECH : est Local Similarity: herry Match:	ESULT 403 (D AAR21597 standard; DE tPA variant - E94A, PN W09202612-A.	B-1992. ) GENENTECH Similarity: h:	2 standiant - 12-A. 1992. GENENT	uery Matcn: RESULT 405 ID AAR22620 standard; ) DE Mutated recombinant PN JP04094684-A.	PD 26-MAR-1992. AA (KANF) KANEKA CORP Sest Local Similarity: Duery Match: RESULT 406	619 standar ed recombin 94684-A. R-1992. ) KANEKA C	GEST LOCAL SIMILATILY: Duery Match: RESULT 407 ID AAR22617 standard; E Mutated recombinant PN JP04694684-A.	PD 26-MAR-1992. PA (KANF) KANEKA CORP- GET LOCAL Similarity: Duery Match: SEGULT 408  ID ARK22621 standard; DE Mutated recombinant	JP04094684-A. 26-MAR-1992. (KANF ) KANEKA CORP

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ID AAR2023 standard; protein; 527 AA.
ID AAR20233 standard; protein; 527 AA.
DE t-PR analogue expressed by pCDM8-018.
PN JF02285680-A.
PD 16-DEC-1991.
PA (SUMU ) SUMITOMO SEIYAKU KK.
Best Local Similarity: 100.00% Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DE t-PA analogue expressed by pCDM8-009.
PN 4P02285680-A.
PD 16-DEC-1991.
PA (SUMU) SUMITOMO SEIYAKU KK.
Best Local Similarity: 100.00$
RESULT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE R465G t-PA analogue.

PN J792285680-A.

PD 16-DEC-1991.

PD 16-DEC-1991.

Best Local Similarity: 100.00% Misma Query Match:

RESULT 414

IRSULT 414

DE t-PA analogue expressed by pCDM8-011.

PN J79228580-A.
DE Mutated recombinant tPA.

DE Mutated recombinant tPA.

PN JP04094684-A.

PD 36-MAR-1992.

PA (KANF) KANEKA CORP.

Best Local Similarity: 100.00$ Misn Query Match:

RESULT 410

ID 74820221 standard; protein; 527 AA.

DE t-PA analogue expressed by pCDM8-013.
                                                                                                                                                                                                                                                                                                                    Query Match:
RESULT 412
ID AAR2020 standard; protein; 527 AA.
DD E PA analogue expressed by pCDM8-012.
PN JP03285680-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR20222 standard; protein; 527 AA.
t-PA analogue expressed by pCDM8-014.
JP03285680-A.
                                                                                                       RESULT 410

ID AAR2021 standard; protein; 527 AA.

ID AAR2022 standard; protein; 527 AA.

ID AAR2022 standard; protein; 527 AA.

BY JP02285680-A.

PD 16-DEC-1991.

PD 16-DEC-1991.

PD 16-DEC-1991.

PD 3-044 Miss

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Ouery Match:
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AAR20216 standard; protein; 527 AA.
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AAR2015 standard; protein; 527 AA.
8462E t-PA analogue.
JP03285680-A.
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PD 16-DEC-1991.
PA SUMU ) SUMITOMO SEIYAKU KK.
Best Local Similarity: 100.00%
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RESULT 415
ID AAR20222
DE T-PA anal
PN JP0328568
PD 16-DEC-19
PA (SUMU)
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RESULT 416
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RESULT 417
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7 AA. M8-010.	Mismatches: Indels:	7 AA.	Mismatches: Indels:	7 AA.	Mismatches: Indels:	7 AA.	Mismatches: Indels:	7 AA.	Mismatches: Indels:	7 AA.	Mismatches: Indels:	7 AA.	Mismatches: Indels:	527 AA. ,A198,A298,A299).	Mismatches: Indels:	7 AA.	Mismatches: Indels:
standard; protein; 527 AA. togue expressed by pCDM8-010 0-A.	SIYAKU KK. 100.00% 3.64%	protein; 527 N50.	INC. 100.00% 3.64%	protein; 527 (N65, S67).	INC. 100.00% 3.64%	protein; 527 N67.	INC. 100.00% 3.64%	protein; 527 (N65, T67).	INC. 100.00% 3.64%	protein; 527 (N67,N103).	INC. 100.00% 3.64%	protein; 527 (N105, S107).	INC. 100.00% 3.64%	protein; 52' (N67,A197,A19	INC. 100.00% 3.64%	; protein; 527 N103.	INC. 100.00% 3.64%
AAR20218 standard; t-PA analogue expr JP03285680-A.	PD 16-DEC-1991.  PA (SUMU) SUMITOMO SEIYAKU KK Best Local Similarity: 100.00% Query Match: 3.64%	ID AAR44808 standard; protein; DE Human tPA variant N50. PN USS-270198-A. PD 14-DEC-1993.	PA (GETH ) GENENTECH : Best Local Similarity: Query Match:	9 standard, PA variant 98-A.	FD 14-DEC 1555.  GETH ) GENENTECH : Best Local Similarity: Query Match: RESULT 421	AAR44811 standard; protein; Human tPA variant N67. US5270198-A.	PD 14-DEC-1993. PA (GETH ) GENENTECH : Best Local Similarity: Query Match: RESUTT 422	0 standard; PA variant 98-A.	• •	standard, A variant 8-a		standard; A variant 8-A.	PD 14-DEC-1993.  PA (GETH ) GENENTECH 1 Best Local Similarity: Ouery Match:	5 standard, PA variant 98-A.	PD 14-DEC-1993.  PA (GETH) GENENTECH Dest Local Similarity:	2 standard PA variant 98-A.	PD 14-DEC-1993. PA (GETH ) GENENTECH 1 Best Local Similarity: Query Match:

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297, A298, A299).	Mismatches: Indels:	27 AA. ).	Mismatches: Indels:	27 AA.	Mismatches: Indels:	527 AA. N103).	Mismatches: Indels:	27 AA. ,A462).	Mismatches: Indels:	527 AA. ,A365,A366).	Mismatches: Indels:	27 AA.	Mismatches: Indels:	527 AA. 2,A434).	Mismatches: Indels:	27 AA.	Mismatches: Indels:	27 AA. A453).
(N67, A296, A297	INC. 100.00% 3.64%	protein; 5 (N105, T107	INC. 100.00% 3.64%	protein; 5 (N60,N103)	INC. 100.00% 3.64%	protein; (N60,N67,	INC. 100.00% 3.64%	protein, 52 (N103, A460,	INC. 100.00% 3.64%	protein; (N67,A364	INC. 100.00% 3.64%	protein; 5: (N67,A410)	INC. 100.00% 3.64%	protein; 5 (N103,A432	INC. 100.00% 3.64%	protein; 52 (N67,A408).	INC. 100.00% 3.64%	protein; 52' (N67,A449,A
tPA variant 3198-A. 3-1993.	(GETH ) GENENTECH St Local Similarity: ery Match: SULT 428	AR4 uma	.993. GENENTECH .milarity:	5 2 8 8 8	31-JAN-1995. (GETH ) GENENTECH st Local Similarity: arganth:	AR270876 standard; DE Human t-PA variant DN 1165365737.	E :-	ID AAR70907 standard; DE Human t-PA variant	32-A. 1995. GENENTECH imilarity:	RESULT 432 ID AAR70863 standard; DE Human t-PA variant PN US5385732-A	PD 31-JAN-1995. PA (GETH) GENENTECH Dest Local Similarity: Query Match: RESULT 433	ID AAR70865 standard; DE Human t-PA variant PN HS5385732-A.	95. ENENTECH ilarity:	AR70903 fuman t-P JS5385732	95. ENENTECH ilarity:	AR70864 Human t-P IS5385732	JAN-1995. TH ) GENENTECH al Similarity: cch:	*30 R70871 standard; man t-PA variant

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Mismatches: Indels:	7 AA. 287). Mismatches: Indels:	7 AA. 417,A418). Mismatches: Indels:	AA. A304). Mismatches: Indels:	7 AA. A342). Mismatches: Indele:	7 AA. A365,A366). Mismatches: Indele:	AA. A417,A418). Mismatches: Indels:	7 AA. Mismatches: Indels:	UNG7, A296, A297, A298, A299). (NG7, A296, A297, A298, A299). (NG7, A296, A297, A298, A299).  Mismatches: 3.64* Indels: protein; 527 AA. (NG7, A339, A342).
INC. 100.00% 3.64%	; protein; 527 AA : (N67,A283,A287) INC. 100.00% 3.64%	: Drotein; 527 AA. : (N67,A416,A417,A418) INC. 100.00% ' Misma 3.64% Indel	: (N103,A303,A304) : (N103,A303,A304) : (N103,A303,A304) : INC. : 100.00% : 3.64%	. (N103,A339,A342) . (N103,A339,A342) INC. 100.00% M	; protein; 527 AA. : (N103,A364,A365),A366) INC. Mismat 100.00% Mismat	protein; 527 AA. 	Drotein; 527 (N103, A440). INC. 100.00\$	i protein; 52 (N67, A296, A INC. 100, 00\$ 3.64\$ ; protein; 52 : (N67, A339, A
PN USS385732-A. PD 31-JAN-1995. PA (GETH) GENENTECH 1 Best Local Similarity: Query Match:	standard A variant -A. 95. ENENTECH	standard; A variant A. 95. ENENTECH	RESULT 439  RESULT 439  ID AARY0894 standard; p  DE Human t-PA variant ( PN US5385732-A.  PD 31-JAN-1995.  PA (GETH) GENENTECH IN  Best Local Similarity: II  Query Match:	6 standard, -PA variant 32-A. 1995. GENENTECH imilarity:	standard, PA variant 2-A. 995. GENENTECH	Standard, -PA variant 32-A. 1995. GENENTECH	4 standard -PA variant 32-A. 1995. GENENTECH imilarity:	B standard -PA variant 32-A. 1995. GENENTECH imilarity: 1 standard -PA variant 32-A.

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Indels:
                                        Query Match:

RESULT 446

Indels:

ID AAR70897 standard; protein; 527 AA.

DE Human t-PA variant (N103, A347, A348, A349, A351)

PN US5385732-A.
                                                                                                                                                          Mismatches:
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PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$ Mismat Query Match: 3.64$ Indels
RESULT 450
ID AAR70895 standard; protein; 527 AA.
ID Human t-PA variant (N103,A331,A332).
PN USSS82732-A.
PN 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$ Misma
                                                                                                                                                                                                                                                                                        Guery Match:

RESULT 448

ID AAR70892 standard; protein; 527 AA.

DE Human L-PA variant (N103,A283,A287).

PN US5385732-A.

PD 31-JAN-1995.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00% Mismanum Match:
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Human t-PA variant (N103,A449,A453).
US5385732-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match: 3.64%
RESULT 454
ID AAR/70899 standard, protein; 527 AA.
DE Human t-PA variant (N103,A408).
PN US5385732-A.
PD 31-JAN-1995.
                                                                                                                                                                       Query Match:
RESULT 447

ID AART/0874 standard; protein; 527 AA.
DE Human t-PA variant (N67,N103).
PN US5385732-A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
RESULT 449
TD AARTO868 standard; protein; 527 AA.
DE Human t-PA variant (N67,A432,A434).
PN US5385732-A.
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RESULT 451

ID AAR70860 standard; protein; 527 AA.

BE Human t-PA variant (N67,A331,A332).

PN US5385732-A.

PD 31-JAN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 453
AAR70872 standard; protein; 527 AA.
Human t-PA variant (N67,A460,A462).
US5385732-A.
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DE Human t-..

PN US5388732-A.

PD 31-JAN-1995.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00$

"uery Match: 3.64$

"uery Atch: ---

" 453 ----
" standard; protein;
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PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
                                                                                                                                                                                                                                            PD 31-JAN-1995.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
Query Match:
RESULT 452
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us-10-015-385a-193.olin2p.rag.spdi

: 100.00% Mis 3.64% Inc	(N67, A426, A42 (N67, A426, A42 (NC.) 100.00\$ 3.64\$	(N67, A440). INC. 100.00\$	d; protein; 527 AA. nt (N103, A267). H INC. : 100.00\$ Mit	d; protein; 527 AA. sue plasminogen acti; ERKE AG. ORP. : 100.00\$ Mis. 3.64\$ In	a S S	d; protein; 527 AA.  sue plasminogen acti:  ERKE AG.  ORP.  100.00\$  Mit. 3.64\$ In	14.70 AA199128 standard; protein; 527 AA. Mutant human tissue plasminogen activ USS501853-A. 26-MAR-1996. (BEHW) BEHRINGWERKE AG. (GHIR) CHIRON CORP. Local Similarity: 100.00\$ Mi. March: 3.64\$ In	T.47. T. 47. T. 47. T. 47. T. 47. T. 47. T. 47. Mata9129 standard; protein; 527 AA. Matant human tissue plasminogen activus 5501853. A. G. F. A. T. 1996. (BEHW ) BEHRINGWERKE AG. (CHIR ) CHIRON CORP. Local Similarity: 100.00\$ Mi. Match: 3.64\$ In T. 472. T. 472. AAR99124 standard; protein; 527 AA.
Siry st	DE Human t-PA variant DE Human t-PA variant PN US5385732-A. PD 31-JAN-1995. PA (GETH ) GENENTECH J Best Local Similarity: Query Match: RESULT 465	st .	ID AAR70891 standard; DE Human t-PA variant PN USS385732-A. PD 31-JAN-1995. PA (GETH) GENENTECH I Best Local Similarity: Query Match:	ID AAR99130 standard; protein; 527 DB Mutant human tissue plasminogen PN US5501853-A. PD 26-WAR-1996. PA (BEHW ) BEHRINGWERKE AG. PA (CHIR ) CHIRON CORP. Best Local Similarity: 100.00\$ Ouery Match:	RESULT 468  ID AAR99125 standard; protein; 527  DB Mutant human tissue plasminogen PN US5501853-A.  PD 26-MAR-1996.  PA (BEHW) BERRINGWERKE AG.  PA (CHIR) CHIRON CORP.  Best Local Similarity: 100.00%	RESULT 469  ID AAR99126 standard; protein; 527  ID E Mutant human tissue plasminogen  PN US5501853-A.  PD 26-WAR-1996.  PA (BEHW) BEHRINGWERKE AG.  PA (CHIR) CHIRON CORP.  Best Local Similarity: 100.00\$	ESOUL 470 ID AAR9918 standard; protein; DE Mutant human tissue plasminn PN USS501853-A. PD 26-MAR-1996. PA (BEHW) BEHRINGWERKE AG. PA (CHIR ) CHIRON CORP. Best Local Similarity: 100.00% Query March: 3.64%	KESULT 4/1  ID AAR99129 standard; prott DE Mutant human tissue platen WS501853-A. PD 26-MAR-1996. PA (BEHW) BEHRINGWERKE AG PA (CHIR) CHIRON CORP. Best Local Similarity: 100.0uery Match: 3.644 RESULT 472. ID AAR99124 standard; prott
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Mismatches: Indels:	Mismatches: Indels:	 A349,A351). Mismatches: Indels:	Mismatches:	orotei Ches:	hes:	: sa	, s	30)
2	\$	7 AA. 348,A349 Mism Inde	7 AA. 449). Misma	7 AA. ctivator prote Mismatches	<b>\$</b>	7 AA. 304). Mismatches Indels: 7 AA.	A291, A298, A299 Mismatches Indels: 7 AA.	Mismatches Indels: 7 AA. A427,A429,A430
INC. 100.00% 3.64%	Jul 435.  ARAT70900 standard; protein; 527 AA.  Human t-PA variant (N103,A410).  US5385732-A.  31-JAN-1995.  Local Similarity: 100.00\$ Mi.  Ty Match: 3.64\$ Inc.	ART/0862 standard; protein; 527 AA.  Human t-PA variant (N67,A347,A348,A349,A351) US5385732-A. US5385732-A. (GETH ) GENENTECH INC. Local Similarity: 100.00\$ Indeals:	sin; 527 AA A445,A449)	, 527 AA en activ	protein; 527 AA (N67,A267). INC. 100.00\$	AAR70859 standard; protein; 527 AA. Human t-PA variant (N67,A303,A304). US538732-A. 31-JAN-1995. (GETH ) GENENTECH INC. Local Similarity: 100.00\$ Mismatche. "Match: 3.64\$ Indels: "I 461 AAR70893 standard; protein; 527 AA.	NC. 100.00% 3.64% protein; 527 AA (N103,A445,A4499)	US5385732-A. US5385732-A. (GETH ) GENENTECH INC. Local Similarity: 100.00\$ Mismatches: Match: Match: AAR70902 standard; protein; 527 AA. Human t-PA variant (N103, A426, A427, A429, A430) US5385732-A. 31.JAN-1995. (GETH ) GENENTECH INC.

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otein; 527 AA.
Lasminogen activator for fibrin clot lysis.
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Lasminogen activator for fibrin clot lysis.
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Lasminogen activator for fibrin clot lysis.
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Indels:
                              otein; 527 AA.
57,A426,A427,A429,A430)
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103, A267).
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R275E,H417E human tissue-type plasminogen activator protein mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW57778 standard; protein; 527 AA.
R275E,H417D human tissue-type plasminogen activator protein mutant.
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R275E,K429Y human tissue-type plasminogen activator protein mutant.
W09821320-A2.
                                                                                                                                                                                                                                                                                                                     AAR99127 standard; protein; 527 AA.

Mutant human tissue plasminogen activator for fibrin clot lysis.
26-MAR-1996.
(BEHW ) BEHRINGWERKE AG.
(CHIR ) CHIRON CORP.
Local Similarity: 100.00% Mismatches: 0
Mutant human tissue plasminogen activator for fibrin clot lysis.
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DE Human tissue plasminogen activator (tPA) protein.

PN W0200240696-A2.

PD 23-MAY-2002.

PA (BOEH) BOEHRINGER INCELHEIM INT GMBH.

Best Local Similarity: 100.00% Mismatches:
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Human tissue plasminogen activator (tPA) protein.
WO200240650-A2.
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Single chain form of the intact t-PA molecule.
WO9802454-A2.
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PA (BOEH) BOEIRINGER INGELHEIM INT GMBH.

Best Local Similarity: 100.00$ Mismatches:

Query Match: 3.64$ Indels:

RESULT 481
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Indels:
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WO200243747-A2.
06-JUN-2002.
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(ISIS-) ISIS INNOVATION LTD.
Local Similarity: 100.00%
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Best Local Similarity: 100.00%
Ouery Match:
3.64%
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PA (SCRI ) SCRIPPS RES INST.
Best Local Similarity: 3.64%
Query Match: 3.64%
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Local Similarity: 100.00%
Match: 3.64%
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                                                                                  PD 26-MAR-1996.
PA (BEHW) BEHKINGWERKE AG.
PA (CHIR) CHIRON CORP.
Best Local Similarity: 100.0
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RESULT 476
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RESULT 478
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RESULT 473
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RESULT 474
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RESULT 479
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AAR07033 standard; protein; 528 AA. Thrombolytic protein with secondary structure of human tissue plasminogen activator.
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                                                                                                                                                                                                                                                                   AAP71449 standard; protein; 528 AA.
Modified human tissue plasminogen activator.
EP238304-A.
                                                                                                                                       AAP71451 standard; protein; 528 AA.
Modified human tissue plasminogen activator.
                                                                                                                                                                                                                                                                                                                                                                                                              AAP71450 standard; protein; 528 AA.
Modified human tissue plasminogen activator.
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Tissue plasminogen activator mutant 2K1 1K2
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t-PA insertion variant i305 H, T, N, K, R,
WO9002798-A.
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ADL92126 standard; protein; 527 AA.
Alteplase protein sequence.
W02003099862-A1.
04-DEC-2003.
(NANO-) APPLIED NANOSYSTEMS BV.
t. Local Similarity: 100.00% Mis.
ry Match:
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T-PA variant R299D.
W09211377-A1.
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Best Local Similarity: 100.00%
Query Match: 3.64%
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P W09211377-A1.
PD 09-UUL-1992.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
Query Match:
RESULT 490
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Local Similarity: 100.00%
Match: 3.64%
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PD 23-SEP-1987.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
Ouery Match:
3.64%
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Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
Query Match: 3.64%
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PD 23-SEP-1987.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100
   ID ADL92126 standard; p. DE Alteplase protein set PN W02003099862-A1. PD 04-DE-2003. PA (NANO-) APPLIED NANO Best Local Similarity: 1
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                                                                                                        Query Match:
RESULT 482
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RESULT 486
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RESULT 488
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RESULT 489
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Sequence encoded by of synthetic gene for mature human tissue plasminogen activator (tPA).
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Sequence of tissue plasminogen activator (t-PA) encoded by plasmid
PTPA25.
WO8601538-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP92277 standard, protein, 530 AA.
Sequence of modified tPA-type thrombolytic proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00
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des(Cys51-Asp87)t-PA with extra finger domain.
EP241210-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR07034 standard; protein; 531 AA. Thrombolytic protein with secondary structure
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Indels:
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Indels:
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                                                                                                                                                                                                                                                                                                                           AAP70449 standard; protein; 530 AA.
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Tissue plasminogen activator deriv.
JP03065184-A.
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T-PA growth domain deletion mutant.
JP03130077-A.
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PA (YAMA ) YAMANOUCHI PHARM CO LTD.
Best Local Similarity: 100.00%
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Best Local Similarity: 100.00$
Query Match: 3.64$
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Best Local Similarity: 100.00$
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PA (CREA/) CREA R.
Best Local Similarity: 100.00$
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PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 29-DEC-1988.
PA (GEMY) GENETICS INST INC.
Best Local Similarity: 100.00%
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PA (BEEC ) BESCHAM GROUP PLC.
Best Local Similarity: 100.00$
                                                                                                                                                                                              100.00$
                                                                     13-AUG-1987.
(GEMY ) GENETICS INST INC.
(LARS/) LARSEN G R.
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PN WO8704722-A.
PD 13-AUG-1987.
PA (GEMY ) GENETICS INS
PA (LARS/) LARSEN G R.
Best Local Similarity: 1
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PA (BIOJ) BIOGEN NV.
Best Local Similarity:
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RESULT 499
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RESULT 501
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RESULT 503
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RESULT 505
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RESULT 506
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RESULT 504
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Thrombolytic protein with t-PA activity where R275 is deleted or replaced and containing a modified N-linked glycosylation site.
W08704722-A.
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Thrombolytic proteins 1-1-1-7 having t-PA activity, where R275 is deleted
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Thrombolytic protein 1-12-1-18 having t-PA activity, deleted or replaced
R275 is and containing a modified N-linked glycosylation site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deleted or replaced
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Sequence of tissue plasminogen activator (TPA) encoded by DUCH.
DE3537176-A.
                     AAK68853 standard, protein; 528 AA.
Bifibronectin domain-delta 52-94-tissue plasminogen activator.
US5376547-A.
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Thrombolytic protein 1-19-1-21 having t-PA activity, deleted of R275 is and containing a modified N-linked glycosylation site.
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Indels:
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                                                                                                                                                                                                                                                                                                                                                              529 AA.
HH.
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t-PA insertion variant i304H, i305H
W09002798-A.
22-MAR-1990.
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                                                                                                                             27-DEC-1994.
(AMHP ) AMERICAN HOME PROD CORP.
Local Similarity: 100.00$
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PA (GEMY ) GENETICS INST INC.
PA (IARS/) LARSEN G R.
Best Local Similarity: 100.00%
Query Match:
RESULT 497
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t-PA insertion variant i304 W09002798-A.
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PD 22-MAR-1990.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00%
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Local Similarity: 100.00$
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
3.64%
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(GEMY ) GENETICS INST INC.
(LARS/) LARSEN G R.
Local Similarity: 100.00%
/ Match:
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WO8704722-A
                 ID AAR68853
DB Bifibrome
PN US5376547
PD 27-DEC-11
PA (AMHP) A
Best Local Sin
Query Macch:
RESULT 491
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RESULT 492
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RESULT 493
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RESULT 495
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RESULT
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Best Local Similarity: 100.00%
Query Match: 3.64%
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RESULT 522
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RESULT 521
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T-PA variant contg. fibronectin for thrombosis lysis (4).
JP03061482-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR13149 standard, protein, 557 AA.
T-PA variant contg. fibronectin for thrombosis lysis (4).
JP03061482-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR13148 standard, protein; 556 AA.
T-PA variant contg. fibronectin for thrombosis lysis (2)
JP03061482-A.
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T-PA with -ve charged finger and/or kringle domain (8).
JP03061483-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR13150 standard; protein; 558 AA.
T-PA with -ve charged finger and/or kringle domain (3)
JP03061483-A.
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                                                                                                                                                                          AAR06238 standard; protein; 555 AA.
Novel mutant tissue plasminogen activator (LPA)
plgnYQTPA.
EP379890-A.
                                                                                                                  Mismatches:
Indels:
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Tissue plasminogen activator analogue.
EP233334-A.
07-DEC-1988.
                AARl1662 standard; protein; 552 AA.
Tissue plasminogen activator deriv.
JP03065184-A.
                                                                                                                                                                                                                                                                                                                                                     AAR23805 standard; protein; 555 AA.
t-PA (Del 296-302) mutant.
WO9206203-A.
16-APR-1992.
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PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00$
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(FUJI) FUJISAWA PHARM CO LTD.
Local Similarity: 100,008
Match: 3.64%
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Match: 3.64%
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                                                                                                                                                                                                                                                                         PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00%
Query Match: 3.64%
                                                                                          (KANF) KANEGAFUCHI CHEM KK.
Local Similarity: 100.00$
Match: 3.64$
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Best Local Similarity: 100.00%
Onerv Match:
3.64%
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RESULT 510
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RESULT 512
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RESULT 514
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RESULT
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RESULT 517
ID AAP94403 standard; protein; 559 AA.
DB Analogue of amino acid sequence of tissue plasminogen activator (t-PA).
PN AU8817430-A.
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AARIJSIS standard; protein; 559 AA.
T-PA with -ve charged finger and/or kringle domain (4)
JP03061483-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain (6)
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T-PA variant contg. fibronectin for thrombosis lysis
JP03061482-A.
18-MAR-1991.
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T-PA with -ve charged finger and/or kringle
JP03061483-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR13154 standard; protein; 559 AA.
T-PA variant having Lys416 substitution (2)
JP03061484-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-PA variant having Ly8416 substitution (6) JP03061484-A.
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                                                     AAP80654 standard; protein; 559 AA.
Tissue plasminogen activator analogue.
EP293934-A.
O7-DEC-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DS-JUL-1991.
(PORT-) PORTON PROD LTD.
(PUBL-) PUBLIC HEALTH LEB SERVIC.
(UNLO) UNIV COLLEGE LONDON.
t Local Similarity: 100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                           AAR13263 standard; protein; 559 AA.
JM1-229 cell line t-PA.
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Local Similarity: 100.00%
Match: 3.64%
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Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
Query Match: 3.64%
RESULT 524
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Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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(NOVO ) NOVO IND AS.
(ZYWO ) ZYMOGENETICS INC.
(EISA ) EISAI CO LTD.
L Local Similarity: 100.00$
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PA (NOVO) NOVO IND AS.
(NOVA) SA (STAD.
BEST LOCAL SIMILARITY: 100.00
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AAP30001 standard; protein; 562 AA.
Sequence of full length tissue plasminogen activator (t-Pa).
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                                                                                                                                                                     Human tPA.
                                                                                                            Query Match:
RESULT 534
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RESULT 538
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RESULT 540
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DE Mouse ischaemic condition related protein sequence SEQ ID NO:41.

PN W0200188188-A2.

PD 22-NOV-2001.

PA (UYNL-) UNIV UNHON SCHOOL JURIDICAL PERSON.

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR12341 standard, protein; 560 AA.
T-PA variant contg. fibronectin for thrombosis lysis (3)
JP03061482-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-PA with -ve charged finger and/or kringle domain (1). JP03061483-A.
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T-PA with -ve charged finger and/or kringle domain (7)
JP03061483-A.
                                                                                                                                                                                                                                                                                                                Human tissue plasminogen activator deletion mutant.
USS55269-A.
12-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP50219 standard; protein; 561 AA.
Tissue plasminogen activator encoded by cDNA clone.
EP143081-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP70020 standard; protein; 561 AA.
Sequence of tissue plasminogen activator (tPA)
28-20236-A.
28-0CT-1987.
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Indels:
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Novel plasminogen activator.
US5504001-A.
                                                                                                                                                                                                                                                                                                     AAW23368 standard; protein; 559 AA.
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AAR96222 standard, protein, 559 AA.
Novel plasminogen activator.
US5504001-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BOEF ) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE T-PA variant contg. fibronectir PN JP03061482-A.
PD 18-MAR-1991.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00%
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(FUJI) FUJISAWA PHARM CO LTD.
Local Similarity: 100.00$
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PD 18-MAR-1991.
PA (FUJI) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00$
                                                                                                                                                                                                                                                                                               ID AAW23368 Standard, proceed to the Human tissue plasminogen active to 12-5055269-A.

PD 12-506-1997.

PA (CHIR ) CHIRON CORP.

PA (BEHW ) BEHRINGWERKE AG.

Best Local Similarity: 100.00%
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3.64%
                                                                         (ZYMO) ZYMOGENETICS INC.
Local Similarity: 100.00%
/ Match:
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Best Local Similarity: 100.00%
Query Match: 3.64%
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PA (CIBA) CIBA GEIGY AG.
Best Local Similarity: 100.00%
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ID AAR96222
DE Novel pl
PN US550400
PD 02-APR-11
PA (ZYMO) S
Best Local Si
Guery Match:
RESULT 525
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RESULT 531
ID AAR12342
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RESULT 532
ID AAR12367
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RESULT 528
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RESULT 533
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AAP70285 standard; protein; 562 AA.
Sequence encoded by human tissue plasminogen activator (t-PA) cDNA clone.
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Sequence of active human uterine tissue plasminogen activator (UTPA).
EP178105-A.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAP60810 standard; protein; 562 AA.
Sequence of modified human tissue plasminogen activator (t-PA).
FR2581652-A.
                                                                                                                                                                                                                                                          AAP60790 standard; protein; 562 AA.
Sequence of human pre-tissue plasminogen activator (pre-t-PA).
GB2173804-A.
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RESULT 539
ID AAP81913 standard, protein, 562 AA.
DE Tissue plasinogen activator encoded by pEMpl-tPA.
PN WO880242-A.
                                            Mismatches:
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Tissue plasminogen activator analogue.
EP293934-A.
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AAP80656 standard; protein; 562 AA.
Tissue plasminogen activator analogue.
EP293934-A.
                                                                                                   AAP50342 standard; protein; 562 AA.
                                                                                                                                               PD 16-AUG-1985.
PD 16-AUG-1985.
PA (GEMY ) GENETICS INST INC.
Best Local Similarity: 100.00%
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PA (NOVO) NOVO IND AS.
PA (EISA ) EISA CO LTD.
Best Local Similarity: 3.64%
Query Match:
3.64%
                                                                                                                                                                                                                                                                                                         PD 22-OCT-1986.
PD GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
PD 09-NOV-1983.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00%
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PA (GENE-) GENETICA.
Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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(ZYMO ) ZYMOGENETICS INC.
(NOVO ) NOVO IND AS.
(EISA ) EISA CO LTD.
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Mismatches:

Indels:

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T 551
AAR09288 standard; protein; 562 AA.
Sequence of tissue plasminogen activator analogue BBNT11 (Ser 67, Leu
PN W08912681-A.
PD 28-DEC-1989.
PA (BRB1-) BRIT BIO-TECHN LTD.
Best Local Similarity: 100.00%
                                                                                                                                                                       PN MCGALCE 1989.
PD 28-DEC-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Best Local Similarity: 100.00%
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RESULT 554
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RESULT 556
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RESULT 550
ID AAR09287 standard; protein; 562 AA.
DE Sequence of tissue plasminogen activator analogue BENT6 (Thr 67, Asp 68).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR07079 standard; protein; 562 AA.
Thrombolytic protein with secondary structure of human tissue plasminogen
                                                                                                                                                                                                                                     AAP82582 standard; protein; 562 AA.
Tissue plasminogen activator with S-119 substd for M and QGI96-98 substd
for NGT.
                                                                                                                                                                                                                                                                                                                                                                                        AAP82580 standard; protein; 562 AA.
Tissue plasminogen activator with G-183 and S-186 substd for S and T.
JP63230083-A.
                                               AAP94380 standard; protein; 562 AA.
Amino acid sequence of tissue plasminogen activator (t-PA) protein.
AU8817430-A.
AU8817430-A.
(GB-DEC-1988
(NOVO ) NOVO IND AS.
(IZYMO ) ZYMOGENETICS INC.
(EISA ) EISAI CO LTD.
LOCAL Similarity: 100.00% Mismatches: 0
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Sequence encoded by native tPA of plasmid pST112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP94238 standard; protein; 562 AA.
Human tissue plasminogen activator (t-PA) gene
WO8900197-A.
   Mismatches:
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Indels:
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Indels:
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Human melanoma t-PA encoded by plasmid pKG12.
EP297066-A.
                      Indels:
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Human tissue plasminogen activator.
JP01174388-A.
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Best Local Similarity: 100.00%
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Best Local Similarity: 100.00$
Querry Match:
RESULT 548
ID AAP94238 standard; protein; 56
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Best Local Similarity: 100.00$
Query Match:
3.64$
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12-JAN-1989.
(GETH ) GENENTECH INC.
Local Similarity: 100.00%
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PD 26-SEP-1988.
A (EISA ) EISAI CO LTD.
Best Local Similarity: 100.00$
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26-SEP-1988.
(EISA ) EISAI CO LTD.
Local Similarity: 100.00%
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PA (KABI ) KABIGEN AB.
Best Local Similarity: 100.00%
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08-FEB-1989
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RESULT 549
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RESULT 547
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RESULT 542
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RESULT 543
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AAR04700 standard; protein; 562 AA. Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S, H420S with altered residues 419 and 420. EP351246-A.
                                    AAR09286 standard, protein; 562 AA.
Sequence of tissue plasminogen activator analogue BBNT5 (Ser 67, Ser 68)
WO8912681-A.
                                                                                                                                                                                                                                                                                                                                                                                           AAR09290 standard; protein; 562 AA.
Sequence of tissue plasminogen activator analogue GF6 (Leu 66, Asp 67,
The 89, Gln 117).
WO8912681-A.
                                                                                                                                                                                                               AAR09289 standard; protein; 562 AA.
Sequence of tissue plasminogen activator analogue BBNT12 (Asp 67, Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AARG6237 standard; protein; 562 AA.
Novel tissue plasminogen activator (tPA) encoded by plasmid pST112.
EP379990-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR09284 standard; protein; 562 AA.
Sequence of tissue plasminogen activator (tPA) mutant Thr 478.
WO8912680-A.
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AAR05388 standard; protein; 562 AA.
Thrombolytic protein.
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PA (YAMA ) YAMANOUCHI PHARM CO LTD.
Best Local Similarity: 100.00$
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Best Local Similarity: 100.00%
Query Match: 3.64%
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PD 28-DEC-1989.
PA (UNIW ) UNIV WASHINGTON.
BEST Local Similarity: 100.00%
                                                                         DE Sequence of tissue plasmino
PN W08912681-A.
PD 28-C1989
PA (BRB-) BRIT BIO-TECHN LTD.
Best Local Similarity: 100.00%
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3.64%
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PD 28-C-1989.
PA (BRBI-) BRIT BIO-TECHN LTD.
Best Local Similarity: 100.00%
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PA (BRBI-) BRIT BIO-TECHN LTD.
Best Local Similarity: 100.00%
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(NOVO ) NOVO-NORDISK AS.
Local Similarity: 100.00%
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	DE T-PA variant having Ly8416 substitution (5). PN JP03061484-A. PD 18-MAR-1991. PA (FUJI ) FUJISAWA PHARM CO LTD. Best Local Similarity: 100.00% Mismatches: Query Match:	SOLI 308 AAR12423 standard, proteir T-PA variant having Lys41( JP03061484-A. 18-MAR-1991.	(FUJI ) FUJISAW st Local Similarit ery Match: SULT 569	standard; protein; 562 AA 31e 1 domain substitution 7-A. 31. ANEGAFUCHI CHEM KK. ilarity: 100.00\$	Query Match:  RESULT 570  ID AAR23802 standard; protein; 562 AA.  DE Zymogen-like t-PA (Ser 292, His 305).  PN W0926203-A.	ائع ٿڌ	KESULI 5/1 ID 14423809 standard; protein; 562 AA. DE t-PA (Glu 299) mutant. PN WO92062013.A.	(TEXA) UNIV TEXAS SYSTEM. St Local Similarity: 100.00% Sry Match: 3.64%	DE 4-PAR-280-3 SCENDARG; DECCEIN; DOZ AA. DE T-PA (Ser 304) mutant. PN W09206203-A. PD 16-APR-1992. PA (TEXA ) IMIV PEXAS SYSTEM	H CE	Standard, process, 382 A.B. 183 A.B. 18	or Local Similarity: 100.00%  ary Match: 3.64%  SUIT 574	standard; ike t-PA -A. 92.	(1EAA ) UNIV 1EAAS SISIEM. St Local Similarity: 100.00\$ STY Match: SULT 575	AAR23811 standard; t-PA (Glu 296, Glu WO9206203-A. 16-APR-1992.	PA (TEXA) UNIV TEXAS SYSTEM.  Best Local Similarity: 100.00% Mismatches: Query Match: RESULT 576  ID AAR23807 standard; protein; 562 AA. DE t-PA (Tyr 297) mutant.
,	0 analogue t-PA K419S with	00	analogue t-PA C87S; K419S	00		00	oligosaccharide side chain.	00		00		00	in (2).	00	in (5).	••
,	indeis: 2 AA. activator (t-PA)	Mismatches: Indels:	AA. activator (t-PA) 9.	Mismatches: Indels:	AA. ator (t-PA).	Mismatches: Indels:	linked	Mismatches: Indels:	AA.	Mismatches: Indels:	AA. half-life.	Mismatches: Indels:	662 AA. and/or kringle domain	Mismatches: Indels:	62 AA. and/or kringle domain	Mismatches: Indels: AA.
1	Vuery March: RESULT Patch: RESULT 3.64* ID AAR04701 standard; protein; 562 DE Sequence of tissue plasminogen a DE altered residue 419. PN EP351246-A.	PA (NOVO ) NOVO-NORDISK AS. PA (NOVO ) NOVO-NORDISK AS. Best Local Similarity: 100.00% Query Match: 3.64%	RESULT 560  ID ARACTO2 standard; protein; 562 AA. DE Sequence of tissue plasminogen activ  With altered residues 87 and 419.	PN EP351246-A. PD 17-JAN-1990. PA (NOVO ) NOVO-NORDISK AS. PA (NOVO ) NOVO-NORDISK AS. Best Local Similarity: 100.00% Query March: 3.64%	699 standard; protein; 562 e tissue plasminogen activa 246-A. N-1990.	PA (NOVO) NOVO-NORDISK AS. PA (NOVO) NOVO-NORDISK AS. Best Local Similarity: 100.00% Query Match: 3.64%	727 standard; protein; 562 7+ mutant with supernumerar 1376-A. G-1991	PA (TEXA) UNIV TEXAS SYSTEM. PA (COLD-) COLD SPRING HABOR LAB. Best Local Similarity: 100.00% Ouery Match: 3.64%	441 standard; protein; 562 3 t-PA variant. 7752-A. G-1991.	PA (MONS) MONSANTO CO. Best Local Similarity: 100.00\$ Query Match: 3.64\$	2 standard; protein; 562 t-PA variant with longer 52-A.	Best Local Similarity: 100.00\$ Querry Match: 3.64\$	343 standard; protein; Ewith -ve charged finger 61483-A.	PA (FUJI) FUJISAWA PHARM CO LTD. Best Local Similarity: 100.00% Query Match: 3.64%	6 standard; protein; 5 th -ve charged finger 193-A.	PD 18-MMK-1991 PA (FUJI) FUJISAWA PHARM CO LTD. Best Local Similarity: 100.00\$ Query Match: 3.64\$ I RESULT 567 ID AAR12425 standard; protein; 562 AA.

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(ZYMO) ZYMOGENETICS INC.
Local Similarity: 100.00%
/ Match: 3.64%
02-APR-1996
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RESULT 594
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Modified tPA MB1012 with two K2 kringle domains.
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Sequence of tissue plasminogen activator (t-PA)
WO9312225-A1.
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Full-length tissue plasminogen activator.
US5504001-A.
                                                          Indels:
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                                                                                      AAR23806 standard; protein; 562 AA. t-PA (Glu 296) mutant. W09206203-A.
                                                                                                                                                                                                      AAR23810 standard; protein; 562 AA.
t-PA (Gly 301) mutant.
WO9206203-A.
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t-PA (Glu 304) mutant.
WO9206203-A.
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Human tPA (R129W).
JP05304992-A.
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(TAKE ) TAKEDA CHEM IND LTD.
Local Similarity: 100.00$
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30-MAR-1993.
(TAKE ) TAKEDA CHEM IND LTD.
Local Similarity: 100.00$
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16-APR-1992.
16-APR-1992.
Local Similarity: 100.00%
3.64%
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Local Similarity: 100.00%
       16-APR-1992.
(TEXA) UNIV TEXAS SYSTEM.
Local Similarity: 100.00%
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16-APR-1992.
(TEXA) UNIV TEXAS SYSTEM.
Local Similarity: 100.00%
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Local Similarity: 100.00%
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Local Similarity: 100.00%
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Local Similarity: 1
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 WO9206203-A
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RESULT 583
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AAU07700 standard, protein, 562 AA.
Human tissue plasminogen activator (t-PA) protein sequence.
WO200232446-A2.
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WO20030333009-A2.
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Human tissue plasminogen activator protein sequence
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Human tissue plasminogen activator protein fragment
WO9957251-A2.
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Human tissue-type plasminogen activator t-PA.
WO200032759-A1.
                                                                                                                                                                                                                                                                                                                                     Tissue plasminogen activator variant R275G. USS714372-A.
03-FEB-1998.
(GETH) GENENTECH INC.
Local Similarity: 100.00$ Mismatche.
1D AAW47536 standard; protein; 562 AA.
DE Tissue plasminogen activator variant R275E.
PN US5714372-A.
PD 03-FEB-1998.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100,00% Mismatche
                                                                                                                                              ARM#/537 standard; protein; 562 AA.
Tissue plasminogen activator variant 1276P.
US5714372-A.
                                                                                                                           Indels:
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Fissue type plasminogen activator, tPA.
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Best Local Similarity: 100.00% M
Ouery Match: 3.64% In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE37130 standard; protein; 562 AA.
                                                                                                                                                                                                                                                                                                                         AAW47535 standard; protein; 562 AA.
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PA (CANG-) CANGENE CORP.
Best Local Similarity: 100.00%
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(GLDS ) LG CHEM LTD.
Local Similarity: 100.00%
                                                                                                                                                                                                                      PD 03-FEB-1998.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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PN US5106741-A.
PD 21-APR-1992.
PA (UPJO ) UPJOHN CO.
Best Local Similarity:
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RESULT 606
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RESULT 608
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RESULT 604
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RESULT 609
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RESULT 610
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RESULT 611
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Human myocardial infarction-associated gene derived protein, SEQ ID 911.
WO2004058052-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM80983 standard; protein; 562 AA.
Tumour-associated antigenic target (TAT) polypeptide PRO4, SEQ:2535.
                                                                                                                                                                                  Differentially expressed breast cancer associated protein #33. US2002156263-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN49698 standard; protein; 562 AA.
Human tissue type plasminogen activator TPA protein SeqID 26.
WO2004033651-A2.
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Human BEC/LEC-related protein sequence SeqID547.
WO2003080640-A1.
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Sequence of tissue plasminogen (TPA) analogue.
WO8703906-A.
                                 Mismatches:
Indels:
                                                                   Human tissue-type plasminogen activator (TPA) WO2003031464-A2.
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Human tPA protein SEQ ID NO:108.
W02004044178-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR22664 standard, protein, 564 AA.
                                                                                                                      PD 17-APR-2003.
PA (NEOS-) NEOSE TECHNOLOGIES INC.
Best Local Similarity: 100.00$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NECS.) NEOSE TECHNOLOGIES INC. Local Similarity: 100.00%
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(LUCN ) LICENTIA LTD.
Local Similarity: 100.00%
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(GETH ) GENENTECH INC.
Local Similarity: 100.00%
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(GETH) GENENTECH INC.
Local Similarity: 100.00%
Match: 3.64%
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PA (UPJO) UPJOHN CO.
PA (MARO/) MAROTTI K R.
Best Local Similarity: 100.00$
                                                                                                                                                                                                                                                                         PA (CHEN/) CHEN H.
Best Local Similarity: 100.00%
                                  100.00%
                                                                                                                                                                                                                                                                                                            3.64%
                  (OMNI-) OMNIO AB.
Local Similarity:
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      24-APR-2003.
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RESULT 603
ID AAR22664
DE tPA anal
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RESULT 598
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RESULT 595
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RESULT 597
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RESULT 600
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RESULT 601
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RESULT 596
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AAP70059 standard; protein; 593 AA.
Hybrid plasminogen activator (PA) contg. urokinase kringle (UKK) 1-131
and tissue plasminogen activator (tPA) 92-527.
EP213794-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP11744 standard; protein; 586 AA.
Bes(CysS1-Asp87)t-PA with extra finger- and growth factor-domains.
EP241210-A.
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Tissue plasminogen activator mutant 1K1 2K2.
WO8997146-A.
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Tissue plasminogen activator mutant 2G.
WO8907146-A.
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Tissue plasminogen activator mutant 2F.
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Ile(277)t-PA with extra finger-domain.
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AARO177 standard; protein; 570 AA.
L-PA variant MB1023.
US4963357-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID AAP71741 standard; protein; 586 AA.
DE t-PA with extra finger domain.
PN EP241210-A.
PD 14-0CT-1987.
PA (BEEC) BEECHAM GROUP PLC.
Best Local Similarity; 100.00$ N
Query Match:
                                                            protein; 568 AA.
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Best Local Similarity: 100.00%
Query Match: 3.64%
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PD 16-OCT-1990.
PA (MONS ) MONSANTO CO.
Best Local Similarity: 100.00$
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PD 10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00$
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PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100,00%
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PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
Ouery Match:
                                                                                                                  PD 27-MAK-2005.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 100.00%
100.00%
                                                                            Novel human protein #231.
WO2003025148-A2.
27-MAR-2003.
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                                                          ADI21256 standard;
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14-OCT-1987
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RESULT 623
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RESULT 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM80709 standard; protein; 615 AA.
Tumour-associated antigenic target (TAT) polypeptide PRO36372, SEQ:1829.
WO2004030615-A2.
15-APR-2004.
                                                                                                             encoded by plasmid plgN
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Human coagulation factor XII (F12) variant polypeptide.
WO200179228-A2.
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                                                                                      Novel mutant tissue plasminogen activator (tPA) delta GFTPA.
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Human coagulation factor XII (F12) polypeptide
WO200179228-A2.
                                              Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADN04180 standard; protein; 615 AA. Antipsoriatic protein sequence #285.WO2004028479-A2.
                                                                                                                                                                                                                                                                                                                                                       ADA50545 standard; protein; 615 AA.
Human factor XII.
US2003073652-AI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM98382 standard; protein; 615 AA.
                                                                                                                                                     PD 01-AUG-1990.
PA (FUJI ) FUJISAWA PHARM CO LTD.
Best Local Similarity: 100.00$
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(GENA-) GENAISSANCE PHARM INC.
Local Similarity: 100.00$
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PA (GENA-) GENAISSANCE PHARM INC.
Best Local Similarity: 100.00$
      EFF412.
14-0CT-1987.
16-0CT-1987.
LOCAL SIMILARITY: 100.00%
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Local Similarity: 100.00%
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Local Similarity: 100.00%
Match: 3.64%
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Local Similarity: 100.00%
Match: 3.64%
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US2004077538-A1.
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PA (POLL/) POLLARD B.
Best Local Similarity:
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                                                                                                                                                                                                                                                                             26-JUL-2001
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EP241210-A
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RESULT 614
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RESULT 620
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RESULT 621
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RESULT 613
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RESULT
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Hybrid plasminogen activator (PA) concg. tissue plasminogen activator (tPA) 1-261, urokinase kringle (UKK) 50-131 and tPA 262-527. EPP13794-A.
                                                                                                                                                                                                                                                                                                                                              Hybrid plasminogen activator (PA) contg. tissue plasminogen activator (tPA) 1-91, urokinase kringle (UKK) 50-131 and tPA 92-527.
AAP71742 standard; protein; 623 AA.
Ile(277)t-PA with extra finger- and extra growth factor-domains.
EP241210-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE06934 standard; protein; 658 AA.
Human membrane-type serine protease (MTSP) 4-S splice variant.
WO200157194-A2.
                                                                                                                                                               AAP71740 standard; protein; 623 AA.
t-PA with extra finger domain and extra growth factor domain.
EP241210-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ46903 standard; protein; 658 AA.
Human transmembrane serine protease (MTSP) polypeptide #5.
US2004001801-A1.
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Human tissue urokinase plasminogen activator.
WO2003087393-A2.
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Human cell surface protease #5.
WO200295007-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP70084 standard; protein; 650 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP90173 standard; peptide; 680 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 11-MAR-1987.
PD 71-MAR-1987.
PA (AMHP) AMERICAN HOME PROD CORP.
Best Local Similarity: 100.00$
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PA (AMHP) AMERICAN HOME PROD CORP.
Best Local Similarity: 100.00$
                                                PN brians 4-007-1987.
PD 14-007-1987.
PA (BEEC ) BEECHAM GROUP PLC.
Best Local Similarity: 100.00%
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PA (CORV-) CORVAS INT INC.
Best Local Similarity: 100.00$
3.64$
                                                                                                                                                                                                                                         PA (BEEC ) BEECHAM GROUP PLC.
Best Local Similarity: 100.00%
Query Match: 3.64%
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Best Local Similarity: 100.00%
Onerv Match:
3.64%
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A (CORV-) CORVAS INT INC.
Best Local Similarity: 100.00$
Anory Match: 3.64$
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Best Local Similarity: 100.00%
Query Match: 3.64%
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Best Local Similarity: 100.00%
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Tissue plasminogen activator mutant 2 Prot 2 CV
                                                                                                                                                                                                                                                                                                                                                                                                                                              AARO6824 standard; protein; 780 AA.
Thrombomodulin analogue / t-PA fusion protein.
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Tissue plasminogen activator mutant 2 Prot 1
WO8907146-A.
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                         AAP90176 standard; peptide; 704 AA.
Tissue plasminogen activator mutant S+N.
                                                                                                                                                             AAP90177 standard; peptide; 718 AA.
Tissue plasminogen activator mutant OMS.
WO8907146-A.
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WO200268649-A2.
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RESULT 630

ID AAP90176 standard; peptide; 70

DE Tissue plasminogen activator n

PN W08907146-A.

PD 10-AUG-1989.

PA (INTE-) INTEG GENETICS INC.

Best Local Similarity: 100.00%
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Human PRO618 protein sequence:
WO9946281-22
16-SEP-1999.
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10-AUG-1989.
PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00*
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PA (INTE-) INTEG GENETICS INC.
Best Local Similarity: 100.00%
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(CODO-) CODON.
Local Similarity: 100.00%
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(CURA-) CURAGEN CORP.
Local Similarity: 100.00%
Match: 3.64%
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(CURA-) CURAGEN CORP.
Local Similarity: 100.00%
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Local Similarity: 100.00%
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Best Local Similarity: 100
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18-APR-2002.
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RESULT 631
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RESULT 634
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RESULT 633
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RESULT 635
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RESULT 636
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RESULT 639
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RESULT
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Human membrane-type serine protease (MTSP) 4-L splice variant.
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Novel human secreted and transmembrane protein PRO618.
US2003050239-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID ABU72218 standard; protein; 802 AA.

DE Novel human secreted and transmembrane protein PRO618

N US2002192706-A1.

PD 19-DEC-2002.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.004 Mismatches: 0
AAB44266 standard; protein; 802 AA.
Human PRO618 (UNQ354) protein sequence SEQ ID NO:169.
WO200053756-A2.
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Human secreted and transmembrane polypeptide PRO618.
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WO200200860-A2.
03-JAN-2002.
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Indels:
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Indels:
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                                                                                                                                      ID AB24052 standard; protein; 802 AA.

DE Human PR0618 protein sequence SEQ ID NO:24.

PN W0200053754-A1.

PD 14-SEP-2000.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00% Mismatche

Query Match: Indels:
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Human PROG18 polypeptide.
US2002169284-A1.
14-NOV-2002.
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                                  PN WO200053755-74.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00%
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PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
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GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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                                                                                                        Query Match:
RESULT 640
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RESULT 642
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RESULT 643
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RESULT 646
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and	INC. 100.00%	3.64%	rotei	and	INC.	100.00% 3.64%	. nrotein. 8	ansmembrane		INC.	100.00%	-	; protein; B ted and tran	100.00%	3.64%	: protein: 8	tide #26.		INC.	100.00%	3.64%	protein; 8	tide #26.		INC.	100.00\$	3.64%	, protein, 8	ansmembrane		INC.	100.00\$	3.64*	, protein, 8	ansmembrane		INC.	3.6		procein; nsmembrane			100.00% 3.64%	1000	ansmembrane	
Novel human secreted a US2003050241-A1.	13-MAR-2003. (GETH ) GENENTECH Local Similarity:	Match:	ID ABO19667 standard;	an secret 240-Al 03	(GETH ) GENENTECH	Jocal Similarity: Match:	r 650 Nna12369 standard	DE Human secreted/transmembrane p	JS2003055216-A1.	(GETH ) GENENTECH	Local Similarity: Match:	RESULT 651	ABO19558 standard; protein; 802 AA. Novel human secreted and transmembrane	Is-MAK-2003. Local Similarity:	Match:	RESULT 652 Th Aph73675 standard: protein: 8	Human PRO polypept	US2003045462-A1.	(GETH ) GENENTECH	Local Similarity:	Query Match: 3.64%	ADB76391 standard	Human PRO polypep	US2003083248-A1.	(GETH ) GENENTECH	Local Similarity:	Query Match:	r 654 ADC43817 standard	Human secreted/tr	US2003054986-A1.	20-MAK-2003. (GETH ) GENENTECH INC.	Local Similarity:	Query Match: RESULT 655	ADC61577 standard	Human secreted/tr US2003049684-Al.	13-MAR-2003.	(GETH ) GENENTECH	best bocal similaficy: Ouery Match:	,	ADC63541 standard; Human secreted/tra	US2003054405-A1.	CGETH ) GENENTECH	Best Local Similarity: Query Match:	RESULT 657	ADCeeetl Brandard; Procein; ouz An. Human secreted/transmembrane protein, HS2003060406-Al.	
	H	Query	ID 7	E E E	PA	Best J Query	RESUL	88	NG G	P. P.	Best 1	RESUL	28	PD	Query	RESUL	OB	PN C	P. P.	Best	Query	TD	30	Z G		Best	Query	KESUL		NA		Best	Query	Ωī	a Na		₽A	Ouery	RESUL	BB	N G	PD <b>PA</b>	Best Query	RESUL	DE D	:

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                                                                                       DE Human secreted/transmembrane protein, PRO618.

BHUMAN SECRETED/transmembrane protein, PRO618.

BN US2003064407-A1.

DO 3-APR-2003.

PA (GETH) GENENTECH INC.

BRESULT 659

ID ADC62825 standard; protein; 802 AA.

DE Human secreted/transmembrane protein, PRO618.

PRO517 659

ID ADC62825 standard; protein; 802 AA.

DE Human secreted/transmembrane protein, PRO618.

PRO518 10-APR-2003.

PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
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Indels:
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Description:

TESULT 665

ID ADE49203 standard; protein; 802 AA.

DE Human secreted/transmembrane protein, PR0618.

PN US2003096744-A1.

PD 22-MAY-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches:
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Indels:
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Human secreted/transmembrane protein, PRO618.
US2003203434-A1.
30-OCT-2003.
                                Mismatches:
Indels:
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DE Human secreted/transmembrane protein, PR0618.
PN 052003104998-A1.
PN 05201104998-A1.
PA (GETH ) GENEWIECH INC.
Best Local Similarity: 100.00% Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                       DE Human secreted/transmembrane protein, PRO618.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches:
Ouery Match: 3.64% Indels:
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Human secreted/transmembrane protein, PRO618.
US2003073624-A1.
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Human secreted/transmembrane protein, PRO618.
US2003073131-A1.
                                                      Query Match:
RESULT 658
ID ADC68765 standard; protein; 802 AA.
DE Human secreted/transmembrane protein; PRO618.
PN US2003064407-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
RESULT 661

ID ADC41210 standard; protein; 802 AA.
BE Human secreted/transmembrane protein, PRO618.
PN US2003072745-A1.
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RESULT 660
ID ADC67890 standard; protein; 802 AA.
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PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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AA (GETH) GENENTECH INC.
Best Local Similarity: 100.00%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
Query Match:
RESULT 662.
PD 27-MAR-ZUUS.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
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RESULT 663
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RESULT 664
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RESULT 666
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Mismatches: Indels:	802 AA. protein, PRO618.	Mismatches: Indels:	802 AA. : protein, PRO618.	Mismatches: Indels:	802 AA. 9 protein, PRO618.	Mismatches: Indels:	802 AA. : protein, PRO618.	Mismatches: Indels:	802 AA. : protein, PRO618.	Mismatches: Indels:	802 AA. : protein, PRO618.	Mismatches: Indels:	802 AA. : protein, PRO618.	Mismatches: Indels:	802 AA. : protein, PRO618.	Mismatches: Indels:	802 AA. #4.
INC. 100.00% 3.64%	protein; ansmembrane	INC. 100.00% 3.64%	protein; { nsmembrane	INC. 100.00% 3.64%	protein; ⁽ nsmembrane	INC. 100.00% 3.64%	protein; ( nsmembrane	INC. 100.00% 3.64%	protein; Ensmembrane	INC. 100.00% 3.64%	protein; { nsmembrane	INC. 100.00% 3.64%	protein; ( nsmembrane	INC. 100.00% 3.64%	protein; { nsmembrane	INC. 100.00% 3.64%	protein; protease INC.
ENENTECH ilarity:	KESULT 65 ID ADB16371 standard; protein; E DE Human secreted/transmembrane PN UGS003203435-A1.	PA (GETH ) GENENTECH ) Best Local Similarity: Querry Match:	KESULT 686 standard; protein; ED ADD72986 standard; protein; EDE Human secreted/transmembrane BD US2003203436-A1.	PA (GETH ) GENENTECH 1 Best Local Similarity: Query Match:	RESULT 669  ID ADD7344 standard; protein; 6 DB Human secreted/transmembrane PN US2003194781-A1.	7 7 1		003. GENENTECH milarity:	rd; tra	003. GENENTECH milarity:	6 standard; ecreted/tra 16561-A1.	20-NOV-2003. (GETH ) GENENTECH 3t Local Similarity: sry Match:	DE Human secreted/transmembrane protein, PN US2003206915-A1.	# 7. F	AESOLI 014 DD ADIGOSC standard; protein; 802 AA. DB Human secreted/transmembrane protein, PN US2003077700-A1.	PD 24-APR-2003.  PA (GETH ) GENENTECH 1  Best Local Similarity:  Query Match:	10 A110377 standard; DE Human cell surface PN W0200295007-A2. PD 28-NOV-2002. PA (CORV-) CORVAS INT

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Mismatches: Indels: 802 AA. protein, PRO618.	Mismatches: Indels:	802 AA. protein, PRO618.									Mismatches:	Indels:	802 AA. protein, PRO618.		Mismatches: Indels:	2 AA.	procein, PRO618.	Mismatches:		802 AA. protein, PRO618.		Indels:	802 AA. : protein, PRO618.
100.00% 3.64% protein; E	INC. 100.00% 3.64%	protein; E nsmembrane	4 ઃમ	ш	Σ Μ	 	. · · ·		i,	Σ	100.00\$	3.64%	protein; 8 1smembrane	Ç	3.64%	protein; 8	ısmembrane	INC. 100.00%	3.64%	protein; E Bemembrane	INC. 100.00%	3.64%	protein; 8 nsmembrane
. Local Similarity: 100.00\$  y Match: 3.64\$  JLT 676  ADE48503 standard; protein; 80 Human secreted/transmembrane p	-2003. ) GENENTECH 1 Similarity: :		• •	ARA N. AROFF	GAC W. GERBER H. GERRITSEN N	нна	LAN K U		SHELTON D I	. S		•	ADF61244 standard; protein; 80 Human secreted/transmembrane p	15345-A1. 2003. CENEWIECH 1	Similarity:	standard;	auman secreted/transmembrane p US2003198994-A1. 23-OCT-2003.	GENENTECH I	•	ADF45732 standard; protein; 80 Human secreted/transmembrane p US2003195148-Al	-2003. ) GENENTECH I Similarity:	•	ADF24128 standard; protein; Human secreted/transmembrane US2003204055-A1.
## Best Local Signery Match: Query Match: RESULT 676 ID ADE48503 DE Human 86 PN US200310	PD 05-JUN-2 PA (GETH) Best Local Si Query Match: RESULT 677	11D ADE89604 DE Human se PN US200313 PD 10-JUL-2	(ASHK/) (BAKE/) (BOTS/) (DESN/)		PA (GERB/) PA (GERB/) PA (GERR/) PA (GODD/)				PA (KOIM/) PA (SHEL/)		(WOOD/ st Local	Query Match: RESULT 678	ID ADF61244 DE Human se	PN US200319 PD 16-OCT-2	Best Local Si Query Match:	ğ	DE HUMAN BE PN US200319 PD 23-OCT-2	PA (GETH ) Best Local Si	9 50	ID ADF45732 DE Human B6 PN US200319	m	>-1	ID ADF24128 DE Human se PN US200320

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Mismatches: Indels:	otein, PRO618.	Mismatches: Indels:	802 AA. : protein, PRO618.	Mismatches: Indels:	AA. cotein, PRO618. Wismarches:	Indels:	COCEIN, PROBLE.		cotein, PRO618.	Mismatches: Indels:	rotein, PRO618.	Mismacches: Indels:	rotein, PRO618.	Mismatches: Indels: 2 AA.	rotein, PRO618.	Mismatches: Indels:	2 AA. rotein, PRO618. Mismatches:	
Best Local Similarity: 100.00% Query Match: 3.64% RESULT 691 In Appr4119 standard: protein: 802	DE Human secreted/transmembrane protein, PN US201394410-A1.	E St	6 standard; protein; E ecreted/transmembrane 95344-Al. 2003.	# <u>7,7</u> F	ID ADG50342 standard; protein; 802 AA. DE Human Becreted/transmembrane protein, PN US2003207803-A1. PD 06-NOV-2003. PA (GETH) GENENTECH INC. PAR (GETH) GENENTECH INC.	Desy March: RESULT 694  ID ADG49718 standard; protein; 802	DE HUMMAN SECFECECATRANSMEMDFANE PIOCEIN, PN US2003215905-A1. PD 20-NOV-2003. PA (GETH ) GENENTECH INC.	t Local Similarity: 100.00\$  rry Match: 3.64\$  full 695	AUGS1590 Btandard Human secreted/tr: US2003215908-A1. 20-NOV-2003.	PA (GEIN ) GENENIECH 100.00% Best Local Similarity: 100.00% Query Match: 3.64% Inde RESULT 696 TO ADGAGOGA standard: protein: 802 AA.	DE Human secreted/transmembrane pi PN US2003216305-A1. PD 20-NOV-2003. PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00% Query Match: RESULT 697 TT DATASATA CHANGERA. PROFESSIONE 807.	DE Human secreted/transmembrane protein, PN US2003216560-A1. PD 20-NOV-2003. PA (GETH ) GENENTECH INC.	Best Local Similarity: 100.00% Query Match: RESULT 698 ID AD50966 standard: protein: 800	DE Human secreted/transmembrane protein, PN US2004005312-A1. PD 08-JMA-2004. PA (GETH ) GENEWIECH INC.	it Local Similarity: 100.00% iry Match: 3.64% SULT 699	ID ADG58910 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PD 08-JAN-2004. PD 08-JAN-2004. PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00\$	
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00% Mismatches: i% Indels:	ein; 802 AA. brane protein, PRO618.		ein; 802 AA. brane protein, PRO618.	00% Mismatches: '% Indels:		.00% Mismatches:	ein, 802 AA. Abrane protein, PRO618.	.00% Mismatches: I% Indels:	protein, 802 AA. Ismembrane protein, PRO618.	.00% Mismatches:	cein; 802 AA. nbrane protein, PRO618.	.00% Mismatches:	protein; 802 AA. nsmembrane protein, PRO618.	.00% Mismatches:	cein; 802 AA. mbrane protein, PRO618.	.00% Mismatches: 1% Indels:	cein; 802 AA. nbrane protein, PRO618.	
PA (GETH) GENENTECH INC. Best Local Similarity: 100.00% QUETY MATCh: 3.64%	KESULI 982  ID ADF40560 standard; protein; 802 A DE Human secreted/transmembrane prot DN 11920011494011-21	PD 23-OCT-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 100.00\$	Query Match: RESULT 683  ID ADF23504 standard; protein; 802 A. DE Human secreted/transmembrane prot DN 1152001301480-21	PD 30-OCT-2003.  PA (GETH) GENENTECH INC. Best Local Similarity: 100.00% Ouery Match: 3.64%	7 standard ecreted/tr 94780-A1. 2003.	PA (GETH) GENENFECH INC. Best Local Similarity: 100.00% Query Match: 3.64% RESULT 685	ID ADF26954 standard; protein; 802 A. DE Human secreted/transmembrane prot. PN US2003199436-A1. PD 23-C77-2003.	# 년	0 standard; ecreted/trar 99437-A1.	PD 23-OCT-2003. PD 23-OCT-2003. Best Local Similarity: 100.00% Query Match: 3.64%	KESULI 687  ID ADF41184 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PN US2003199435-A1. PD 23-OCT-2003.	PA (GETH) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.64%	3 standard; ecreted/tran 11091-A1.	7 K	D PRESC129 standard; protein; 802 AA. DE Human secreted/transmembrane protein, by US200311092-A1.	PA (GETH) GENENTECH INC. Best Local Similarity: 100.00% Ouery Match: 3.64%	0 standard ecreted/tr 99674-A1. 2003. GENENTECH	

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á	SEQ ID 52.	Mismatches: Indels:	· AA	Mismatches: Indels:	970 AA. human protease #42		AA. 1 SEQ ID 50.		1 AA.	Mismatches: Indele:	4 N	Mismatches:	∢	Mismatches: Indels:	6 AA. #14579.	Mismatches: Indels:	6 AA. #7861. Mismatches:
Ĕ	DE Human NOV12b CG92293-02 protein PN WO20021625-A2. PD 17-OCT-2002	CURA-) CURAGEN CORP.  St Local Similarity: 100.00%  Bry Match: 3.64%  SULT 710	ADK43/18 Btandard Human protease PR' WO200220736-A2. 14-MAR-2002	PA (INCY-) INCYTE GENOMICS INC. Best Local Similarity: 100.00\$ Query Match: 3.64\$	ID AAU82743 standard; protein; 970 DE Amino acid sequence of novel hu WO200200860-A2. PD 03-JAN-2002.	SUGEN INC. milarity: 100.00% 3.64%	ID ABU12065 standard; protein; 986 DE Human NOV12a CG92293-01 protein PN WO200281625-A2. PD 17-CPT-2002	(CURA.) CURACEN CORP. Local Similarity: 100.00% Match: 3.64%	standard; protein; man protein. SEQ ID 105-A1.	PA (SMIK ) SMITHKLING BEECHAM COKE PA (SMIK ) SMITHKLING BEECHAM PLC. PA (GLAX ) GLAXO GROUP LTD. Beet Local Similarity: 100.00%	SULT 714 AAP80692 standard; Hybrid plasminogen/	PD 23-NOV-1988. PD 23-NOV-1988. PA (BEEC) BEECHAM GROUP PLC. Beet Local Similarity: 100.00%	SULT 715 SULT 715 AAP80691 standard; Hybrid plasminogen/	PN EEV29.2246-A. PD 23-NOV-1988. PA (BEEC ) BEECHAM GROUP PLC. Beet Local Similarity: 100.00%	T 716 ABG14588 standard; Novel human diagnos WO200175067-A2.	PD 11-OCT-2001. PA (HYSE) HYSEQ INC. Best Local Similarity: 100.00% Query Match: 3.64%	RESULT 717  ID ABG07870 standard; protein; 1576 AA.  ID NO.01175067-A2.  PD 11-OCT-2001.  PA (HYSE-) HYSEQ INC.  Best Local Similarity: 100.00% Mi
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			ce SEQ ID NO:169.		:ide #4.								262-527.				
	PRO618.	ches: 0	ein sequence	ches: 0	) polype	ches: 0 :	0618.	ches: 0	0618.	ches: 0		ches: 0 : 0	] t-PA	ches: 0 : 0		ches: 0	ches: 0
Indels		Mismatche Indels:	802 AA. related protein	. Mismatche	12 AA. tease (MTSP)	Mismatches Indels:	12 AA. rotein, PR	Mismatche Indels:	12 AA. rotein, PR	Mismatches Indels:	2 AA.	Mismatches Indels:	rotein; 807 AA. [Arg298-299->Gln298-299	Mismatches Indels:	3 AA.	Mismatches Indels:	3 AA. 1 #24237. Mismatchee Indels:
3.64%	d; protein; 80 ransmembrane p	H INC. : 100.00% 3.64%	d; protein; 80 n homologue re	H INC. : 100.00%	d; protein; 80 ane serine pro	NT INC. : 100.00% 3.64%	d; protein; 80 ransmembrane p	H INC. : 100.00% 3.64%	d, protein, 80 ransmembrane p	H INC. : 100.00% 3.64%	d; protein; 802 tein sequence.	H INC. : 100.00% 3.64%	d; protein; 80 541 [Arg298-29	GROUP PLC. : 100.00% 3.64%	d; protein; 86 e ID 7484157CL	GENOMICS INC. :Y: 100.00% 3.64%	d; protein; 91 nostic protein C. C. 3.64\$
Query Match: RESILT 700	ID ADG62366 standard; protein; 802 AA. DE Human secreted/transmembrane protein, DN 1152004006219-21	PD 08-JAN-2004. PA (GETH ) GENENTECH Best Local Similarity: Ouery Match:	KESULI /01 ID ADH25391 standard; protein; DE Human neurotrimin homologue PN EP136431-A1	ž,	RESULT 702 ID ADJ46901 standard; protein; 802 AA. DE Human transmembrane serine protease PN US2004001801-A1.	PD 01-JAN-2004. PA (CORV-) CORVAS INT INC. Best Local Similarity: 100.00% Query Match: 3.64%	RESULT 703 ID ADM17168 standard; protein; 802 AA. DE Human secreted/transmembrane protein, PRO61: PN :::2004048312-a1	PD 11-MAR-2004.  PA (GETH ) GENENTECH INC.  Best Local Similarity: 100  Query Match: 3.6	ğ	PD 01-AFK-2004. PA (GETH) GENENTECH INC. Best Local Similarity: 100 Query Match: 3.6	KESOLI (02)  DE Human PRO618 protein; 80  PN AU2002317529-A1.	PD 10-APR-2003.  PA (GETH) GENENTECH INC. Best Local Similarity: 100 Query Match: 3.6	}	PD 12-DEC-1991. PA (BEEC ) BEECHAM GROUP PLC Best Local Similarity: 100.00 Query Match: 3.64%	1D ABB98140 standard; protein; 863 AA. DE Human PAWM Incyte ID 7484157CD1. PP W0200246383-A2. PD 13-JUN-2002.	(INCY-) INCYTE st Local Similarit ery Match: SULT 708	ID ABG24246 standard; protein; 913 AA. DE Novel human diagnostic protein #24237 PN W020175067-A2. PD 11-OCT-2001. PA (HYSE-) HYSEQ INC. Best Local Similarity: 100.00% Miss Query Match: 1nd

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(PFIZ ) PFIZER PROD INC.
(OXPO-) OXFORD GLYCOSCIENCES UK LTD.
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PA (ENGE-) ENGENEOS INC.
Best Local Similarity: 100.00%
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A (FUSO) FUSO PHARM IND LTD.
Best Local Similarity: 100.00%
Ouery Match: 3.36%
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Query Match: 3.36%
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Best Local Similarity:
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(TANO-) TANOX INC.
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RESULT 729
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Alzheimer's Disease-associated protein isoform, API-26, SEQ ID 68.
WO2003028543-A2.
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ADN31742 standard; peptide; 18 AA.
Human Alzheimer's disease-API tryptic digest peptide - SEQ ID 68.
EP1408333-A2.
14-APR-2004.
                                                                                                                                                                                                                                                                                                                       AA772112 standard, peptide, 12 AA.
Peptide fragment #12 related to human serine protéase.
WO200068247-A2.
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Human gene 4 encoded serine protease fragment #1.
WO200198476-A1.
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Human serine protease serine active site domain.
US2002119925-A1.
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Human API-180 tryptic digest peptide #4.
WO200175454-A2.
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Human API-26 tryptic digest peptide #3.
WO200175454-A2.
                                                           Novel human diagnostic protein #19878.
W0200175067-A2.
11-OCT-2001.
(HYSE-) HYSEQ INC.
Local Similarity: 100.00% Mism
                                                                                                                                                                                                       Novel human diagnostic protein #10209.
WO200175067-A2.
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Mis Carl Similarity: 100.00% Mis / Match: 3.36% Inc.
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(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
(PPIZ ) PFIZER INC.
Local Similarity: 100,00$
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PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
BEST LOCAL Similarity: 100.00% Mi
Query Match: 3.36% Ir
              Query Match: 3.64% In
RESULT 718
ID ABG19887 standard; protein; 1576 AA.
                                                                                                                                                                                        ABG10218 standard; protein; 1576 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity: 100.00%.
Query Match:
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Match: 3.36%
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Best Local Similarity: 100.00%
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(HYSE-) HYSEQ INC.
Local Similarity:
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RESULT 726
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RESULT 720
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RESULT 721
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JT 728
BBE63477 standard, protein, 141 AA.
Drosophila melanogaster polypeptide SEQ ID NO 17223.
WO200171042-A2.
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Human kallikrein 15, marker of endocrine cancer.
WO2004029285-A2.
                                                                                                                                                                                                                                                                                                   AAU79393 standard; protein; 171 AA.
Novel human kallikrein KLK15, splice variant #3.
WO200214485-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU82735 standard; protein; 222 AA.
Amino acid sequence of novel human protease #34.
WO200200860-A2.
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              Query Match:
RESULT 727
ID ADR72151 standard; peptide; 40 AA.
DE Human kallikrein 15 splice form 3 peptide.
PN US2004180380-A1.
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Human endothellase 1 protease domain.
WC200136664-A2.
P5-MAY-2001.
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Human neurosin amino acid sequence.
WO200031284-AI.
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RESULT 733
ID AAR89430 standard; protein; 232 AA.
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Best Local Similarity: 100.00%
Ouerv Match: 3.36%
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gry tr	PD 08-MAY-2003. PD 08-MAY-2003. PA (MILL-) MILLENNIUM PHARM INC. Best Local Similarity: 100.0% Mismatches: 0 Query Match: 3.36% Indels: 0 RESULT 746 ID ADB80567 standard; protein; 244 AA. DE Ovarian cancer-associated protein #66. PN W02002102238-A2.	i ji ji	۲ <u>۲</u> ۲ ۲ ۲ ۲ ۲ ۲ ۲ ۲ ۲ ۲ ۲ ۲ ۲ ۲ ۲ ۲ ۲	i ji ji	Sir Sir	Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 3.36\$ Indels: 0 RESULT 751 ID ADN29289 standard; protein; 244 AA. DE Human Kallikrein 6 associated protein. PN US2004097452-A1. PD 20-MAY-2004.	Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 3.36\$ Indels: 0 RESULT 752 ID ADQ89076 standard; protein; 244 AA. DE Human urological disorder related protein 2047 SEQ:28.	st sur st
PA (CORV-) CORVAS INT INC.  Best Local Similarity: 100.00\$ Mismatches: 0  Query Match: 3.36\$ Indels: 0  RESULT 736  ID AD110391 standard; protein; 233 AA.  DE Human cell surface protease #11.	PN WOZUOZSJON-AZ. PD 28-NOV-2002. PA (CORV-2 2002. PA (CORV-2) CORVAS INT INC. Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 3.36\$ Indels: 0 RESULT 737 ID ADJ46915 standard; protein; 233 AA. DE Human transmembrane serine protease (MTSP)-related polymentide #1.	INC. 100.00% Mismatches: 0 1.36% Indels: 0	FN WCJOUGASTY-76-AZ. PD 14-SEP-2000. PA (WOUN ) MOUNT SINAI HOSPITAL. PA (WOUN ) MOUNT SINAI HOSPITAL. PBEST Local Similarity: 100.00\$ Mismatches: 0 QUETY MATCH: 3.36\$ Indels: 0 RESULT 739 ID ADASG482 standard; protein; 241 AA. PD Human protease SEQ ID NO:80. PN WC2003040393-A2.	PD 15-MAY-2003. PA (DECO-) DECODE GENETICS EHP. Mismatches: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 3.36\$ Indels: 0 RESULT 740 ID AAR44532 standard; protein; 244 AA. DE Zyme APP-cleaving protease.	PA (ELIL) LILLY & CO ELI.  Best Local Similarity: 100.00\$ Mismatches: 0  Query Match: 3.36\$ Indels: 0  RESULT 741  1D AAW22985 standard; protein; 244 AA.  DE Human serine protease 59 (SP59).	PA (SUNR) SUMTORY LTD.  Best Local Similarity: 100.00\$ Mismatches: 0  Query Match: 3.36\$ Indels: 0  RESULT 742  ID AAWS1006 standard; protein; 244 AA.  DR Protease M, a novel serine protease.  PN W09811238 A2.	PA (DAND) DANA FARBER CANCER INST INC.  Best Local Similarity: 100.00\$ Mismatches: 0  Query Match: 3.36\$ Indels: 0  RESULT 743  ID AAB21323 standard; protein; 244 AA.  BD Human zyme.	FIN MCJOURS JOETAL.  PD 14-SEP-2000.  PA (MOUN ) MOUNT SINAI HOSPITAL.  Best Local Similarity: 100.00\$ Mismatches: 0  Query Match: 3.36\$ Indels: 0  RESULT 744  ID ABG96357 standard; protein; 244 AA.  DE Human ovarian cancer marker OV33.  PD 19-SEP-2002.  PD 4MILL-) MILLENNIUM PHARM INC.

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ABBÓ6965 standard, protein; 417 AA.
Mouse airway specific trypsin-like protease protein SEQ ID NO:2.
WQ200218562-A1.
                         ADJ83072 standard; protein; 345 AA.
Human protein which is similar to DESC protein - SEQ ID 63.
US2003170630-A1.
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Bovine AST protein sequence SEQ ID NO:33.
WQ200218562-A1.
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Novel mouse protein #20.
WO2003089644-A1.
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WO200226947-A2.
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PA (RIKE) RIKEN KK.
PA (DNAP-) DNAFORM KK.
PA (DNAP-) DNAFORM CK.
PA (MITU) MITSUBIGHI CHEM CORP.
Best Local Similarity: 100.00%
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(ELLE/) ELLERMAN K.
(MACD/) MACDOUGALL J R.
(SMIT/) SMITHSON G.
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FERNANDES E R.
RIEGER D K.
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JP2002065266-A.
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SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
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                                                                                         ALSOBROOK J P
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PA (TEIJ) TEIJIN LTD.
Best Local Similarity: 1
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PA (PEKE) PE CORP NY.
Best Local Similarity: 1
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BOLDOG F L.
                                                                                                                                                                                   LEPLEY D M.
BURGESS C E
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Best Local Similarity:
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MILLET I.
SCIORE P.
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(PATT/)
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RESULT 766
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RESULT 768
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                                           Human ovarian cancer-related tumour marker kallikrein 6 (hK6) protein. WO2004075713-A2.
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DE Drosophila melanogaster polypeptide SEQ ID NO 17217.

PN W0200171042-A2.

PD 27-SEP-2011.

PA (PEKE) PE CORP NY.

Best Local Similarity: 100.00% Mismatches: 0
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Drosophila melanogaster polypeptide SEQ ID NO 19374.
W0200171042-A2.
27-SEP-2001.
(PEKE ) PE CORP NY.
(PEKE ) PE CORP NY.
3.36*
Indels:
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Drosophila melanogaster polypeptide SEQ ID NO 40248.
WO200171042-A2.
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Drosophila melanogaster polypeptide SEQ ID NO 35004
WO200171042-A2.
                                                                                                                                                                                                                                                                                                              28356
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Drosophila melanogaster polypeptide SEQ ID NO 9798.
W7200171042-A2.
27-SER-2001.
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Drosophila melanogaster polypeptide SEQ ID NO
WO200171042-A2.
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                RESULT 754
ID ADR72876 standard; protein; 244 AA.
                                                                                                                                                      AAP90531 standard; protein; 256 AA.
Hypodermin B of ATCC # 67613.
EP326419-A.
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19-7UN-2002.
(UTVA-) UNIV NANJING MEDICAL.
Local Similarity: 100.00%
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(USDA ) US SEC OF AGRIC.
(CODO-) CODON.
st Local Similarity: 100.00$
                                                                                         (MOUN ) MOUNT SINAI HOSPITAL.
Local Similarity: 100.00%
Match: 3.36%
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(PEKE) PE CORP NY.
Local Similarity: 100.00$
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(PEKE ) PE CORP NY.
Local Similarity: 100.00%
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PA (PEKE) PE CORP NY.
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RESULT 762
ID ABB63475
DE Drosophi:
PN WO220171(PD 27-SEP-2(PA C) PA C) PA C)
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RESULT 760
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RESULT 761
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RESULT 756
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DE
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Best
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Query Match: RESULT 770

Query Match: RESULT 771

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ABB06964 standard; protein; 418 AA.
Human airway specific trypsin-like protease protein SEQ ID NO:1.
WO200218562-A1.
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Macaca fascicularis AST protein sequence SEQ ID NO:29.
07-MAR-2002.
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Indels:
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Guinea pig AST protein sequence SEQ ID NO:37.
WO200218562-A1.
                                                             ID ARBI3769 standard; protein; 418 AA.

DE Human lung tumour-specific protein L86S-46.

PN W0200172295-A2.

PD 04-0CT-2001.

PA (CORI-) CORIXA CORP.

Best Local Similarity: 100.00$ Mismatche
Query Match: 13.36$
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Human lung tumour-specific protein L86S-36.
WO200172295-A2.
                                                                                                                                                                                                                                                                                                                                                            Human lung tumour-specific protein L86S-46 WO200172295-A2.
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Rabbit AST protein sequence SEQ ID NO:35.
WO200218562-A1.
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PA (TEL) TELJIN LTD.
Best Local Similarity: 100.00%
              100.00%
3.36%
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(CORI-) CORIXA CORP.
Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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JP2002065266-A.
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Best Local Similarity:
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                Best Local Similarity:
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PA (FARB ) BAYER AG.
Best Local Similarity:
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RESULT 781
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RESULT 785
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RESULT 786
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RESULT 782
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RESULT
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WO9938973-A2.
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Human lung tumour protein L86S-36 predicted extended protein sequence.
WO9938973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human lung tumour protein L865-46 predicted amino acid sequence. W09938973-A2.
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Human lung tumour-specific antigen encoded by cDNA #48.
12-OCT-2000.
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Human lung tumour-specific antigen encoded by cDNA #49.
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Human airway trypsin-like protease (HAT) protein.
WO200157194-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB44428 standard; protein; 418 AA.
Human lung tumour-specific antigen encoded by
WO200060077-A2.
                                Mismatches:
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                                                                           Hamster AST protein sequence SEQ ID NO:39.
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Trypsin-like enzyme.
AU9527248-A.
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(CORI-) CORIXA CORP.
Local Similarity: 100.00%
3.36%
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(CORI-) CORIXA CORP.
Local Similarity: 100.00%
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PA (CORI-) CORIXA CORP.

Best Local Similarity: 100.00%
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PA (COR-) CORIXA CORP.

Best Local Similarity: 100.00%
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(CORI-) CORIXA CORP.
Local Similarity: 100.00%
PA (TELJ ) TELJIN LTD.
Best Local Similarity: 100.00%
3.36%
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PD 07-MAR-2002.
PA (TELU) TELUIN LTD.
Best Local Similarity: 100.00$
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Best Local Similarity: 100.00$
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Local Similarity: 100.00%
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                                              Query Match:
RESULT 769
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Query Match: RESULT 774

Query Match: RESULT 775

Query Match: RESULT 776

Query Matc RESULT 777 Best ]

VERNET C A M.

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Human lung tumour-specific related protein, SEQ ID No 62. 21-NOV-2002.
                                                                                                                                        ADD66391 standard; protein; 418 AA.
Human lung tumour-specific related protein, SEQ ID No 83.
WO200292001-A2.
                                        82.
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US2003170630-A1.
                                       SEQ ID No
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                         ADD66390 standard; protein; 418 AA.
Human lung tumour-specific related protein,
WO200292001-A2.
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US2003118599-A1.
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Human lung tumour antigen polypeptide #22.
US2003118599-A1.
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Human lung tumour antigen polypeptide #31.
US2003118599-A1.
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                                        DE Human lung tumour-specific re
PN WO200292001-A2.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 100.00%
Query Match:
RESULT 788
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26-JUN-2003.
(CORI-) CORIXA CORP.
Local Similarity: 100.00%
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(CORI-) CORIXA CORP.
Local Similarity: 100.00%
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PA (CORI-) CORIXA CORP.
Best Local Similarity: 100.00%
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A (CORI-) CORIXA CORP.
Best Local Similarity: 100.00$
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DE Human lung tumour-specific
PN WO200292001-A2.
PD 21-WV-2002.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 100.00%
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TCHERNEV V T.
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BURGESS C E.
SHIMKETS R A.
GROSSE W M.
SZEKERES E S.
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PATTURAJAN M.
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SPYTEK K A.
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PA (CORI-) G
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RESULT 793
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RESULT 791
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RESULT 789
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RESULT 790
Query Match:
RESULT 787
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RESULT
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Human transmembrane serine protease (MTSP)-related polypeptide #7.01-JAN-2004.
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Human airway trypsin-like protease HAT.
WO2004053496-Al.
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ADJ46926 standard; protein; 418 AA.
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Human DESC1 protein variant #2.
WO200050061-A1.
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Human endotheliase 1 protein.
WO200136604-A2.
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Human DESC1 protein variant #1.
WO200050061-A1.
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PA (OHIS) UNIV OHIO STATE RES FOUND.
Best Local Similarity: 100.00%
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Best Local Similarity: 100.00$
                                                                                                        MILLET I.
SCIORE P.
SCIORE P.
MILLERANN K.
MACDOUGALL J R.
SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                    DE CORVER CORVER INT INC.
Best Local Similarity: 100.00%
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Query Match: 3.36%
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Best Local Similarity: 100.00%
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                                       GANGOLLI E A. FERNANDES E R.
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(HINZ/) HINZMANN B.
(HEIDZ/) HEIDEN E.
(HEEM/) HERMANN K.
(ROSE/) ROSENTHAL A.
                                                                 RIEGER D K.
EDINGER S R.
GUNTHER E.
CASMAN S J.
BOLDOG F L.
                                                                                                                                                                              Local Similarity:
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RESULT 796
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RESULT 797
                                                                                                              (MILL/)
(SCIO/)
(ELLE/)
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(SMIT/)
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                           (GORM/)
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RESULT 800
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RESULT 801
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AAY99414 standard; protein; 423 AA.
Human PRO1461 (UNQ742) amino acid sequence SEQ ID NO:269.
WO200012708-A2.
09-MAR-2000.
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Human TANGO 361, variant #4 amino acid sequence.
WO200121631-A2.
29-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU01400 standard; protein; 423 AA.
Human TANGO 361, variant #2 amino acid sequence.
WO200121631-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU01401 standard; protein; 423 AA.
Human TANGO 361, variant #3 amino acid sequence.
WO200121631-A2.
29-MAR-2001.
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Human TANGO 361, variant #1 amino acid sequence.
WO200121631-A2.
                      Mismatches:
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DE Human PRO polypeptide sequence #160.
PN W0200168848-A2.
PD 20-SEP-2001.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mich
                                                                                                                                                                                                                                                                                                            ID AAU01344 standard; protein; 423 AA.

DE Human TANGO 361 amino acid sequence.

PN W0200121631-A2.

PD 29-MAR-2001.

PA (MILL-) MILLENNIUM PHARM INC.

Best Local Similarity: 100.00% Mi
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RESULT 816
ID AAB87578 standard; protein; 423 AA.
                                                                                                                                                                                        AAB66163 standard; protein; 423 AA.
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D 29-MAR-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 100.00%
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PA (MILL-) MILLENNIUM PHARM INC.
Best Local Similarity: 100.00%
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Best Local Similarity: 100.00$
Query Match: 3.36$
                                                                                                                                                                                                     Protein of the invention #75.
WO200078961-A1.
28-DEC-2000.
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Best Local Similarity: 100.00%
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WO200116318-A2.
08-MAR-2001.
(GETH ) GENENTECH INC.
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Human transmembrane serine protease (MTSP)-related polypeptide #11.
US2004001801-A1.
01-0JNN-2004.
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Human transmembrane serine protease (MTSP)-related polypeptide #4.
US2004001801-Aį.
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Lung cancer-associated polypeptide #120.
WO200286443-A2.
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Human DESC1 protein - SEQ ID 64.
US2003170630-A1.
                                                                                                                                                                                     ADI10410 standard; protein; 422 AA.
Human cell surface protease #21.
WO200295007-A2.
28-NOV-2002.
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PA (BOSB-) EOS BIOTECHNOLOGY INC. Best Local Similarity: 100.00$
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28-NOV-2002.
(CORV-) CORVAS INT INC.
'Acal Similarity: 100.00$
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LOCAL Similarity: 100.00%
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(CORV-) CORVAS INT INC.
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ZERHUSEN B D.
PATTURAJAN M.
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DE COL	17 017 18055903 standard, protein, 423 AA. Human secreted/transmembrane protein PRO14 US2002119130-A1.	protein; 4 smembrane	123 AA. protein PRO1461.		
PD PA PA Best 1	29-AUG-2002. (GETH ) GENENTECH I Local Similarity: Match:	INC. 100.00% 3.36%	Mismatches: Indels:	00	
ID OE OE	KESULI 818  ID ABP43883 standard; F DE Human PRO1461 protei PN WO200231111-A2.	orotein; in.	423 AA.		
PA PA Best ] Query	PD 18-AFA-2002. PA (HYSE-) HYSEQ INC. Best Local Similarity: Query Match:	100.00% 3.36%	Mismatches: Indels:	00	
RESUL ID DE PN	ወደጠ		423 AA.		
PD Best Query	PD 06-FBB-2003. Best Local Similarity: Query Match:	100.00\$	Mismatches: Indels:	00	
RESUL ID DE PN	Jr 820 ABU88107 standard; protein; Novel human secreted and tr US2003032127-Al.	protein; 'ed and tra	n; 423 AA. transmembrane protein	. PRO1461.	
# £	PD 13-FEB-2003. Best Local Similarity: Query Match:	100.00% 3.36%	Mismatches: Indels:	00	
RESUL ID DE PN	rr 821 ABU84422 standard; protein; 4 Human secreted/transmembrane US2003032112-Al.	protein; nsmembrane	423 AA. protein (PRO) #160	. 0	
PD Best Query	13-FEB-2003. Local Similarity: Match:	100.00% 3.36%	Mismatches: Indels:	00	
KESOT DE DE	KESULI 8/2/ ID ARR66296 standard; protein; DE Human secreted polypeptide   PN US2003027278-A1.	protein; ypeptide P	423 AA. PRO1461, SEQ ID NO:	:320.	
PD Best Query	ED 08-FEB-2003. Best Local Similarity:	100.00% 3.36%	Mismatches: Indels:	00	
E E E E E E E E E E E E E E E E E E E	Jul 823 ARK65686 standard; protein; 4 Human secreted polypeptide PR US2003036159-Al.	protein; ypeptide P	423 AA. PRO1461, SEQ ID NO:	.320.	
m (1)	PD 20-FEB-2003. Best Local Similarity: Query Match:	100.00%	Mismatches: Indels:	00	
RESUI ID DE PN	Jr 824 ABU99626 standard; protein; 4 Human secreted/transmembrane US2003040070-A1.	protein; nsmembrane	423 AA. : protein (PRO) #160	. 03	
m 41 6	Z/-FBB-Z003. Local Similarity: / Match:	100.00% 3.36%	Mismatches: Indels:	00	
ID BE	Jul 923 BUB0865 standard, protein; 4 Human PRO polypeptide #160. US2003032113-Al.	protein; ide #160.	423 AA.		
ED (I) E	Best Local Similarity: Query Match:	100.00% 3.36%	Mismatches: Indels:	00	
	ABU89986 standard; protein; 423 AA Novel human secreted and transmemb US2003036147-Al.	protein; ed and tra	otein; 423 AA. and transmembrane protein	n PRO1461.	· <u></u>
PD Best	20-FEB-2003. Local Similarity:	100.00\$	Mismatches:	0	_

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ID ABU99112 standard; protein; 423 AA.

ID ABU99112 standard; protein; 423 AA.

Bo US2003017544-A1.

PD 23-JAN-2003.

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.36% Indels: 0
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Novel human secreted and transmembrane protein PRO1461.
US2003036144-A1.
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Novel human secreted and transmembrane protein PRO1461
US2003013153-A1.
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Human secreted polypeptide PRO1461, SEQ ID NO:320.
US2003040056-A1.
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Human secreted polypeptide PRO1461, SEQ ID NO:320.
US2003044926-Al.
                          ARR66235 standard; protein; 423 AA.
Human secreted polypeptide PRO1461, SEQ ID NO:320.
US2003027264-A1.
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DE Human secreted/transmembrane protein (PRO) #160.

PN US2003040062-A1.

PD 27-FEB-2003.

Best Local Similarity: 100.00% Mismatches: Query Match: 3.36% ThABLE.
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ABU92719 standard; protein; 423 AA.
Human secreted/transmembrane protein (PRO) #160.
US2003036149-A1.
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Human secreted/transmembrane protein (PRO) #160.
US2003044923-A1.
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Human PRO polypeptide #160.
10/52003036140-Al.
20-FRB-2003.
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PD 20-FEB-2003.
Best Local Similarity: 100.00% Query Match: 3.36% RESULR 830
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Query Match:
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ABU91818 standard; Novel human secrete 082003027277-Al. 06-FEB-2003. Local Similarity:	protein; ed and tran	ABU91818 standard; protein; 423 AA.  Novel human secreted and transmembrane protein PRO1461 US2003027277-A1.  06-FEB-2003.  Mismatches: 0	PRO1461. 0	Query Match: RESULT 847 ID ABR92334 standard; protein; DE Human secreted polypeptide P PN US2003036160-Al.
7. Match: 3.36% ABU89511 standard; protein; Human PRO polypeptide #160.		Indels: 423 AA.	0	PD 20-FEB-2003. Best Local Similarity: .100.00\$ Query Match: 3.36\$ RESULY 848
US2003036141-A1. 20-FEB-2003. Local Similarity: y Match:	100.00%	Mismatches: Indels:	00	ID ABO18965 standard; protein; DE Human secreted/transmembrane PN US2003044925-A1. PD 06-MAR-2003.
RESULT 839  ID ABU86352 standard;  DE Human secreted/tran	rd; protein; transmembrane	rd; protein; 423 AA. transmembrane protein (PRO) #160		# KE
. B:	INC. 100.00% 3.36%	Mismatches: Indels:	0 0	ABK78386 standard Human secreted po. US2003054474-A1. 20-MAR-2003. (GETH ) GENENTECH
5 standa ecreted/ 36162-A1	protein; 4	rd; protein; 423 AA. transmembrane protein (PRO) #160	á	Best Local Similarity: 100.00\$ Query Match: 3.36\$ RESULT 850 ID ABU72004 standard; protein;
Ξü	INC. 100.00% 3.36%	Mismatches: Indels:	00	DE Novel human secreted and tra PN US2003018183-A1. PD 23-JAN-2003. PA (GETH) GENENTECH INC. POOF TOTAL SIGNIFICATION ONS
ABU80593 standard; protein; Human PRO protein #160. IS2003036137-A1		423 AA.		Match: T 851
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8 standard; uman secret:	protein; 4ed and tran	Jr 842 ABU90928 standard; protein; 423 AA. Novel human secreted and transmembrane protein	PRO1461.	3.36% SULT 852 ABOOUSCI standard, protei
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anda ted/ 3-A1	protein; 4 nsmembrane	rd; protein; 423 AA. transmembrane protein PRO1461.		KESULT 853  DE ABO11593 standard; protein; DE Human secreted/transmembrane PN US2003036124-A1.
2003. GENENTECH imilarity:	INC. 100.00% 3.36%	Mismatches: Indels:	00	PD 20-FEB-2003. Best Local Similarity: 100.00\$ Query Match: 3.36\$ RESULT 854
RESULT 844 ID ABR99511 standard; DE Human secreted poly PN US2003040063-A1.	protein, ypeptide	423 AA. PRO1461, SEQ ID NO:320	.20.	ID ABO02238 standard; protein; DE Human secreted/transmembranc PN US2003040054-A1. PD 27-FEB-2003.
PD 27-FEB-2003. Best Local Similarity: Query Match:	100.00% 3.36%	Mismatches: Indels:	0 0	# K.E
anda ted 4-A1	protein; ypeptide	. 423 AA. PRO1461, SEQ ID NO:320	120.	1D ABUSBELZ Standard; protein; DE Novel human secreted and tra PN US2003036133-A1. PD 20-FEB-2003
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1846 ABO16424 standard; Human secreted/trar US2003027267-A1. 06-FEB-2003.	protein; 423 AA nsmembrane prote	rd; protein; 423 AA. transmembrane protein (PRO) #160		DE Human secreted/transmembrane PN US2003036134-A1. PD 20-FEB-2003. Best Local Similarity: 100.00%
imilarity:	100.001	Mismatches:		Unery March: 3.36%

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	8	3R92	protein; 423 AA.	SEO ID NO.32	Ġ
		US2003036160-A1.			•
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	ID	R78386 standard;	protein, 423		,
		Human secreted poly US2003054474-A1.	peptide	1, SEQ ID NO:320	
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	OI SE	ABU72004 standard; Novel himan secret	protein; 423 AA. ed and transmembrane	protein	PRO1461.
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		3032101-A1.			
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		27-FEB-2003.			
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<u>.</u>		Abossov, Brandard; procesn; . Human secreted/transmembrane	procein; 123 AA.	ein (PRO) #160.	
		US2003036134-A1.			
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ABU95368 standard; protein; 423 AA. Novel human secreted and transmembrane protein PRO1461. US2003036117-A1. 00 00 00 00 00 00 00 00 00 00 ABR67211 standard; protein; 423 AA. Human secreted polypeptide PRO1461, SEQ ID NO:320. US2003027266-A1. 06-FEE-2003. Human secreted/transmembrane protein (PRO) #160. US2003054483-A1. 20-MAR-2003. AB003763 standard; protein; 423 AA. Human secreted/transmembrane protein (PRO) #160. US2003036128-A1. Mismatches: ABU56095 standard; protein; 423 AA. Human secreted/transmembrane protein, PRO1461. US2003022298-A1. Mismatches: Indels: Mismatches: Indels: Mismatches: Mismatches: Indels: Mismatches: Mismatches: Mismatches: Mismatches: Mismatches: Indels: Indel8: Indels: Indels: ABU72339 standard; protein; 423 AA. Human PRO polypeptide #53. US2002182638-A1. ABUGG423 standard; protein; 423 AA. Human PRO polypeptide #160. US2003032102-A1. ABU71271 standard; protein; 423 AA. 423 AA. ABR70122 standard; protein; 423 AA. AB007576 standard; protein; 423 AA. Human PRO polypeptide #160. US2003032117-A1. T 870 ABO15814 standard; protein; 423 AA. ABO07881 standard; protein; Human PRO polypeptide #160. US2003032130-A1. 100.00% 100.00% 3.36% Best Local Similarity: 100.00% Query Match: 3.36% RESULT 874 100.00% 100.00% 100.00% 3.36% 100.00% 3.36% 100.00% 3.36% PD ZU-WARL & C.V...

A. (GETH ) GENENTECH INC.

BEST LOCAL SIMILATITY: 100.00\$ PD 05-DEC-2002. PA (GETH) GENENTECH INC. Best Local Similarity: 100.00% 3.36% Human PRO1461 protein. US2003036143-A1. Best Local Similarity: Query Match: Best Local Similarity: Best Local Similarity: Best Local Similarity: PD 20-FEB-2003. Best Local Similarity: Best Local Similarity: Best Local Similarity: 20-FEB-2003 30-JAN-2003 13-FEB-2003 20-FEB-200 13-FEB-200 13-FEB-2003 Query Match: RESULT 875 Query Match: RESULT 876 Match: Query Match: Query Match: RESULT 869 Query Match: RESULT 870 Query Match: RESULT 868 Query Match: Query Matc RESULT 877 RESULT 873 Query M RESULT

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l, SEQ ID NO:320 Mismatches: Indels:	SEQ ID NO	Mismatches: Indels:		Mismatches: Indels:		Mismatches: Indels:	SEQ ID NO:320	Mismatches: Indels:		Mismatches: Indels:	SEQ ID NO:32	Mismatches: Indels:	SEQ ID NO:33	Mismatches: Indels:	SEQ ID NO:33	Mismatches: Indels:	SEQ ID NO	Mismatches: Indels:
PRO1461,	423 AA. PRO1461,	ΣH	423 AA.	ΣΗ	423 AA.	ΣH	423 AA. PRO1461,	ΣН	423 AA.		423 AA. PRO1461,	ΣĤ	423 AA. PRO1461,	ΣH	423 AA. PRO1461,	ΣĤ	, 423 AA. PRO1461,	ΣĤ
polypeptide cr INC. y: 100.00%	1, protein; olypeptide	100.00%	, protein; :ide #160.	INC. 100.00% 3.36%	protein; cide #160.	100.00%	rd; protein; polypeptide	100.00% 3.36%	protein; ide #53.	INC. 100.00% 3.36%	protein, Peptide	100.00% 3.36%		100.00% 3.36%		100.00% 3.36%	protein; peptide	INC. 100.00% 3.36%
Human secreted US2003032138-A1 13-FEB-2003. (GETH ) GENENTE LOCAL Similarit	5 standard ecreted po 36132-Al.	Local Similarity: Y Match:	6 standard, RO polypept 08353-Al. 2003.	(GETH ) GENENTECH Local Similarity: / Match:	8 standard, RO polypept 17542-A1.	ED 23-04N-2003. Best Local Similarity: Query Match:	5 standa ecreted 32137-A1	Local Similarity:	L1 885 BWD1012 standard; protein; Human PRO polypeptide #53. US200018168-Al.		ASSESSION STANDARD, protein, Human secreted polypeptide US2003027269-A1.	Ub-FEB-2003. Local Similarity: / Match:	LI 884 ABR5318 standard, protein Human secreted polypeptide US2003027268-Al.	Local Similarity: // Match:	0 standard; ecreted poly 27274-A1.	>	ABR71952 standard; protein; Human secreted polypeptide US2003032135-A1.	13-f55-203. (GETH ) GENENTECH I Local Similarity: Y Match: LT 887
DE PN PD PA Best Quer	N D D D D D	Best Query	DE DE S	PA Best Query	DES	Best Query	DE DE CE	Best	PN	PA Best Query	See	Best Ouer	DE D	Best Quer	See	Best Quer		PA (C Best Lo Query N RESULT

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Novel human secreted and transmembrane protein PRO1461. US2003032123-A1.
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Novel human secreted and transmembrane protein PRO1461.
US2003032108-A1.
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DE Novel human secreted and transmembrane protein PRO1461.

PN US2003032119-A1.

PD 13-FEB-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.36% Indels:
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Human secreted polypeptide PRO1461, SEQ ID NO:320.
US2003027271-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR65013 standard; protein; 423 AA.
Human secreted polypeptide PRO1461, SEQ ID NO:320.
US2003027263-A1.
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Human secreted/transmembrane polypeptide PRO1461.
US2003009012-A1.
                                                                                                               ABU89122 standard; protein; 423 AA.
Human secreted/transmembrane protein (PRO) #160.
US2003022297-A1.
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Human secreted/transmembrane protein (PRO) #160.
US2003032105-A1.
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Human secreted/transmembrane protein (PRO) #160.
US2003032111-A1.
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ABU85412 standard; protein; 423 AA.
Human PRO polypeptide #160.
US2003022295-A1.
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PA (GETH ) GRNENTECH INC.
BEST LOCAL SIMILARITY: 100.00%
Query Match: 3.36%
ID. ABU85432 standard; pD Human PRO POJypeptic
PN US200302225-A1.
PD 30-JAN-2003.
Best Local Similarity: 1
Query Match:
                                                                                                                 ID ABU89122 standard; pD Human secreted/trans
PN US2003022297-A1.
PD 30-JAN-2003.
Best Local Similarity: 1
Query Match:
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RESULT 891
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100.00%	na, protein; polypeptide L.	100.00% 3.36%	protein; ide #160.	100.00%	prote ed and	100.00%	protei ed and	100.00%	protein; ide #160.	100.00% 3.36%	protein; nsmembran	100.00% 3.36%	protein; ide #160.	100.00% 3.36%	protein; insmembran	INC. 100.00\$ 3.36\$	protein; ed and tr	100.00\$
PD 20-FEB-2003.  Bet Local Similarity: 100.00\$ Mis Query March: 3.36\$ Ind RESULT 898	sreted Sreted 5068-A1	Best Local Similarity: Query Match: RESULT 899	ABU57090 standard; protein; Human PRO polypeptide #160. U52003027280-A1.	FD 00-FED-2003. Buest Local Similarity: Query Match:	042 sta human 3022300	Best Local Similarity: Query Match:	KESULI 901 ID ABU82329 standard; DE Novel human secret	PN USZUGJOSISS-AI. PD 20-FEB-2003. Best Local Similarity: Querry Match:	ii 902 ABU87340 standard; pro Human PRO polypeptide US2003036138-A1.	Best Local Similarity: Query Match:	ME SULI 90.  ID AB103812 standard; protein; 423 AA.  DE Human secreted/transmembrane protein  NUSCO03032109-A1.	ED 13-FEB-2003. Best Local Similarity: Query Match:	11 904 ABO08186 standard; protein; Human PRO polypeptide #160. US2003040066-A1.	Best Local Similarity: Query Match: RRSHT 905	ABU92528 standard; protein; 423 AA. Human secreted/transmembrane protein US2003045684-A1.	PD 08-MAK-2003.  PA (GETH ) GENENTECH Best Local Similarity: Query Match:	14 308 Mousel By standard, protein; Novel human secreted and tr US2003032104-Al.	PD 13-FEB-2003. Best Local Similarity: Onew Match.

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DE Novel hume...

PN US2003036155-A1.

PD 20-FEBS-2003.

Best Local Similarity: 100.00$ ...

Query March: 3.36$ Indels:

RESULT 91

ID ABU99931 standard; protein; 423 AA.

DE Novel human secreted and transmembrane protein PRO1461.

PN US200302226-A1.

10-JAM-2003.

10-JAM-2003.

3.36$ Indels: 0

3.36$ ...

Th NO:320.
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ABO53112 standard; protein; 423 AA.
Novel human secreted and transmembrane protein PRO1461.
US2003027986-A1.
06-PEB-2003.
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RESULT 910
ID ABU94078 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2003036155-A1.
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DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
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DE GETH J GENENTECH INC.
DE BEST LOCAL Similarity: 100.00% Mismatches: 0
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
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Human secreted polypeptide PRO1461, SEQ ID NO:320.
US2003032120-A1.
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Human secreted/transmembrane protein (PRO) #160.
US2003032129-A1.
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Human PRO polypeptide #160.
US2003017540-A1.
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Human PRO polypeptide #160.
US2003032106-A1.
                                                                                                                     ID ABU81198 standard; protein; 423 AA.

DE Human secreted polypeptide PRO1461.

PN US2003027212-A1.

PD 06-FEB-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00$ M:

Query Match: 13.36$
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PD 13-FEB-2003.
Best Local Similarity: 100.00%
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PD 23-JAN-2003.
Best Local Similarity: 100.00%
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Query Match: 3.36%
PD 20-FEB-2003.
Best Local Similarity: 100.00$
Query Match:
RESULT 908
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RESULT 915
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Mismatches: Indels:	.n; 423 AA. transmembrane protein	Mismatches: Indels:	423 AA.	Mismatches: Indels:	423 AA.	Mismatches: Indels:	423 AA. PRO1461, SEQ ID NO:320	Mismatches: Indels:	423 AA.	Mismatches: Indels:	423 AA. PRO1461, SEQ ID NO:320	Mismatches: Indels:	423 AA. PRO1461, SEQ ID NO:320	Mismatches: Indels:	423 AA.	Mismatches: Indels:	423 AA. : protein (PRO) #160	Mismatches: Indels:	423 AA.	Mismatches:
100.00% 3.36%	protein; ed and tra	100.00% 3.36%	protein; ide #160.	100.00% 3.36%	protein; ide #160.	100.00% 3.36%	protein; 7peptide F	100.00%	protein; ide #160.	100.00% 3.36%		INC. 100.00% 3.36%	protein; /peptide F	100.00% 3.36%	protein; ide #160.	100.00%	protein; nsmembrane	100.00% 3.36%	protein; ide #160.	100 008
PD 13-FEB-2003. Best Local Similarity; Query Match: PESTIT 010	KESUL1 318 1D ABU86962 standard; protein; DB Novel human secreted and tra PP UGSCO30302131-A1. PD 13-FEB-2003.	# K	1D ABU94751 standard; protein; DE Human PRO polypeptide #160. PN US2003032103-A1.	PD 13-FEB-2003. Best Local Similarity: Query Match: RESULT 920	ID ABO04678 standard, protein, DE Human PRO polypeptide #160. PD 13-PEB-2003.	Best Local Similarity; Query Match: RESULT 921	ID ABR70427 standard; protein; 423 AA. DE Human secreted polypeptide PRO1461, PN US2003032139-A1.	FD 13-FEB-2003. Best Local Similarity: Query Match:	A 20098592 standard; protein; 4: DE Human PRO polypeptide #160. PN US200302201-A1.		ID ABR6591 standard; protein, DE Human secreted polypeptide PN US2003036165-A1.	ZO-FEB-2003. (GETH ) GENENTECH St Local Similarity: STY Match:	rbsoll 324 ID ABR64708 standard; protein; DE Human secreted polypeptide; PN US2003027262-Al.	PD 06-FEB-2003. Best Local Similarity: Query Match:	1D ABU79633 standard; protein; DE Human PRO polypeptide #160. PN US2003032110-A1. PD 13-PER-2003	π ÿ Ë	4 standard; ecreted/tra 36142-A1.	الله الله	resold 357 1D ABU95983 standard; protein; DE Human PRO polypeptide #160. PN US2003036145-Al.	Ť.

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ABU91203 standard; protein; 423 AA.
Novel human secreted and transmembrane protein PRO1461.
US2003036154-A1.
20-PBB-2003.
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US2003036153-A1.
20-PBB-2003.
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ABU098315 standard; protein; 423 AA.

Novel human secreted and transmembrane protein PRO1461.

US2002183493-A1.

O5-DEC-2002.

(GETH ) GENETRECH INC.

Local Similarity: 100.00* Mismatches: 0

/ Match: 3.36* Indels: 0
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Novel human secreted and transmembrane protein PRO1461.
US2003036634-A1.
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Human secreted polypeptide PRO1461, SEQ ID NO:320.
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3.36$ Indels:
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AB009711 standard; protein; 423 AA.
Human secreted/transmembrane protein (PRO) #160.
05-MAR-2003.
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ABO10983 standard; protein; 423 AA.
Human secreted/transmembrane protein (PRO) #160.
US2003036150-A1.
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Human secreted/transmembrane protein (PRO) #160.
US2003032116-A1.
13-FEB-2003.
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Human PRO polypeptide #160.

US2003032128-A1.

13-FEB-2003.

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nalarity: 100.00\$ masmacches:  5.36\$ Indels:  6 standard, protein; 423 AA.  68882-A1.  68882-A1.  68882-A1.  68882-A1.  68882-A1.  68882-A1.  68882-A1.  73.00\$ Mismatches:  1 standard; protein; 423 AA.  689701-A1.  73.36\$ Indels:  1 milarity: 100.00\$ Mismatches:  1 milarity: 100.00\$ Mismatches:  80 polypeptide #160.  68701-A1.  68701-A1.  73.36\$ Indels:  73.36\$ Indels:  80 standard; protein; 423 AA.  68755-A1.  68755-A1.  68755-A1.  68755-A1.  68764 Protein; 423 AA.	mainarity: 100.00\$ masmacches:  6 standard, protein; 423 AA.  668682-A1.  608682-A1.  60803.  milarity: 100.00\$ Mismatches:  1 standard; protein; 423 AA.  68701-A1.  68701-A1.  68701-A1.  73.36\$ Indels:  1 standard; protein; 423 AA.  Mismatches:  3.36\$ Indels:  68701-A1.  68701-A1.  68701-A1.  68701-A1.  68701-A1.  68701-A1.  68701-A1.  73.36\$ Indels:  1 milarity: 100.00\$ Mismatches:  1 indels:  2 standard; protein; 423 AA.  68755-A1.  68765-A1.  687675-A1.  687675-A1.  687675-A1.  73.36\$ Indels:  2 standard; protein; 423 AA.  68705-A1.  68707-A180-A1.	(GETH)	INC.		•	
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US2003068755-A1.  10APR.2003.  (GETH ) GENENTECH INC.  1o.cal Similarity: 100.00\$ Mismatches:  / Match: 3.36\$ Indels:  ADA7072 standard; protein; 423 AA.  Human secreted/transmembrane protein (PRO) #160.	US2003068755-A1.  10-ARR-2003.  (GETH ) GENENTECH INC.  Local Similarity: 100.00\$  Mismatches:  1.05		ide #160.			
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2 standard, protein; 423 AA. ecreted/transmembrane protein (PRO) #160.	s standard; protein; 423 AA. ecreted/transmembrane protein (PRO) #160. 73180-A1.	/ Match	3 6	Indels:	. 0	•
2 standard; protein; 423 AA. ecreted/transmembrane protein (PRO)	<pre>2 standard; protein; 423 AA. ecreted/transmembrane protein (PRO) 73180-A1.</pre>	ESULT 966			•	•
Human secreted/transmembrane protein (PRO)	Human secreted/transmembrane protein (PRO) US2003073180-A1.	D ADA78072 standard	; protein;	423 AA.		
	US2003073180-A1.		ansmembrane	(PRO)		

17-APR-2003.

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DE Human secreted/transmembrane protein (PRO) #160.

DE Human secreted/transmembrane protein (PRO) #160.

PN US2001036131-A1.

PD 20-FEB-2003.

Best Local Similarity: 100.00$ Mismatches: 0 Query Match: 3.36$ Indels: 0 RESULT 969

ID ABR90409 standard; protein; 423 AA.

DE Human secreted polypeptide PRO1461, SEQ ID NO:320.

PD 27-FEB-2003.
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Human secreted polypeptide PRO1461, SEQ ID NO:320.
US2003054459-A1.
                                                                                       1D ABM24885 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003104539-A1.
PD 05-UW-2003.
Best Local Similarity: 100.00% Mismatches: 0
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DE Human secreted polypeptide PRO1461, SEQ ID NO:320.

PN US2003044930-A1.

PD 06-MAR-2003.

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.36% Indels: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query_Match: 3.36% Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR97876 standard; protein; 423 AA.
Human secreted polypeptide PRO1461, SEQ ID NO:320.
US2003064452-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DE Human secreted/transmembrane protein (PRO) #160.

NUS2003064471-A1.

PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1D ADB17163 standard; protein; 423 AA.

DE Human transmembrane PRO polypeptide (SeqID 106).

PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00*

Mismatches:
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Indels:
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Indels:
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Indels:
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RESULT 976
ID ABR87664 standard; protein; 423 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID ABM17323 branker.,
DE Human secreted polypeptide PRC NG2003054459-A1.
PD 20-MRR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
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3.36%
"" (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
Onerv Match: 3.36$
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Query Match: 3.36%
RESULT 970
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RESULT 974
ID ABO21612
DE Human sec
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RESULT 967
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RESULT 971
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PRO1461, 8	Mis	423 AA. PRO1461,	Min	423 AA. PRO1461,	Min	423 AA. PRO1461,	Minor	423 AA. PRO1461,	Min	423 AA. PRO1461,	Mi	423 AA. PRO1461,	Mi	423 AA. e protein		423 AA. PRO1461,	Mi	423 AA. e protein
polypeptide E	INC. 100.00% 3.36%		INC. 100.00% 3.36%	••	100.00%		INC. 100.00% 3.36%		INC. 100.00% 3.36%	ard; protein; polypeptide	INC. 100.00% 3.36%		INC. 100.00% 3.36%	protein; nsmembrane	INC. 100.00% 3.36%	protein; ypeptide 1	INC. 100.00% 3.36%	protein; nsmembran
ted 5-A1	ENTECH arity:	05 standard; protein secreted polypeptide (054473-A1.	· ENTECH arity:	35 standard; protein secreted polypeptide (064440-A1.	milarity:	ABMO6216 standard; protein Human secreted polypeptide US2003068704-Al.	003. GENENTECH milarity:	ABM03722 standard; protein Human secreted polypeptide US2003068722-Al	-2003. ) GENENTECH ] Similarity:	standa reted 183-A1	03. ENENTECH ilarity:	T 982 ABMZ6410 standard; protein Human secreted polypeptide US2003104549-A1.	1-2003. ) GENENTECH : Similarity:	'H 983 ABO48192 standard; protein; 4 Human secreted/transmembrane US2003049749-Al.	R-2003. ) GENENTECH : Similarity:	andard; ted pol 2-Al.	ENTECH arity:	standard; sreted/tra s159-A1.
Human secreted US2003068705-A1	PD 10-APK-2003 PA (GETH ) GEN Best Local Simil Query Match:	1F 977 ABM77705 standa Human secreted US2003054473-A1 20-MAR-2003	PA (GETH ) Best Local Si Query Match:	ABM27935 standa Human secreted US2003064440-Al	Local Si Match:	ID ABM06216 DE Human see	10-APR-2 (GETH ) Local Si Match:	ABM03722 Human se	PD 10-APR-2 PA (GETH) Best Local Si Query Match:	.T. 981 ABM35173 Human 86 US200307	PD 17-APR-20 PA (GETH ) G Best Local Sim Query Match:	RESULT 982 ID ABM26410 DE Human ser	PD 05-JUN-2 PA (GETH ) Best Local Si Query Match:	ABO48192 Human se US200304	PD 13-MAR-2 PA (GETH ) Best Local Si Query Match:	ABR92934 Human sec	-AF	ABO24695 Human sec US2003065
DE DE	PD PA Best Query	DE DE CO	PA Best Query	RESUL ID DE PN	Best Query	ID DE	PD PA Best Query	I DE S	PD PA Best Query	RESUL ID DE	PD PA Best Query	RESUL ID DE PN	PD PA Best Query	KESUL ID DE PN	PD PA Best Query	RESULT ID AE DE HI	PD 03 PA (G Best Lo Query M	ID DE

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PD 03-APR-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00$ Mismatches: 0
Query Match: 3.36$ Indels: 0
RESULT 986

ID ABM11706 standard; protein; 423 AA.

DE Human secreted polypeptide PR01461, SEQ ID NO:320.

PN US2003064447-A1.

PD 03-APR-2003.

PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00$ Mismatches: 0

Onerv Match: 3.36$ Indels: 0
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DB Human secreted polypeptide PRO1461, SEQ ID NO:3200.

DB US2003.07184-A1.

PD 17-APR-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 3.36% Indels: 0
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Human secreted polypeptide PRO1461, SEQ ID NO:320.
US2003064463-A1.
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DE Human secreted polypeptide PRO1461, SEQ ID NO:320.

PN US2003068721-A1.

PD 10-APR-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100,00% Mismatches: 0
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RESULT 992
TD ABM21225 standard; protein; 423 AA.
DE Human secreted polypeptide PR01461, SEQ ID NO:320.
PN US2003068707-A1.
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DE Human secreted polypeptide PR01461, SEQ ID NO:320.

PN US2003068699-A1.

PD 10-APR-2003.

PA (GETH ) GENEWTECH INC.

PAS (GETH ) GENEWTECH INC.

Dest Local Similarity: 100.00% Mismatches: 0

Query Match: 3.36% Indels: 0
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DE Human secreted polypeptide PR01461, SEQ ID NO:3200.

PN US2003073175-A1.

PD 17-APR-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0
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Human secreted/transmembrane protein (PRO) #160.
US20031068695-A1.
10-ARR-2003.
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Human secreted/transmembrane protein (PRO) #160.
US2003064451-A1.
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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RESULT
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PN US2003036130-A1.  PD 20-FEB-2003.  Best Local Similarity: 100.00% Mismatches: 0 Query Match: 3.36% Indels: 0	RESULT 1005  ID ABR73782 standard; protein; 423 AA.  DE Human secreted polypeptide PR01461, SEQ ID NO:320.  PN US2003054468-A1.  PD 20-MAR-2003.  PA (GETH ) GENEVIECH INC.  Best Local Similarity: 100.00\$ Mismatches: 0	7. Match: 7. 1006 ABO17034 standard; protein; 423 AA- Human secreted/transmembrane prote US2003054470-A1.	Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 3.36\$ Indels: 0 RESULT 1007 ID ABR9459 standard; protein; 423 AA. DB Human secreted polypeptide PRO1461, SEQ ID NO:320.	D 06-MAR-2003.  PD 06-MAR-2003.  Best Local Similarity: 100.00% Mismatches: 0  Query Match: 3.36% Indels: 0  RESULT 1008	DE Human secreted polypeptide PRO1461, SEQ ID NO:320. PN US2003044229-A1. PD 06-MAR-2003. Best Local Similarity: 100.00% Mismatches: 0 Query Match: 3.36% Indels: 0	ABR71342 standard Human secreted po. US2003059880-A1. 27-MAR-2003.	<pre>9 standard; protein; 423 AA. secreted polypeptide PRO1461, SEQ ID NO:320 4465-A1. 2003. GENENTECH INC.</pre>	Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 3.36\$ Indels: 0 RESULT 1011 ID ARR93644 standard; protein; 423 AA. THUMAN serveted nolymentide Debota61	US2003054478-A1. 20-MAR-2003. (GETH ) GENENTECH INC. t Local Similarity: 100.00% Mismatche ery Match: 3.36% Indels:	RESULT 1012  ID ABR87969 standard; protein; 423 AA.  DE Human secreted polypeptide PRO1461, SEQ ID NO:320.  PN US2003068118-A1.	st.	ID AB033556 standard; protein; 423 AA.  DE Novel human serreted and transmembrane protein PRO1461.  PD 17-APR-2003.	ή.
(GETH ) GENENTECH INC. st Local Similarity: 100.00% ery Match: 3.36% SULT 995	ID ABO36256 standard; protein; 423 AA.  DE Human PRO polypeptide #160.  PN US2003068703-A1.  PD 10-APR-2003.  PA (GETH ) GENENTECH INC.  Best Local Similarity: 100.00\$ Mismatches: 0  Query Match: 0	996 043785 standard; protein; 423 AA. man PRO polypeptide #160APR-2003. ETH ) GENENTECH INC.	Match: 13.6% The Party of Match of Matc	ery SUI	US2003104548-A1. 05-UTN-2003. 65-UTN-2003. st Local Similarity: 100.00\$ Mismatche: Indels:	ABMASSOO standard, protein, 423 AA. Human secreted polypeptide PRO1461, SEQ ID NO:320 US2003104542-A1. 05-JUN-2003.	DE Human secreted polypeptide PRO1461, SEQ ID NO:320. PN US2003104543-A1. PD 05-JUN-2003. Best Local Similarity: 100.00% Mismatches: 0 Query Match: 3.36% Indels: 0	KESULI 1001 ID ABO03458 standard; protein; 423 AA. DE Human secreted/transmembrane protein (PRO) #160. PN US2003636127-A1. PD 20-FRR-7003.	at Sul	PN 052003-040061-Al. PD 27-FEB-2003. Best Local Similarity: 100.00% Mismatches: 0 Query Match: 3.36% Indels: 0	ID ABO4291 standard; protein; 423 AA. DE Human secreted/transmembrane polypeptide PRO 1461. PN US2003018172-A1. PD 23-JAN-2003.	gr.	ID ABR90714 standard; protein; 423 AA. DE Human secreted polypeptide PRO1461, SEQ ID NO:320.

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3.36*	protein; nsmembrane	INC. 100.00% 3.36%	protein; ısmembrane	INC. 100.00% 3.36%	protein; ide #160.	INC. 100.00% 3.36%	protein; peptide 1	INC. 100.00% 3.36%	protein; /peptide 1	INC. 100.00% 3.36%	protein; nsmembrane	INC. 100.00% 3.36%	protein; ide #160.	INC. 100.00% 3.36%	protein; nsmembrane	INC. 100.00% 3.36%	rd; protein; 423 AA. polypeptide PRO1461,	INC.
.cn:	tandard; eted/trar 54-A1.	GENENTECH 1 Similarity:	Jr 1015 ABO30104 standard; protein; 4 Human secreted/transmembrane HS2003064461-Al.	03-APR-2003. 03-APR-2003. (GETH ) GENENTECH 1 Local Similarity:	17 1016 A ABO33313 standard, protein, Human PRO polypeptide #160. US2003068724-Al.	AFK-2003. TH ) GENENTECH INC Al Similarity: 10.	T 1017 ABMO501 standard; protein; 423 AA. Human secreted polypeptide PR01461, US2003068727-A1.	10-APR-2003. (GETH ) GENENTECH INC Local Similarity: 101 Match: 3.0	ABM08961 standard; protein; 423 AA. Human secreted polypeptide PRO1461, US2003068772-A1.	10-APR-2003. (GETH ) GENENTECH 1 Local Similarity: Match:	n 1013 Bools561 standard; protein; 423 AA. Human secreted/transmembrane protein (PRO) US2003068714-A1.	303. SENENTECH nilarity:	Manan PRO polypeptide #160. US2003068758-A1.	10-APR-2003. (GETH ) GENENTECH I Local Similarity: Match:	1 1721 AB039611 standard; protein; 423 AA. Human secreted/transmembrane protein (PRO)	10-APR-2003. (GETH ) GENENTECH : LOCAL Similarity: Match:	6 standa ecreted 69407-A1	-2003. GENENTECH Similarity:
RESTER 10	10 ABO27969 s DE Human secr PN US20030644	e a	RESULT 10 ID ABO3 DE Huma	بري بر اي بر	KESULT 10 ID ABO3 DE Huma PN US2	PD 10-AFK-PA (GETH ) Best Local S Query Match:	Ĕ	PD 10-APR- PA (GETH ) Best Local S Query Match:	ID ABMO DE Huma PN US20	ក ក្តី	Ž.	PD 10-APR- PA (GETH ) Best Local S Query Match:	ID ABO35646 DE Human PR(	# K	ID ABO	PD 10-APR-1PA (GETH ) Best Local S Query Match:	ID ABMI DE Hume	اید

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ADA19968 standard; protein; 423 AA.
Novel human secreted and transmembrane protein PRO1461.
US2003069394-A1.
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Ph 0.5.003.09.0939.9.4.1.

Ph (GETH ) GENENTECH INC.

Best Local Similarity: 100.00$ Mismatches: 0

Query Match:

RESULT 1027

DE Human secreted/transmembrane protein (PRO) #160.

Ph 0.3.FEB-2003.

Ph 13-FEB-2003.

Best Local Similarity: 100.00$ Mismatches: 0

Query Match:

RESULT 1028

ID ADB1751 standard; protein; 423 AA.

DE Human transmembrane PRO polypeptide (SeqID 106).

Ph 0.52003050465-A1.

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RESULT 1030
ID ABR87054 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003-49778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00$ Mismatches: (
Rest Local Similarity: 3.36$
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RESULT 1023

ID ABM12011 standard; protein; 423 AA.

DE Human secreted polypeptide PR01461, SEQ ID NO:320.

PN US2003104555-A1.

PD 05-JUN-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0
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Query Match:

RESULT 1029

ID ABR97266 standard; protein; 423 AA.

DE Human secreted polypeptide PRO1461, SEQ ID NO:320.

PN US2003054481-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0
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Human secreted polypeptide PRO1461, SEQ ID NO:320.
US2003049782-A1.
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Indels:
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DE Human PRO polypeptide #160.

PN US2003049771-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00$ M?

Query Match:

13-36$
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Human PRO polypeptide #160.
US2003049768-A1.
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ABM28240 standard; protein; 423 AA.
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PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
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PD 13-MR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
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RESULT 1032
ID ABM28240
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RESULT 1025
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RESULT 1026
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	Ç.	100.00% 3.36%	protein; 423 nsmembrane pi	INC. 100.00% 3.36%	protein; ypeptide	INC. 100.00% 3.36%	protein; 423 ypeptide PRO1	INC. 100.00% 3.36%	••	INC. 100.00% 3.36%		INC. 100.00% 3.36%	protein; 423 ypeptide PRO1	INC. 100.00% 3.36%	protein; 423 nsmembrane px	INC. 100.00% 3.36%	protein; 423 ypeptide PRO1	INC. 100.00% 3.36%

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PN USZUDACZIONER PN USZUDACZIONER PN USZUDACZIONER PA (GETH) GENETYECH INC.

Best Local Similarity: 100,00% Mismatches: 0
ODERY Match: 3.36% Indels: 0
RESULT 1048
ID ABR97571 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN USZO03059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
PA (GETH) GENENTECH INC.
Best Local Similarity: 100,00% Mismatches: 0
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3.36 Indels:
0 RESULT 1049
ID ABRO671 standard; protein; 423 AA.
DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
PN US2003049740-A1.

        Query Match:
        3.36*
        Indels:
        0

        RESULT 1050
        1.050
        0
        0

        ID ABM01282 standard; protein; 423 AA.
        DE Human secreted polypeptide PR01461, SEQ ID NO:320.
        PN US2003049770-A1.

        PD 13-MAR-2003.
        PA
        (GETH ) GENENTECH INC.

        Best Local Similarity: 100.00*
        Mismatches: 0

        Query Match:
        Indels: 0

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US2003054480-A1.
                                                                                                                                                                                                                                                                                       DE Human secreted/transmembrane protein (PRO) #160.

BHOWN US2003049777-A1.

PA (GETH) GENERAL

BEST LOCAL Similarity: 100.00$ Mismatches:

Ouery Match:
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RESULT 1044
DE ABU99321 standard; protein; 423 AA.
DE Human secreted/transmembrane protein (PRO) #160.
PN US2003040055-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JT 1046
ABO06003 standard; protein; 423 AA.
Human secreted/transmembrane protein (PRO) #160.
US2003040074-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted/transmembrane protein (PRO) #160.
US2003036164-A1.
                                                                Mismatches:
Indels:
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Indels:
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Ouery Match: 3.36$ II
RESULT 1045
ID ABO04373 standard; protein; 423 AA.
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                                                                                                                            423 AA.
                                                                                                                      DE Human PRO polypeptide #160.

DE Human PRO polypeptide #160.

PN US2003049773-A1.

PD 13-MAR-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100,00%
PN US2003087374-A1.
PD 08-MAY-2003.
Best Local Similarity: 100.00%
Query Macch:
RESULT 1042
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Best Local Similarity: 100.00%
Query Match:
RESULT 1046
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PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00$
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2003096353-A1.

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A. 1, SEQ ID NO:32	Mismatches: Indels:	AA. :61, SEQ ID NO:32	Mismatches: Indels:	SEQ ID	Mismatches: Indels:	#1	Mismatches: Indels:	A. ein (PRO) #160	Mismatches: Indels:	SEQ ID	Mismatches: Indels:	A. .ein (PRO) #160	Mismatches: Indels:	A. ii, seq id no:3	Mismatches: Indels:	SEQ ID	Mismatches: Indels:	AA. 31, SEQ ID NO
n, 423 A e PRO146	ale.	n; 423 A e PRO146	ake	n; 423 A e PRO146	do.	n; 423 AA ane prote	ogo.	n; 423 AA ane prote	#0	n; 423 A le PRO146	*	n; 423 AA ane prote	*	in; 423 A le PRO146	*	in; 423 AA. de PRO1461,	*	in; 423 / le PRO146
protei lypeptid	100.00% 3.36%	protein; lypeptide	INC. 100.00% 3.36%	, protein; lypeptide	INC. 100.00% 3.36%	; protein; ansmembran	INC. 100.00% 3.36%	, protein; ansmembran	INC. 100.00% 3.36%	, protei lypeptid	INC. 100.00 3.36%	; protein; ansmembran	INC. 100.00% 3.36%	; proted	INC. 100.00% 3.36%	, protein; lypeptide	100.00\$	; prote
Jr 1051 ABR88884 standard; protein, 423 AA. Human secreted polypeptide PRO1461, US2003073169-A1.	ocal Similarity: Match:	ABM13536 standard; protein; 423 AA. Human secreted polypeptide PRO1461, SEQ US2003064457-A1.	PD 03-APR-2003.  PA (GETH ) GENENTECH Best Local Similarity: Query Match: RESHIT 1053	ABMZ0920 standard; protein; 423 AA. Human secreted polypeptide PR01461, US2003068711-A1.	10-APR-2003. (GETH ) GENENTECH Local Similarity: Match:	KESULI 1054 ID ABO42051 standard; protein; 423 AA. DE Human secreted/transmembrane protein (PRO) PN US2003049745-A1.	3-MAR-2003. GETH ) GENENTECH ocal Similarity: Match:	RESULT 1055 ID ABO42661 standard; protein; 423 AA. DE Human secreted/transmembrane protein (PRO) PN US2003049751-A1.	3-MAR-2003. GETH ) GENENTECH ocal Similarity:	KESULT 1018.  ID ABMIOLIS standard; protein; 423 AA. DE Human secreted polypeptide PRO1461, PN USSO03067478-A1.	PD 10-AFK-ZOOS. PD 10-AFK-ZOOS. Best Local Similarity: 100.00% Query Match: 3.36%	standard creted/tr 8773-A1.	PD IO-AFK-2003. PA (GETH) GENENTECH Best Local Similarity: Query Match:	Jr 1058  ABM32936 standard; protein; 423 AA. Human secreted polypeptide PRO1461, US2003073185-A1.	PA (GETH ) GENERATECH INC. Best Local Similarity: 100 Query Match: 3.3	T 1059 ABM2750 standard; protein; 423 AA. Human secreted polypeptide PRO1461, US2003087373-A1.	08-MAY-2003. Local Similarity: Match: m 1050	RESULT 1000 ID ABM74961 standard; protein; 423 AA. DE Human secreted polypeptide PRO1461, SEQ ID NO:320.
RESULT ID AI DE HI PN U	# K	ID DE PN H DI	ir ir		PD 1 PA ( Best L	ID A ID A DE H	PD 1 PA ( Best L Query	RESULT ID A DE H	PD 1 PA ( Best L Query	RESULT ID DE DE PN	PA ( Best L Query	RESULT ID A DE H PN U	ř,ř	RESULT ID A DE H PN U	PA (Best L	RESULT ID A DE H PN U	Best I Query	IDE T

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BM29765 standard; protein; 423 AA.
BM29765 standard; protein; 423 AA.
Uman secreted polypeptide PRO1461, SEQ ID NO:320.
S2200064456-A1.
13-APR-2003.
(GETH ) GENENTECH INC.
Cocal Similarity: 100.00$ Mismatches: 0
Match: 3.36$
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BETH ) GENEWTECH INC.

Acch: Indiarity: 100.00$ Mismatches: 0
Acth: 1006

BMI6713 standard; protein; 423 AA.

BMI6713 secreted polypeptide PR01461, SEQ ID NO:320.
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BM23970 standard; protein; 423 AA.
BM23970 standard; protein; 423 AA.
Uman secreted polypeptide PR01461, SEQ ID NO:320.
S2000366735-A1.
GETH ) GENENTECH INC.
GCAl Similarity: 100.00% Mismatches: 0
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PBTH ) GENEWTECH INC.
Acal Similarity: 100.00$ Mismatches: 0
Acat. 100.4
1064
18886444 standard; protein; 423 AA.
180303049758-A1.
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JR86749 standard; protein; 423 AA.
Jman secreted polypeptide PRO1461, SEQ ID NO:320.
S2003049772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1063
WN02502 standard; protein; 423 AA.
Secreted polypeptide PRO1461, SEQ ID NO:320.
:2003059886-A1.
                                                                                                                                                                                                                                                                                                                                                                                                           R96351 standard; protein; 423 AA.
man secreted polypeptide PR01461, SEQ ID NO:320.
2003054458-A1.
                                                                                                             1061
A79864 standard; protein; 423 AA.
A79864 stansmembrane protein (PRO) #160.
2003073173-A1.
                               Mismatches:
Indels:
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1.3.36*

ABO29108

ABO29108

ABO203068693-A1.

10-APR-2003.

(GETH ) GENENTECH INC.

LOCAL Similarity: 100.00*

Mismatches:

MAtch:

3.36*

Indels:
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3.36%
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BETH ) GENENTECH INC.

Cal Similarity: 100.00%

datch: 3.36%
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	SEQ ID	Mismatches Indels:	SEQ ID	Mismatches Indels:	423 AA. le protein (PRO)	Mismatches Indels:	423 AA. PRO1461, SEQ ID	Mismatches Indels:	423 AA. PRO1461, SEQ ID	Mismatches Indels:	SEQ	Mismatches Indels:	SEQ ID	Mismatches Indels:	SEQ ID	Mismatches Indels:	SEQ ID	Mismatches: Indels:
	protein; ypeptide	INC. 100.00% 3.36%	protein; ypeptide	INC. 100.00% 3.36%	protein; nsmembrar	INC. 100.00\$ 3.36\$	protein peptide	100.00% 3.36%	protein, ypeptide	100.00\$	protein; ypeptide	INC. 100.00% 3.36%	protein, ypeptide	INC. 100.00% 3.36%	protein; ypeptide	INC. 100.00% 3.36%	protein; ypeptide	INC. 100.00% 3.36%
ESTIT 1070	AESOLI 1707 ABM23360 standard; protein; 423 AA. DE Human secreted polypeptide PRO1461, PN US2003068753-A1.	-2003. ) GENENTECH Similarity: :		os. SNENTECH Llarity:	hesoli 423 AA.  1D AB037781 standard; protein; 423 AA.  DE Human secreted/transmembrane protein (PRO)  PN US2003068756-A1.  DD 10-APR-2003	A (GETH) GENENTECH est Local Similarity: uery Match:	DE Human Secreted poly PN US2003082715-A1.	Best Local Similarity: Query Match:	ID ABM28850 standard; protein. DE Human secreted polypeptide PN US2003082716-A1.	PD 01-MAY-2003. Best Local Similarity: Query Match:	ESOLI 17.9 SENDI 17.9 SENDI 17.9 AN. DE Human secreted polypeptide PRO1461, PN US2003068737-A1.	PD 10-APR-2003. PA (GETH ) GENENTECH Best Local Similarity:	RESOLT 1076 Standard; protein; 423 AA. DE Human secreted polypeptide PRO1461, DD 7003104547-A1.	ENTECH arity:	DE Human secreted polypeptide PRO1461, by US2003096359-A1.	(GETH ) GENENTECH (GETH ) GENENTECH STMINISTICS:	To Sale	PD 29-MAY-2003. PA (GETH) GENENTECH Best Local Similarity: Query Match:

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iry Match:

SULT 1082

SULT 1082

ADA20140 standard; protein; 423 AA.

ADA20140 standard; protein; 423 AA.

NO200305222-AI.

1 US200305222-AI.

2 O-MAR-2003.

A (GETH ) GENENTECH INC.

est Local Similarity: 100.00% Mismatches: 0

and Adaptive included indels: 0
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ABO34219 standard; protein; 423 AA.
ABO34219 standard; protein; 423 AA.
Human secreted/rransmembrane polypeptide PRO 1461.
U22003060601-A1.
27-MAR-2003.
(GETH ) GENENTECH INC.
st Local Similarity: 100.00* Mismatches: 0
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ULT 1084
ABR96656 standard; protein; 423 AA.
Human secreted polypeptide PRO1461, SEQ ID NO:320.
20-MAR-2003.
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Human secreted polypeptide PRO1461, SEQ ID NO:320.
US20030949753-A1.
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DE Human secreted polypeptide PR01461, SEQ ID NO:320.

PN US2003073172-A1.

PD 17-APR-2003.

Best Local Similarity: 100.00% Mismatches: 0
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3.36* Indels:
ULT 1081
AB022222 standard; protein; 423 AA.
Human secreted/transmembrane protein (PRO) #160.
US2003054477-A1.
Human secreted/transmembrane protein (PRO) #160.
US2003032125-A1.
                                                                                                                                                                                                                                                    Human secreted/transmembrane protein (PRO) #160.
US2003054454-A1.
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CO-MAR-2003.

(GETH) GENENTECH INC.

LOCAL Similarity: 100.00%
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t Local Similarity: 100.00%
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t Local Similarity: 100.00%
ry Match: 3.36%
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st Local Similarity: 1
ery Match:
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t Local Similarity:
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		n (PRO) #160.	Mismatches: Indels:	SEQ ID NO:32	Mismatches: Indels:	SEQ ID NO:320	Mismatches: Indels:	n (PRO) #160.	Mismatches: Indels:		Mismatches: Indels:	, SEQ ID NO:320	Mismatches: Indels:	in (PRO) #160.	Mismatches: Indels:	in (PRO) #160.	Mismatches: Indels:	in (PRO) #160.	Mismatches: Indels:	
		protein; 423 AA. nsmembrane protein		protein; 423 AA. Peptide PRO1461,	de	protein; 423 AA. ypeptide PRO1461,	*	protein; 423 AA. nsmembrane protein		protein; 423 AA. ide #160.		23 AA 01461		protein; 423 AA. insmembrane protein		protein; 423 AA. Insmembrane protein		andard; protein; 423 AA. ted/transmembrane protein 0-A1.		; protein; 423 AA
•	Str	ABO29799 standard; fyroteln; f Human secreted/transmembrane US2003068700-Al.	겨서	RESULT 1090 ID ABM2365 standard; protein; DE Human secreted polypeptide	g št	SULT 1091 ABM29460 standard; protei Human secreted polypeptic	7 7	SULT 1092 ABO38391 standard; protein; ( Human secreted/transmembrane	20 00	SULT 1093  ABO45691 standard; protein; 4  E Human PRO polypeptide #160.  1 US2003073182-A1.	£ 6	SULT 1094  ABM20615 standard; protein; 4  Human secreted polypeptide PR  US2003104557-Al.	6 0	SSULT 1095  ADA81591 standard; protein; 's Human secreted/transmembrane v US2003092121-Al.	ery	0167 man 2003	ery	SULT 1097 ABO18355 8t Human secre US200304492	PD US-MAK-2003. Best Local Similarity: Query Match: PESITA 1098	D ABO22782 standard;
	88		S B B B B B B B B B B B B B B B B B B B	ă C C S	O B B D O	ğ 0 8	SERBS	2 C C S	PD PD O	S DE DE	S E E E	B B B B B	S & B B			2022	2 g g	PNEUR	i w Q	4 Ĥ

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DE Human PRO Polypeptide #100.

Bet Local Similarity: 100.00$ Mismatches: 0

CGFF02035-A1.

DE GERES-2003-A1.

RESULT 100.00 Indels: 0

DE MARCA-2003.

DE MARCA-2004.

DE Human PRO Polypeptide #160.

DE MARGA-2004.

DE MARGA-2004.

DE Human Secreted Polypeptide PRO1461, SEO ID NO:320.

DE MARGA-2003.

DE Human secreted Polypeptide PRO1461, SEO ID NO:320.

DE MARGA-2003.

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	PD 10-APR-2003. PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 3.36\$ Indels: 0	ID ABM14146 standard; protein; 423 AA. DE Human secreted polypeptide PRO1461, SEQ ID NO:320. PN US2003068683-A1.	PD 10-APR-2003.  Best Local Similarity: 100.00% Mismatches: 0  Query Match: 3.36% Indels: 0	, , ,	68754-A1. 2003. GENENTECH INC. imilarity: 100.00%	3.36% Indels: SULT 1233 ABO40221 standard; protein; 423 AA.	ecreted/transmembrane prote 68681-A1. 2003. imilarity: 100.00%	3.36* Indel8: andard; protein; 423 AA. ted polypeptide PRO1461, SEQ ID NO:320 1-A1.	PD 22-MAY-2003.  PA (GETH ) GENENTECH INC.  Best Local Similarity: 100.00\$ Mismatches: 0  Querty 1236 Indels: 0	ID ABM33851 standard, protein, 423 AA. DE Human secreted polypeptide PRO1461, SEQ ID NO:320. PN US2003096558-A1.	PD 22-MAY-2003.  PA (GETH ) GENENTECH INC.  Best Local Similarity: 100.00\$ Mismatches: 0  Ouery Match: 3.36\$ Indels: 0	in; 423 AA. de PRO1461, SEQ ID NO:320	PD 05-JUN-2003.  PA (GETH ) GENENTECH INC.  Best Local Similarity: 100.0% Mismatches: 0 Query Match: 3.36% Indels: 0	in; 423 AA. rane protein (PRO) #160.	ئز ٿڌ	RESULT 1238 ID ABR72867 standard; protein; 423 AA. DE Human secreted polypeptide PRO1461, SEQ ID NO:320. PN IRSONANATIO-1	PD 20-FEB-2003. Best Local Similarity: 100.00\$ Mismatches: 0 Ouery Match: 3.36\$ Indels: 0 PRESHT. 1239	ID ABOLS509 standard; protein; 423 AA. DB Human secreted/transmembrane protein (PRO) #160. PN US2003036121-A1. PD 20-FRR-2003.	st
•	DE Human secreted polypeptide PRO1461, SEQ ID NO:320. PN US2003054456-A1. PD 20-MAR-2003. Best Local Similarity: 100.00\$ Mismatches: 0 Onerw March.	5 standard; protein; 423 AA. ecreted/transmembrane protein (PRO) #160.	US2003054482-A1. 20-WAR-2003. (GETH ) GENENTECH INC.		ABK93849 standard Human secreted po US2003054457-A1. 20-MAR-2003.	PA (GETH ) GENENTECH INC.  PA Mismatches: 0  Query Match: 1336* Indels: 0	RESULT 1224 BENO1892 standard; protein; 423 AA. DE Human secreted polypeptide PRO1461, SEQ ID NO:320. PN US200359883-A1.	# <u>4</u> 2 2	ID ABW78315 standard; protein; 423 AA. DB Human secreted polypeptide PRO1461, SEQ ID NO:320. PD US2003049764-A1. PD JAMAR-2003. PA (GETH ) GENEWTECH INC	# £ £	ID AB033533 standard; protein; 423 AA.  DE Novel human secreted and transmembrane protein PRO1461.  PN US2003073129-A1.  PD 17-APR-2003.	F E	ID ABR90104 standard; protein; 423 AA. DB Human secreted polypeptide PR01461, SEQ ID NO:320. PN US200373177-A1. PD 17-APR-2003.	in it	ABM27630 standard Human secreted po US2003064442-A1. 03-APR-2003.	PA (GETH) GENENTECH INC. Best Local Similarity: 100.00% Mismatches: 0 Query Match: 3.36% Indels: 0 RESHIT. 1229	ID ABM13231 standard; protein; 423 AA. DE Human secreted polypeptide PRO1461, SEQ ID NO:320. PN US203064450-A1. PD 01-APR-2003.	PA (GETH) CENENTECH INC. Best Local Similarity: 100.00% Mismatches: 0 Query Match: 3.36% Indels: 0 RESHLY 1230	ID AB031934 standard; protein; 423 AA. DE Human secreted/transmembrane protein (PRO) #160. PN US2003068731-A1.

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procein; 423 AA. /peptide PRO1461,	100.00% 3.36%		100.00% 3.36%	rd; protein; 423 transmembrane pro	100.00% 3.36%	ard; protein; 423 polypeptide PRO14 1.	100.00% 3.36%	ırd; protein; 423 polypeptide PRO14	INC. 100.00% 3.36%	n; 423 le PRO1	INC. 100.00% 3.36%	พษ	INC. 100.00% 3.36%	, 423 PRO1	INC. 100.00\$ 3.36\$	lard; protein; 423   polypeptide PRO1	INC. 100.00% 3.36%	ard; protein; 423 polypeptide PRO1
ч го ш		8 7 9 6	k-2003. Similarity: h:	standa ecreted/ 10077-A1	E E	standa creted 4928-A	k-2003. Similarity: h:	standa reted	K-2003.   ) GENENTECH   Similarity:   h:	Mr 1245 ABM77095 standard; protei Human secreted polypeptid US2003054464-A1.	K-ZOUS. ( ) GENENTECH . Similarity: (h:	ABO28274 standard; protein; 42 Human secreted/transmembrane p US2003064459-A1.	R-2003. ( ) GENENTECH Similarity: h:	T 124/ ABM23055 standard; protein Human secreted polypeptide US2003068757-Al.	R-2003. I) GENENTECH Similarity:	75 stand secreted	(GETH ) GENENTECH COCAL SIMIlarity: Match:	35 stand secreted
DE Human 8 PN US20030 PD 27-FEB-	st Lo ery M	4 4 6 7	PD 06-MAK-3 Best Local S Query Match:		a L	ID ABM17628 DE Human se PN US200304	Best Local Query Match	ID ABR85529 DE Human Bec PN US2003045	PD 13-MAK-2 PA (GETH ) Best Local Si Query Match:	RESULT 124 ID ABM77 DE Human PN US200	PD ZO-MAK-ZO PA (GETH ) G Best Local Sin Query Match:	ID ABO28 DE Human	PD 03-APR-2 PA (GETH ) Best Local Si Query Match:	KESULT 124 ID ABM23 DE Human PN US200	ery		ery	resoni 1243 ID ABM21835 DE Human se

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PA (GETH ) GENENTECH Best Local Similarity: Ouery Match:	0000	10-AFK-2003. (GETH ) GENENTECH Local Similarity:	RESULT 1251 D ABM15061 standard, protein; DE Human secreted polypeptide PN US2003068766-A1.	PD 10-APR-2003. PA (GETH ) GENENTECH Best Local Similarity: Query Match:	LT 1252 ABO41136 stand Human secreted US2003068694-A	PD 10-APK-Z003. PA (GETH ) GENENTECH Best Local Similarity: Query Match:	LT 1253 ABO36866 stand Human secreted US2003068715-A	10-APR-2003. (GETH ) GENENTECH Local Similarity: y Match:	RESULT 1254 ID ABO37476 stand DE Human secreted PN US2003068726-A		1255 3M752 IMan 32003	05-JUN-2003. (GETH ) GENENTECH Local Similarity: Y Match:	Jul 1256 BM33546 standard, protein, Human secreted polypeptide P US2003096357-A1.	22-MAY-2003. (GETH-') GENENTECH Local Similarity: Y Match:	ABO46301 standard; Human PRO polypepti	A B B B B B B B B B B B B B B B B B B B	125 782 782 782 783 784 784
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100.00% 3.36%	protein; ed and tr	INC. 100.00\$ 3.36\$	protein; /peptide	100.00% 3.36%	protein; /peptide	INC. 100.00% 3.36%	protein; nsmembran	INC. 100.00% 3.36%	protein;	INC. 100.00%	protein;	INC. 100.00% 3.36%	protein; ein.	INC. 100.00% 3.36%	protein; sin.	INC. 100.00% 3.36%	protein; peptide	TNC
Best Local Similarity: Query Match: RESULT 1259	ADB85679 standard; Novel human secrete		Mr 1260 ABM31900 standard; protein; Human secreted polypeptide US2003068680-A1.		LLT 1261 ABNJ1290 standard; protein; 423 AA. Human secreted polypeptide PRO1461, US2003068762-A1.	10-APR-2003. (GETH ) GENENTECH I Local Similarity: y Match:	KESULT 1262 ID ADB86063 standard; protein; 423 AA. DE Human secreted/transmembrane protein DN US2003054472-A1.		ILT 1263 ABM32205 standard; protein; 423 AA. Human secreted polypeptide PRO1461,	10-APR-2003. (GETH ) GENENTECH 1 LOCAL Similarity:	RESULT 1264 ID ABM32510 standard; protein; 423 AA. BE Human secreted polypeptide PRO1461,	PD 10-APR-2003. PD 10-APR-2003. PA (GETH ) GENENTECH I Best Local Similarity: Obery March:	DE Human PRO1461 protein, DE Human PRO1461 protein. PN US2003065161-A1.	03-APR-2003. (GETH ) GENENTECH 1 Local Similarity: T Match:	AESOLI 1280 ID ADB68165 standard; protein; DE Human PRO1461 protein. PN IRS7013060600-21	PD 27-WAR-2003.  PA (GETH ) GENENTECH 1  Query Match:	ABM31595 standard; protein; 423 AA. Human secreted polypeptide PRO1461, 1152003068761-A1	10-APR-2003. (GETH ) GENENTECH 3
Query RESU	0 8 8	PD PA Best Query	RESU ID DE PN	PD Best Query	RESUL DB DB	PD PA Best Query	RESUL ID DE	PD PA Best Query	KESU ID DE	PD PA Best	RESUI DE DE	PD PA Best Query	PNE	PD PA Best Query	DE DE SE	PD PA Best Query	888	2 2 2

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Duery Match:
RESULT 1274

ID ADC52434 standard; protein; 423 AA.

DE Novel human secreted and transmembrane protein PRO1461.

PN US2003138882-A1.

PD 24-UL-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00$ Mismatches: 0

Best Local Similarity: 13.36$ Indels:
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DE Novel human secreted and transmembrane protein PRO1461.

PN US2003073208-A1.

PD 17-APP 2003.

PA (GETH ) GENERITECH INC.

Best Local Similarity: 100.00* Mismatches: 0

Query Match: 3.36* Indels: 0
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DE Novel human secreted and transmembrane protein PR01461.

PN US2003083473-A1.

PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00* Mismatches: 0

Query Match: 3.36* Indels:
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RESULT 1268

ID ABM30985 standard; protein; 423 AA.

DE Human secreted polypeptide PRO1461, SEQ ID NO:3200.

PN US2003068771-A1.

PD 10-APR-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00$ Mismatches: C
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Query Match:
RESULT 1278
RESULT 1278
ID ADD05793 standard; protein; 423 AA.
ID ADD05793 standard; protein; 423 AA.
ID ADD05793 standard; protein; (PRO) #160.
PN U52003097376-A1.
PD 08-MAY-2003.
PA (GETH) GENEWTECH INC.
Best Local Similarity: 100.00$ Mismatches:
Rest Local Similarity: 3.36$ Indels:
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RESULT 1276
ID ADD70784 standard; protein; 423 AA.
DE Human secreted/transmembrane protein PRO1461.
PD 29-MAY-2003.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches:
Query Match:
RESULT 1277
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RESULT 1272
DE Mammalian PRO polypeptide (SeqID 106).
PN U32003065143-A1.
PD GARRATECH INC.
PA (GETH ) GENENTECH INC.
BA (GETH ) GENENTECH INC.
BA (GETH ) GENENTECH INC.
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Guery Match:

RESULT 1270

ID ADC07062 standard; protein; 423 AA.

DE Human PR01461 protein.

PN US2003060602-A1.

PD 27-MAR-2003.

PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00% Mis
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RESULT 1271
D ADC18138 standard; protein; 423 AA.
DE Human PRO polypeptide #75.
PN US2003064925-A1.
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DE Human PRO polypeptide #75.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
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RESULT 1273
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Novel human secreted and transmembrane protein PRO1461.
US2003105298-A1.
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Human secreted/transmembrane protein PRO1461.
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ADESOSSS standard; protein; 423 AA.
Human secreted/transmembrane protein PRO1461
US2003069179-A1.
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US2003092883-A1
ADD39861 standard; protein; 423 AA.
Human secreted/transmembrane protein PRO1461.
US2003083462-A1.
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Human secreted/transmembrane protein PRO1461.
US2003096954-A1.
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Human secreted/transmembrane protein PRO1461
US2003092061-A1.
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Human secreted/transmembrane protein PRO1461.
US2003054406-A1.
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ADD38428 standard; protein; 423 AA.
Human secreted/transmembrane protein PRO1461
US2003096955-A1.
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Local Similarity: 100.00%
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ADGUL495 Standard, protein; 423 AA.
Novel human secreted and transmembrane protein PRO1461.
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US2003207398-A1.
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ID ADG08664 standard; protein; 423 AA.
DE Novel human secreted and transmembrane protein PRO1461.
PN US2001180793-A1.
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Novel human secreted and transmembrane protein PRO1461.
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Novel human secreted and transmembrane protein PR01461.
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US2003082628-A1.
01-MAY-2003.
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ADFSSeSs standard, protein; 423 AA.
Human secreted/transmembrane protein PRO1461.
US2003204054-A1.
Human secreted/transmembrane protein PRO1461.
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ADF30065 standard; protein; 423 AA.
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ADE21640 standard; protein; 423 AA.
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PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00%

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MESOLIA 1320, Most human secreted and transmembrane protein PRO1461.

DE Novel human secreted and transmembrane protein PRO1461.

PN US2003180905-A1.

PA (GETH ) GENENTECH INC.

BASEL Local Similarity: 100.00% Mismatches: 0

Query Match:

RESULT 1308

ID ADH24308 standard; protein; 423 AA.

DE Novel human secreted and transmembrane protein PRO1461.

PN US2003180934-A1.

PA (GETH ) GENENTECH INC.

BASEL Local Similarity: 100.00% Mismatches: 0

Query Match: 3.36% Indels: 0
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RESULT 1309
ID AD43602 standard; protein; 423 AA.

DE Novel human secreted and transmembrane protein PRO1461.

PN US2003181643-A1.

PD 25-SEP-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00$ Mismatches: 0

Query Match: 3.36$ Indels: 0

RESULT 1310

ID AD683723 standard; protein; 423 AA.

DE Human PRO polypeptide #53.

PN US2003180794-A1.

PD 25-SEP-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00$ Mismatches: 0

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ID ADH27647 gtandard; protein; 423 AA.
B Novel human secreted and transmembrane protein PRO1461.
PN US2003180906-A1.
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PN US2003181648-A1.

PD 25-SEP-2003.

PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: Onerw March March
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Human secreted and transmembrane protein PRO1461.
US20031647-A1.
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nilarity:	andard; ted and 9-A1.	25-SEP-2003. (GETH ) GENENTECH It Local Similarity:	KESULT 1115  ID ADH57441 standard; protein; 423 AA.  E Novel Human secreted and transmembrane protein by responsionant	80920-A1. 2003. GENENTECH ] imilarity:	ULT 1316 ADH53583 standard; Novel human secrete	PD 25-SEP-2003. PA (GETH ) GENENTECH I Best Local Similarity: Query Match:	Ę	PN USZUGJENEAT-AI. PD 25-SEP-2003. PA (GETH ) GENENTECH I Best Local Similarity: Query Match:	RESULT 1318  ID ADH52089 standard; protein; DE Novel human secreted and tra	PN USZOJJEBSB-A1.  PD 25-SEP-2003.  PA (GETH) GENENTECH I Best Local Similarity: Ouerv Match:	NULT 1319 ADH49944 standard; Novel human secrete	FN USZUGJEJESP-AI. PD 25-SEP-2003. PA (GETH ) GENENTECH I BEST LOCAl Similarity: Query Match:	<pre>SULT 1320 ADI25454 standard; Novel human secrete US2003181696-A1.</pre>	-2003. ) GENENTECH 1 Similarity:	RESULT 1321 D ADH90247 standard; protein; DE Novel human secreted and tra N US2003181698-Al.	PA (GETH) GENENTECH INC. Best Local Similarity: 100 Query Match:	RESULT 1322  DD AD125624 standard; protein; DE Novel human secreted and tra PN US2003181669-A1.	PD 25-SEP-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 100

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ADH98138 standard; protein; 423 AA.
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Novel human secreted and transmembrane protein PRO1461.
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Novel human secreted and transmembrane protein PRO1461.
US2003181657-A1.
   мынун648 standard; protein; 423 AA.
Novel human secreted and transmembrane protein PRO1461.
USPO3111708-A1.
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Novel human secreted and transmembrane protein PRO1461.
US2003180848-A1.
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Novel human secreted and transmembrane protein PRO1461.
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Novel human secreted and transmembrane protein PRO1461.
US2003181676-A1.
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US2003181699-A1.
25-SEP-2003.
(GETH ) GENENTECH INC.
3.16 Local Similarity: 100.00$
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25-SEP-2003.
(GETH ) GENENTECH INC.
Local Similarity: 100.00%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
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Local Similarity: 100.00%
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Local Similarity: 100.00%
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LOCAL Similarity: 100.00%
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RESULT 1332
ID ADH98648 standard; p
DE Novel human secreted
PN US200131708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH IN
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25-SEP-2003.
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RESULT 1333
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RESULT 1335
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RESULT 1340
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RESULT 1341
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RESULT
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ADI01353 standard; protein; 423 AA.
Novel human secreted and transmembrane protein PRO1461
US2003190669-A1.
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Novel human secreted and transmembrane protein PRO1461.
US2002190716-A1.
                                                                                                                      ADMY/968 standard; protein; 423 AA.
Novel human secreted and transmembrane protein PRO1461
USCO03181674-A1.
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Novel human secreted and transmembrane protein PRO1461
US2003181652-A1.
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ID ADI03306 standard; protein; 423 AA.
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ADH77985 standard; protein; 423 AA.
Human PRO polypeptide #53.
US2003181666-A1.
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Human PRO polypeptide #53.
US2003181681-A1.
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ID ADH77985 standard; protein; 9
DE Human PRO polypeptide #53.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.008
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(GETH ) GENENTECH INC.
LOCAL Similarity: 100.00%
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00$
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100
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RESULT 1342
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RESULT 1348
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RESULT 1344
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RESULT 1347
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US2003181651-A1.
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Novel human secreted and transmembrane protein PRO1461.
US2003191289-A1.
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Novel human secreted and transmembrane protein PR01461.
Novel human secreted and transmembrane protein PRO1461. US2003191290-A1.
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US2003181677-A1.
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Novel human secreted and transmembrane protein PRO1461.
US2003191288-A1.
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Novel human secreted and transmembrane protein PRO1461.
US2003181678-A1.
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Novel human secreted and transmembrane protein PRO1461.
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Novel human secreted and transmembrane protein PRO1461.
25-SEP-2003.
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US2003171550-A1.
11-8EP-2003.
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Novel human secreted and transmembrane protein PRO1461
US2003181675-A1.
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(GFTH ) GENENTECH INC.
Local Similarity: 100.00%
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(GETH) GENENTECH INC.
Local Similarity: 100.00%
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Best Local Similarity: 100.00%
Onerv Match: 3.36%
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Local Similarity: 100.00%
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Best Local Similarity: 100.00%
Onerv Match:
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(GETH ) GENENTECH INC.
Local Similarity: 100.00%
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Local Similarity: 100.00%
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imilarity: 100.00%
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ADI04700 standard;
                                                    (GETH ) GENENTECH Local Similarity:
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ADI05300 Btandard;
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RESULT 1353
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RESULT 1356
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RESULT 1357
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RESULT 1
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RESULT
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ADL93789 standard; protein; 423 AA.
Novel human secreted and transmembrane protein PRO1461.
US2003040013-A1.
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Novel human secreted and transmembrane protein PRO1461.
US2003073813-A1.
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Novel human secreted and transmembrane protein PRO1461.
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ADH80059 standard; protein; 423 AA.
Movel human secreted and transmembrane protein PRO1461.
US2003191287-A1.
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Novel human secreted and transmembrane protein PRO1461.
USZOGO181671-A1.
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Novel human secreted and transmembrane protein PRO1461.
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ADI25794 standard; protein; 423 AA.
                                                                                           protein; 423 AA.
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PA (GETH) GENENTECH INC.
Best Local Similarity: 100.00%
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PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00%
3.36%
CS-SEP-2003.
(GETH) GENENTECH INC.
Local Similarity: 100.00%
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Best Local Similarity: 100.00%
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US2003181667-A1.
US-5-SER-2003.
(GETH ) GENENTECH INC.
Local Similarity: 100.00$
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100
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ID ADH78155 Btandard;
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DE Novel human secreted and transmembrane protein PRO1461. PN US2003166848.A1. PD 04-SEP-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 100.00% Mismatches: 0 Query Match: 3.36% Indels: 0	ID ADH06336 standard, protein; 423 AA.  DE Novel human secreted and transmembrane protein PRO1461.  PN US2003180854-A1.  DD 25-SEP-2003.  PA (GETH ) GENEWTECH INC.  Best Local Similarity: 100.00\$ Mismatches: 0  Query Match: 3.36\$ Indels:	RESULT 1398  ID ADH30166 standard; protein; 423 AA.  DE Novel human secreted and transmembrane protein PRO1461.  PN US2003180856-A1.  PD 25-SEP-2003.  PA (GETH) GENENTECH INC.  PA (GETH) GENENTECH INC.  PAST (ACCAL Similarity: 100.00\$ Mismatches: 0	423 AA. cansmembrane protein PR	Match: 3.36* 1.400 ADH3219 standard; protein; 423 AA Human PRO polypeptide #160.	# £ £	US2003180844-A1. 25-SEP-2003. (GETH ) GENENTECH INC. 5t Local Similarity: 100.00\$ Mismatches: 5r Match: 3.36\$ Indels:	ID ADHO7870 standard; protein; 423 AA.  DE Novel human secreted and transmembrane protein PRO1461.  PN US2003180851-A1.  PD 25-SEP-2003.  PA (GETH ) GENENTECH INC.  Best Local Similarity: 100.00\$ Mismatches: 0  Query Match: 3.36\$ Indels: 0	ID ADG85882 standard; protein; 423 AA.  DE Novel human secreted and transmembrane protein PRO1461.  PN US2003180861-A1.  PD 25-SEP-2003.  PA (GETH ) GENENTECH INC.  Best Local Similarity: 100.00\$ Mismatches: 0  Query Match: 3.36\$ Indels: 0	ID ADH39428 standard; protein; 423 AA.  DE Novel human secreted and transmembrane protein PRO1461.  PN US2003180316-A1.  PD 25-SEP-2003.  PA (GETH ) GENENTECH INC.  Best Local Similarity: 100.00\$ Mismatches: 0  Query Match: 3.36\$ Indels: 0  RESULT 1405  ID ADH33620 standard; protein; 423 AA.  DE Human PRO polypeptide #53.
bin, 423 AA.  Drane protein PRO1461.  Mismatches: 0  Indels: 0	423 AA. Mismatches:	Indels: 423 AA. ansmembrane protein PR	nity: 100.00% Indels: 0 Indels: 0 Indard, protein; 423 AA. secreted and transmembrane protein PRO1461.	00% Mismatches: 0 Indels: 0 sin; 423 AA. i transmembrane protein PRO1461.	00% Mismatches: 0 s Indels: 0	orane protein PRO1461.  Orane protein PRO1461.  Orane protein PRO1461.	ein; 423 AA. brane protein PRO1461. 00% Mismatches: 0	; 423 AA. ransmembrane protein PR Mismatches:	, 423 AA. Mismatches: Indels:
ID ADH03157 standard; protein; 423 AA. DE Human secreted/transmembrane protein PRO1461 PN US2003216562-A1. PD 2C-NOV-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 100.00\$ Mismatches Onerv Match: Alch: Inden:	3 standard RO polypep 80839-A1. 2003. GENENTECH	0 sta uman 80845 2003.	ary Match:  SULT 1390  ADG69437 sta  Novel human US2003180846  Z5-SEP-2003.	denewlech milarity: standard; man secret	gir u	DE ADMAIL SCALLGALU; 723 AN: DE Human secreted/transmembrane protein PRO1461 PN US2003220471-A1. PD 27-NOV-2003. PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00\$ Mismatches Query, March: 3.36\$ Indels:	RESULT 1393  ID ADH03634 standard; protein; 423 AA.  DE Human secreted/transmembrane protein PR01461  PN US2003224478-A1.  PD 04-DEC-2003.  PA (GETH ) GENENTECH INC.  PA (GETH ) GENENTECH INC.  PA (ABPAN MATCH MATCH INC.  A 364 TANDAR TANDAR MATCH INC.  A 364 TANDAR TANDAR TANDAR MATCH INC.	RESULT 1394  ID ADH26250 standard; protein; 423 AA.  ID Novel human secreted and transmembrane prote PN US2003068770-A1.  PD 10-APR-2003.  PA (GETH ) GENENTECH INC.  PA (GETH ) 100-1000 Mismatches Pleat Local Similarity: 100.000 Mismatches Pleat Local Similarity: 136.	Guery Macuit RESULT 1395 ID ADG83998 standard; protein; 423 AA DE Human PRO polypeptide #53. PN USCO18180842-A1. PD 25-5EP-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 100.00\$ RESULT 1396 ID ADG85542 standard; protein; 423 AA

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ADG69777 standard; protein; 423 AA.
Novel human secreted and transmembrane protein PRO1461.
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Novel human secreted and transmembrane protein PRO1461.
US2-003180847-A1.
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Novel human secreted and transmembrane protein PRO1461.
US2003180862-A1.
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Novel human secreted and transmembrane protein PRO1461.
US2003180909-A1.
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Novel human secreted and transmembrane protein PRO1461.
US203180915-A1.
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Human PRO polypeptide #53.
US2003180838-A1.
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Human PRO polypeptide #53.
US2003180840-A1.
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линиявив standard; protein; 423 AA.
Novel human secreted and transmembrane protein PRO1461.
US2001180908-A1.
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US2003180849-A1.
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NOVEL human secreted and transmembrane protein PRO1461.
US2003180911-A1.
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Novel human secreted and transmembrane protein PRO1461
US2003181642-A1.
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US2003180863-A1.
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Human secreted/transmembrane protein PRO1461.
US2004005626-A1.
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RESULT 1421
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PA (GETH) GENENTECH INC. Best Local Similarity: 100.00% Query Match:	RESULT 1424  ID ADH49624 standard; protein; 423 AA.  DE Novel human secreted and transmembrane prote  PN 102003180857-A1.	25-SEP-2003. (GETH ) GENENTECH I st Local Similarity:	Query Match: 3.36% Indels: RESULT 1425 ID ADH90587 standard; protein; 423 AA. DE Novel human secreted and transmembrane protein	PN US2003181700-A1. PD 25-SEP-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 100.00\$	Query Match: RESULT 1426 ID ADI11323 standard; protein; DE Human PRO polypeptide #53. PN US2003181683-A1.	it it	KESULI 142. DE Novel human secreted and transmembrane protein PN US2003190698-A1.	PD 09-OCT-2003. PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.36%	RESULT 1428  ID AD102218 standard; protein; 423 AA.  DE Novel human serreted and transmembrane protein	PN USZUGISPOSP-AL. PD 09-OCT-2003. PA (GETH) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.36%	RESULT 1429  ID ADH61589 standard; protein; 423 AA.  DE Human secreted/transmembrane protein PRO146  PN US2004014130-A1.	PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.36%	ID ADH90757 standard; protein; 423 AA. DE Novel human secreted and transmembrane prote PN US2003181701-A1.	# E	RESULT 1431  ID ADJ54958 standard; protein; DE Human PRO polypeptide #160. PN US2004023321-A1.	PD 05-FEB-2004. PA (GETH ) GENENTECH INC. Best Local Similarity: 100.00% Query Match: 3.36%	RESULT 1432  ID ADJ98632 standard; protein; 423 AA.  DE Novel human secreted and transmembrane prot.  PN US2003187197-A1.  PD 02-0CT-2003.	

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Indels:	in; 423 AA. transmembrane protein	Mismatches: Indels:	rane protein	Mismatches: Indels:	T 1444 DAM40477 standard, protein, 423 AA. Novel human secreted and transmembrane protein PRO1461 US2004048335-A1.	Mismatches: Indels:	423 AA.	Mismatches: Indels:	423 AA. protein PRO1461.	Mismatches: Indels:	123 AA. nsmembrane protein	Mismatches: Indels:	123 AA. lated protein 32409	Mismatches: Indels:	431 AA.	Mismatches: Indels:	13 AA. le (3).	Mismatches: Indels:
3.36%	prote: ed and	INC. 100.00% 3.36%	protein; 'ed and tra	INC. 100.00% 3.36%	protein; ed and tra	INC. 100.00% 3.36%		INC. 100.00% 3.36%	protein; insmembrane	INC. 100.00% 3.36%	protein; 423 AA ed and transmemb:	INC. 100.00% 3.36%	protein; 423 AA. Hsorder related p	100.00% 3.36%		100.00\$ 3.36\$	protein;	100.00% 3.08%
Query Match:	1447 431625 sta vel human	FN USZUGAUSASSAFAL. PD 11-MAR-2004. PA (GETH ) GENENTECH Best Local Similarity: Query Match:	200	PN US2004053358-Al. PD 18-MAR-2004. PA (GETH ) GENENTECH Best Local Similarity: Query Match:	RESULT 1444  ID ADM40477 standard; DE Novel human secret PN US2004048335-A1.	1, 7, 1	ESOUL 1445 ID ADM80961 standard; protein; DE Human PRO polypeptide #53. PN US2004058411-A1.	π ř.	KESULI 1446 ID ADD:94788 standard; protein; 423 AA. DE Human secreted/transmembrane protein PRO1461 PN US2004073015-A1. DN 1-2-app-2004	ائع تد	RESULT 1447  MESULT 1447  DE NOVEL human secreted and transmembrane protein PN US2004091959-A1.	ř. ř.	3	PD 05-AUG-2004. PA (MILL-) MILLENNIUM PHARM INC Best Local Similarity: 100.00% Query Match: RESHLY 1449	ID AAR06459 standard; protein; DE v-PA beta.	# 4	ID AAR14930 standard; protein; 12 DE OT-2 antibody binding peptide PN W09117258-A. PD 14-NOV-1991.	t Local Si ery Match:

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INSTITUTION ARE TO CARGARY, peptide, 14 AA.

BY MAIN transmembrane serine procease related type I fibronectin domain #1.

BY WORDSCHIESTS.

BARING MARKET STRANGER AND THE STRAN
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ADN62858 standard; protein; 119 AA.

Iuman NOV11d.
IS2004038223-A1.

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AARŠ3961 standard, protein, 105 AA.
Hepatocyte growth factor converting protease fragment.
EP596524-A2.
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ADA05694 standard; protein; 119 AA. Human NOV11d protein SEQ ID NO:54. WO2003029424-A2.
10-APR-2003.
(CURA-) CURAGEN CORP.
SET Local Similarity: 100.00$ Missing Match: 3.08$ Ind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID ADAGS to standard; protein; 119 AA.

DE Human NOV11g protein SEQ ID NO:60.

PN W02003029424-A2.

PD 10-APR-2003.

PA (CURA-) CURAGEN CORP.

Best Local Similarity: 100.00% Miss Query Match: 3.08% Indian
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ADN62860 standard; protein; 102 AA.
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PD 11-MAY-1994.
PA (MITU) MITSUBISHI KASEI CORP.
Best Local Similarity: 100.00$
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(GANG/) GANGOLLI E A.
(RIEG) RIEGER D K.
(SPAD/) SPADENA S K.
t Local Similarity: 100.00%
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PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
LEACH M D.
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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BERGHS C.
DIPIPPO V A.
EISEN A.
GANGOLLI E A.
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ZERHUSEN B D.
ANDERSON D W.
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PATTURAJAN M.
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PEYMAN J A.
KEKUDA R.
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RASTELLI L.
                                                                 SMITHSON G.
                   fuman NOV11e.
JS2004038223-A1.
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RESULT 1462
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ESSUIT 1466
ID ADG75740 standard; protein; 141 AA.
ID Human protein modification and maintenance molecule polypeptide SeqID64.
PN W02003083084-A2.
PD 09-OCT-2003.
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Indels:
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Human NOV11a protein SEQ ID NO:48.
WO2003029424-A2.
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ADN62852 standard; protein; 142 AA.
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PD (CURA.) CURAGEN CORP.
Best Local Similarity: 100.00%
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3.08%
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Best Local Similarity: 100.00%
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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(ROTH/) ROTHENBERG M E.

(LEACH M D.

(AGRE/) AGRE M D.

(AGRE/) BERCHS C.

(DIPL/) DIPLPPO V A.

(EISE/) EISEN A.

(GANG/) GANGOLLI E A.

(RIEG/) RIEGER D K.

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(SPAD/) SPADERNA S K.
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SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
LEACH M D.
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ANDERSON D W.
ZHONG M.
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PATTURAJAN M.
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                           MILLET I.
PEYMAN J A.
KEKUDA R.
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PEYMAN J A.
KEKUDA R.
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          SMITHSON G.
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US2004038223-A1.
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26-FEB-2004.
(SMIT/) SMIT
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(ELLE/)
(MALY/)
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PEYM/)
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RESULT 1467
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(MILL/)
(RAST/)
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RESULT
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Indels:
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Indels:
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ADN62856 standard; protein; 147 AA.
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Human NOV11c protein SEQ ID NO:52.
WO2003029424-A2.
                                                                                   (SHIM/) SHIMKETS R A.
(ROTH/) ROTHENBERG M E.
(LEAC/) LEACH M D.
(AGEE/) AGEE M L.
(BERG/) BERGHS C.
(DIPI/) DIPIPPO V A.
(EISE/) EISEN A.
(GANG/) GANGOLLI E A.
(RIEG/) RIEGER D K.
(SPAD/) SPADERNA S R.
(SPAD/) SPADERNA S T.
Y MATCH:
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PA (CURA-) CURAGEN CORP.
Best Local Similarity: 100.00%
Query March: 3.08%
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Match: 3.08%
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RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHENOY S R.
ROTHKETS R A.
LEACH M D.
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RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
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LEACH M D.
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PATTURAJAN M.
SPYTEK K A.
EDINGER S R.
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MALYANKAR U M.
ZERHUSEN B D.
ANDERSON D W.
               ZHONG M.
CATTERTON E.
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ANDERSON D W.
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PEYMAN J A.
KEKUDA R.
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CATTERTON E.
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US2004038223-A1.
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RESULT
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Human diagnostic and therapeutic pprotein SEQ ID NO:4913. WO2004023973-A2. ABR41514 standard; protein; 156 AA. Human DITHP protein modification/maintenance protein. WO200297031-A2. 00 00 Mismatches: Indels: Mismatches: Mismatches: Mismatches: Mismatches: Mismatches: Indels: Mismatches: Mismatches: Indels: Indels: Indels: Indels: ADE13246 standard; protein; 149 AA. Protease domain from human protease M. US2003170707-A1. ADE13374 standard; protein; 157 AA. Protease domain from human TADG-12 #2. US2003170707-A1. 11-SER-2003. RESULT 1471

ID AAU68926 standard; protein; 149 AA.
DE Human protease domain of protease M.
PD US6294663-B1.
PD 25-SEP-2001. Query Match: RESULT 1473 TD ADH78455 standard; protein; 149 AA. Ŗ ADP43664 standard; protein; 162 AA. Human PMMM-21 protein SEQ ID NO:21. WO2004053068-A2. I 1479 ABM84664 standard; protein; 165 AA. ADH78458 standard; protein; 157 AA. Human protease M protease domain. US2003207316-A1. AAU68929 standard; protein; 157 F Human protease domain of TADG-12 US6294663-B1. Human TADG-12 protease domain US2003207316-A1. PN NCC-2002.
PA (INCY-) INCYTE GENOMICS INC.
Best Local Similarity: 100.00\$ PD 25-SEP-2001.
PA (UYR-) UNIV ARKANSAS.
Best Local Similarity: 100.00\$ PD 06-NOV-2003.
PD 06-NOV-2003.
PA (UYAR-) UNIV ARKANSAS.
Best Local Similarity: 100.00\$ PD 25-2501.
PD 25-2001.
PA (UYAR-) UNIV ARKANSAS.
Best Local Similarity: 100.00% PA (OBRI) O'BRIEN T J. Best Local Similarity: 100.00% Query Match: 3.08% PD 11-SEP-ZUUS.

PA (OBRI/) O'BRIEN T J.

Best Local Similarity: 100.00\$

3.08\$ PD 25-MAR-2004.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Best Local Similarity: 100.00\$ PD 06-NOV-2003. PA (UYAR-) UNIV ARKANSAS. Best Local Similarity: 100.00% PA (INCY-) INCYTE CORP.
Best Local Similarity: 100.00% 3.08% 11-SEP-2003 24-JUN-2004 Query Match: RESULT 1477 Query Match: RESULT 1478 Query Match: RESULT 1480 Query Match RESULT 1472 RESULT 1474 Query M RESULT

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Human transmembrane serine protease (MTSP) polypeptide #16.
US2004001801-A1.
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Human delta tryptase variant protein SEQ ID NO:3.
WO2004033494-A1.
                            RESULT 1488
ID AAY28641 standard; protein; 207 AA.
DE Human secreted protein from cDNA clone HKAET41.
PN W09940183-A1.
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ID ADI17075 standard; protein; 225 AA.

ID Murine NOVX protein homologue SeqID 611.

PN WO200268649-A2.

PD 06-SEP-2002.

PA (CURA-) CURAGEN CORP.

Best Local Similarity: 100.00% Mismatch
         Indels:
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                                                                                                                                                                                                                  T 1489
ABR4819 standard; protein; 207 AA.
Human Plasminute.
WO200294864-A2.
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Novel human protein sequence #2356.
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AAB21312 standard; protein; 228 AA.
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Best Local Similarity: 100.00%
Query Match:
3.08%
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Best Local Similarity: 100.00%
Query Match: 3.08%
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PD 12-201-1999.
PA (HUMA-) HUWAN GENOME SCI INC.
Best Local Similarity: 100.00$
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Best Local Similarity: 100.00%
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PA (CORV-) CORVAS INT INC.
Best Local Similarity: 100.00$
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PA (GEST ) GENSET.
Best Local Similarity: 100.00%
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PA (UNIX ) UNISEARCH LTD.
Best Local Similarity: 100.00%
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28-JUL-2004.
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RESULT 1493
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RESULT 1494
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RESULT 1496
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RESULT 1495
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RESULT
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Human proble...

BE Human proble...

PN W0200198467-A2.

PD 3-DEC-2001.

PA (FARB ) BAYER AG.

Best Local Similarity: 100.00$ Mismatches:

Query Match: 3.08$ Indels: 0

RESULT 1481

ID AD11632 standard; protein; 181 AA.

DE Human protein modification and maintenance molecule (PMMM) protein #17.

PN W02003100016-A2.

O4-DEC-2003.

O4-DEC-2003.

O4-DEC-2003.

O4-DEC-2003.

Indels: 0

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Indels: 0
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ADJ55806 standard; peptide; 199 AA.
Peptide homologous to a fragment of a human NOV12 protein SeqID 98.
US2003199465-A1.
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Human NOV12 protein-related protein fragment SeqID98.
WO2004009634-A2.
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Human delta tryptase variant protein.
WO2004031494-Al.
22-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG42737 standard; protein; 199 AA.
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) ELLERMAN K.
/) MACDOUGALL J R.
/) SMITHSON G.
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Local Similarity: 100.00%
Match: 3.08%
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PADIGARU M.
TAUPIER R J.
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(MACD/) MACDOUGALL J
(SMIT/) SMITHSON G.
Local Similarity: 1
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-USER=US10015385_@CGN_1_1 46_@runat_05032005_173710_18160 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEDUERY -NGG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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| 11. ADDI 1. 1332 7. 2.0 9 5 PCT-US95-14442A-10 SEGMENCE 10 | 2, Appli c133 7 1.9 10 12.07-969-378-20 Sequence 2. 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; Patent No. 6566498
; GREMEAL INFORMATION:
; TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides
; TITLE REFERENCE: PP391
; CURRENT APPLICATION NUMBER: US/09/244,111
; CURRENT PILING DATE: 1999-02-04
; EARLIER PILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
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; Sequence 812.1. Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VEWTER, U. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PLILING DATE: 2000-10-20
; PRIOR PLILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8151
; LENGTH: 249
                                                                                                                                                                                                                                     540
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                                         ACCAGCAGCGTTCAACCCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGC
LysllePheAsnGlyThrGluCysGlyArgAsnSerGlnProTrpGlnValGlyLeuPhe
                           GAGGGCACCAGCCTGCGGGGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGCG
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Matches:
Conservative:
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Percent Similarity:
Best Local Similarity:
Query Match:
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ORGANISM: Human
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US-09-949-016-8151
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5223425-6
;Patent No. 5223425
; APPLICANT: FLIER, JEFFREY S.;SPIEGELMAN, BRUCE M.;ROSEN,
;BARRY M.;WHITE, TYLER R.
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5223425-6
;Patent No. 5223425
; APPLICANT: FLIER, JEFFREY S.;SPIEGELMAN, BRUCE M.;ROSEN,
;BARRY M.;MHITE, TYLER R.
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 188
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Mismatches:
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                                                                                                                                                                                              US-10-015-385A-193 (1-1091) x 5200340-4 (1-138)
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/277,963
FILING DATE: 30-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34,203
FILING DATE: 02-APR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/277,963
FILING DATE: 30-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34,203
FILING DATE: 02-APR-1987
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NUMBER OF SEQUENCES: 19
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Best Local Similarity:
Query Match:
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;SEQ ID NO:4:
; LENGTH: 138
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110 CysGlnGlyAspSerGlyGlyProLeuValCysGlyGlyValLeuGlnGlyLeuValSer 129
                                                                                                                                                                                                                                                                         646 TATCCCGGGAGAATCACCAGCAACATGGTGTGCAGGGGGGGCGTCCCGGGGCGAGGATGCC 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Patent No. 5200340
; APPLICANT: FOSTER, DONALD C.;MULVIHILL, EILEEN R.;O'HARA,
;PATRICK J.;PINGEL, KURT;YOSHITAKE, SHINJI
TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Patent No. 5200340
; APPLICANT: FOSTER, DONALD C.;MULVIHILL, BILEEN R.;O'HARA,
;PATRICK J.;PINCEL, KURT;YOSBITAKE, SHINJI
TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
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NUMBER OF SEQUENCES: 34

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/53,412

FILING DATE: 22-MAY-1987
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/53,412
FILING DATE: 22-MAY-1987
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   ; ORGANISM: Homo sapiens
US-09-244-111-6
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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LENGTH: 138
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Pred. No.:
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5200340-4
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US-10-015-385A-193 (1-1091) x 5223425-5 (1-238)
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                                                                                                                                                                                     NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/277,963
FILING DATE: 30-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34,203
FILING DATE: 02-APR-1987
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APPLICATION NUMBER: US/07/277,963
FILING DATE: 30-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34,203
FILING DATE: 02-APR-1987
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Patent No. 5223425
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LENGTH: 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                   USEFUL FOR DETECTING AND TREATING DISEASES
                                                                                                                                                                                                                                                         GENERAL INCORMATION MAURICE
APPLICANT: COLDITYS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: RIASS, MICHAEL N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWART, NOWEL SERINB PROTEASE REAGENTS
TITLE OF INVENTION: NOVEL SERINB PROTEASE REAGENTS
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
                                                                                                 750
                                                                                                                                   176 GlyAspSerGlyGlyProLeuValCysGlyGlyValLeu 188
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Conservative:
Mismatches:
Indels:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
                                                             US-10-015-385A-193 (1-1091) x 5223425-6 (1-222)
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       Indel8:
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PRIOR APPLICATION DATA:
PAPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                            Sequence 44, Application US/08944483
Patent No. 6232456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 44:
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MOLECULE TYPE: No. 6232456e
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TYPE: amino acid
STRANDEDNESS: single
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US-08-944-483-44
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712 GGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGGGGTCCTT 750

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APPLICANT: FLIER, JEFFREY S., SPIEGELMAN, BRUCE M., ROSEN, BARRY M., WHITE, TYLER R. TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT; D ACTIVITY
Patent No. 5223425

APPLICANT: FILER, JEFFREY S.;SPIEGELMAN, BRUCE M.;ROSEN,
APPLICANT: TYLER R.
HITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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; Sequence 70, Application US/08944483
; Patent No. 622456
; GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
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Sequence 72, Application US/08944483

Sequence 72, Application US/08944483

Patent No. 6232456

GENERAL INFORMATION:
APPLICANT: COLEN. MAURICE
APPLICANT: COLEN. MAURICE
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: STEMMAP, PAULA N.
APPLICANT: STEMMAP, APPLICANT: STEMMAP, APPLICANT: STEMMAP, APPLICANT: STEWMAP, D.
APPLICANT: STEWMAP, APPLICANT: STEWERT, GENT D.
APPLICANT: STEWDER, GENT D.
APPLICANT: STEWDER, GENT D.
APPLICANT: STEWDER, TENDER STEWEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                            5223425-4
;Patent No. 5223425
; APPLICANT: FLIER, JEFFREY S.;SPIEGELMAN, BRUCE M.;ROSEN,
;BARRY M.;WHITE, TYLER R.
TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
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Matches:
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Mismatches:
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Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/277,963
FILING DATE: 30-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34,203
FILING DATE: 02-APR-1987
                                                                                                                                                                                                                                                                                                                                                                   712 GGTGATTCTGGGGGCCCCCCTGGTG1
                                                          APPLICATION NUMBER: 34,203
FILING DATE: 02-APR-1987
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Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                                                                                  LENGTH: 250
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Pred. No.:
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US-08-944-483-72
                                                                                                SEQ ID NO:4:
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APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDDARDD N.
APPLICANT: GRANADOS, EDDARDD N.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWART, KENT D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANALESS:
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;Patent No. 5223425
; APPLICANT: FILER, JEFFREY S.;SPIEGELMAN, BRUCE M.;ROSEN,
;BARKY M.;WHITE, TYLER R.
; TITLE OF INVENTION: DNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
;D ACTIVITY
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Mismatches:
Indels:
Gaps:
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OPERATING SYSTEM: DOS
SOFTWARE: F884SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
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Matches:
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CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAMM: BECYER, Cheryl L.
REGISTRATION NUMBER: 35,441
REGISTRATION NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/277,963
FILLING DATE: 30-NOV-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                     ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                CITY: Abbot Park
STATE: IL
CONTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 70:
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US-08-944-483-70
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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TELEFAX: 847/938-2623
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-09-027-337-8

US-09-027-337-8

Sequence 8, Application US/09027337B

Sequence 8, Application US/09027337B

Seturn No. 5975616

GENERAL INFORMATION:

APPLICANT: O'FINITY O'FINITY O'FINITY O'HITOCOSHI

TITLE OF INVENTION: Breast and Ovarian Carcinomas

TITLE OF INVENTION: Breast and Ovarian Carcinomas

TITLE OF INVENTION: Breast and Ovarian Carcinomas

CURRENT APPLICATION NUMBER: US/09/027,337B

CURRENT FILING DATE: 1998-02-20

SEQ ID NO 8

LENGER 253

LENGER 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Serine protease catalytic domain of tissue plasminogen CTHER INFORMATION: activator (Tpa) homologous to similar domain in TADG-15 US-09-027-337-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
                                                                                                          CURRENT APPLICATION DATA:
SOUTHWARE: FRASESCY for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 31,441
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: No. 6232456e
                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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INFORMATION FOR SEQ ID NO: 'SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
COUNTRY: USA.
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino a STRANDEDNESS:
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Pred. No.:
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Ouery Match: 3.64% Indels: 0
DB: 2
Caps: 0
US-10-015-385A-193 (1-1091) x US-09-027-337-8 (1-253)
Oy 700 GATGCCTGCCAGGGTGATTCTGGGGGCCCCTGGTGTT 738
Db 198 AspAlaCysGlnGlyAspSerGlyGlyProLeuValcys 210
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Search completed: March 5, 2005, 23:47:13 Job time : 50.5 secs

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coagulation factor recagulation factor u-plasminogen acti u-plasminogen acti u-plasminogen acti u-plasminogen acti plasmin (EC 3.4.21 plasmin (EC 
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tryptase (EC 3.4.2
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G-box binding fact
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myonase (EC 3.4.-.
                                               trypsin (BC 3.4.21 serine proteins as trypsin (BC 3.4.21 trypsin (BC 3.4.21 trypsin (BC 3.4.21 trypsin (BC 3.4.21 probable serine probable serine propabale serine preceinase serine preserine prese
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mast cell proteina
natural killer cel
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serine proteinase
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granzyme M (EC 3.4
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S44462
S173245
S17537
S17537
S17630
S69370
JE0151
812
1004
2616
4548
30
 Command line parameters:
-MODEL=frame+-n2p.model -DEV=xlp
-G9-(cgn2.1/0SFV) cgpodl.p/U3101385/runat_05032005_173710_18168/app_guery.fasta_1.1287
-G9-(cgn2.1/0SFV) cgpodl.p/U310151385/runat_05132005_173710_18168/app_guery.fasta_1.1287
-DB=PIR_79-OFWT=fastan -SUFFIX=olidp-TRANS=human40.cdi-LIST=1500
-UNITS=bits -START=1 -END=-1 -MATRIX=olidp-TRANS=human40.cdi-LIST=1500
-UNITS=bits -START=1 -END=-1 -MATRIX=01000-TRANS=human40.cdi-LIST=1500
-UNITS=bits -START=1 -END=-1 -MATRIX=000000000
-USER=USI0015385 @CGN 1 1 63 @runat_05032005_173710_18168 -NCPU=6 -ICPU=3
-NORM=ext -HEAPSIZE=500 -MINLENE-0 -WAIT -DSPBLOCK=100 -LONGLOG
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A;Title: The plasminogen activator family from the salivary gland of the vampire bat Desn A;Reference number: JSO597; MUID:92039036; PMID:1937019
A;Recession: JSO599
A;Molecule type: mRNA
A;Residues: 1-431 «KRA>
A;Ross-references: UNIPROT:P98121; GB:M63989; NID:g166076; PIDN:AAA31594.1; PID:g166077
C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat homc C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-21/Domain: signal sequence #status predicted <BIC>
F;37-431/Product: plasminogen activator beta #status predicted <PLA>
F;41-74/Domain: EGF homology <KRG>
F;31-74]/Product: plasminogen activator beta #status predicted <PLA>
F;180-45/Domain: kringle homology <KRG>
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F;191-52,46-63,65-74,82-163,103-145,134-158,168-299,211-227,219-288,313-388/Disulfide bonc F;193-352/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;19-180/Cleavage site: His-Ser (Plasmin) #status predicted
F;226,775,382/Active site: His-Ser (Plasmin) #status predicted
F;226,775,382/Active site: His-Ser #status predicted
F;345-361,378-406/Disulfide bonds: #status predicted
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A; Reference number: JS0597; MUID:92039036; PMID:1937019
A; Recession: JS0600
A; Residues: 1-394 «KRA»
A; Residues: 1-394 «KRA»
A; Residues: 1-394 «KRA»
A; Cross references: UNIPFOT: P49150; GB:M63990; NID:9166078; PIDN: AAA31595.1; PID:9166079
A; Residues: 1-394 «KRA»
A; Cross references: UNIPFOT: P49150; GB:M63990; NID:9166078; PIDN: AAA31595.1; PID:9166079
A; Residues: 1-394 plasminogen activator; EGF homology; fibronectin type I repeat hom C; Superfamily: tissue plasminogen activator; Brditted «SIG»
F; 12-1/Domain: signal sequence #status predicted «PRO»
F; 12-36/Domain: propeptide #status predicted «PRO»
F; 12-36/Domain: kringle homology «KRA»
F; 45-126, Domain: kringle homology «KRA»
F; 45-126, Ge-108, 97-121, 131-262, 174-190, 182-251, 276-351, 308-324, 341-369/Disulfide bonds: F; 142-143/Cleavage site: His-Ser (plasmin) #status predicted
F; 18-1345/Cleavage site: His-Ser (plasmin) #status predicted
F; 18-135/Binding site: carbohydrate (Asn) (covalent) #status predicted
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305599
t-plasminogen activator (EC 3.4.21.68) beta precursor - common vampire bat
t-plasminogen activator
N.Alternate names: tissue plasminogen activator
CiSpeciaes: Desmodus rotundus (common vampire bat)
CiSpeciaes: Desmodus rotundus (common vampire bat)
CiSpeciaes: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
CiAccession: JS0599
RiKraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don
Gene 105, 229-237, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don Gene 105, 229-237, 1991
A;Title: The plasminogen activator family from the salivary gland of the vampire bat Des A;Reference number: J80597; MUID:92039036; PMID:1937019
                                             C; Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase F;1-18/Domain: signal sequence #status predicted <$15>F;19-246/Product: complement factor D (fragment) #status experimental <MAT>F;19-241/Domain: trypsin homology <fra>Fixy
F;44-60,141-207,172-188,197-222/Disulfide bonds: #status predicted F;59,105,201/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS0600
t-plasminogen activator (EC 3.4.21.68) gamma precursor - common vampire bat
N.Alternate names: tissue plasminogen activator
C;Species: Desmodus rotundus (common vampire bat)
C;Species: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                         738
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                 C; Superfamily: trypsin; trypsin homology
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t-plasminogen activator (EC 3.4.21.68) precursor - mouse C;Species: Mus musculus (house mouse)
C;Daccies: Mus musculus (house mouse)
C;Daccies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A29941; S48205; S48207; S48206
R;Rickles, R.J.; Darrow, A.L.; Strickland, S.
J. Biol. Chem. 263, 1563-1569, 1988
A;Fitle: Molecular cloning of complementary DNA to mouse tissue plasminogen activator mRh A;Reference number: A29941; MUID:88087303; PMID:2826484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: A29941
A;Molecule type: MRNA
A;Rosidues: 1-559 «RIC>
A;Residues: 1-559 «RIC>
A;Cross-references: UNIPROT:P11214; GB:J03520; NID:g202109; PIDN:AAA40470.1; PID:g202110
R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994
A;Fille: Characterization of the murine plasma fibrinolytic system.
A;Reference number: $48202; MUID:95010076; PMID:7523120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 33-37, X', 39-40 «LIW»
A; Residues: 33-37, X', 39-40 «LIW»
A; Residues: 33-37, X', 39-40 «LIW»
C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat home C; Reywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
E; 1-17/Domain: signal sequence #status predicted «SIG»
F; 10-20/Domain: signal sequence #status predicted «RIS»
F; 30-559/Product: t-plasminogen activator #status predicted «MAT»
F; 30-559/Product: t-plasminogen activator chain A #status predicted «ACH»
F; 33-16/Domain: EGF homology «EGF»
F; 31-294/Domain: kringle homology «KR1»
F; 31-294/Domain: kringle homology «KR2»
F; 310-553/Domain: trypsin homology «KR2»
F; 310-553/Domain: trypsin homology «TR2»
F; 310-553/Domain: trypsi
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A,Residues: 33-37,'X',39-40 <LIJ>A,Accession: 848207
A,Molecule type: protein
A,Residues: 309-316 <LIZ>A,Accession: 848206
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                                                                                                      t-plasminogen activator (EC 3.4.21.68) alpha-1 precursor - common vampire bat N,Alternate names: tissue plasminogen activator C;Species: Desmodus rotundus (common vampire bat) C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004 C;Accession: J30597 R;Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don Gene 105, 229-237, 1991
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A; Residues: 1-562 - CBES
A; Robiccule type: DNA
A; Residues: 1-562 - CBES
A; Robiccule type: DNA
A; Residues: 1-562 - CBES
A; Robiccule type: DNA
A; Residues: 1-562 - CBES
A; Cic. Biol. Chem. 55, 1255-1232, 1991
A; Tic. Biol. Chem. 55, 1255-1232, 1991
A; Reference number: JTO562; MUID: 91291340; PMID: 1368681
A; Reference number: JTO562; MUID: 91291340; PMID: 1368681
A; Reference number: DBJ: DO1036; NID: 9220128; PIDN: BAA00881.1; PID: 9441174
A; Residues: 31-562 - CITA
A; Residues: 31-562 - CITA
A; Residues: DBJ: DO1036; NID: 91291340; PIDN: BAA00881.1; PID: 9441174
A; Residues: 304, 234-221, 1983
A; Rober part of this sequence, including the amino end of the mature protein, was confirm A; Note: part of this sequence, including the amino end of the mature protein, was confirm A; Reference number: A93293; MUID: 83115262; PMID: 6337343
A; Reference number: A93293; MUID: 83115262; PMID: 6337343
A; Rolecule type: mRNA
A; Residues: 1562 - PEN
A; Tritle: Cloning and expression of human tissue-type plasminogen activator cDNA in Escher A; Residues: 1562 - PEN
A; Tritle: Chiak Res. 16, 5695, 1988
A; Residues: 1562 - Rels. Res. 16, 5695, 1988
A; Reference number: S02125; MUID: 88262579; PMID: 3133640
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A;Residues: 1-562 (SAS)

A;Residues: 1-562 (SAS)

A;Cross-references: EMBL:X07393; NID:g37243; PIDN:CAA30302.1; PID:g37244

A;Cross-references: EMBL:X07393; NID:g37243; PIDN:CAA30302.1; PID:g37244

A;Reperimental source: fetal lung cells

FEBS Lett. 189, 145-149, 1985

A;Reference number: A91343; MUID:85285620; PMID:3896853

A;Reference number: A91343
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A, Residues: 1-38, (%, 86-433,'E', 435-562 cKAG>
A, Experimental source: Detroit 562 cells; ATCC 138
R, Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephson, S.
Proc. Natl. Acad. Sci. US.A. 80, 349-352, 1983
A, Fitle: Isolation of cDNA sequences coding for a part of human tissue plasminogen active
A, Reference number: A93951; MUID:83169656; PMID:6572897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: A93951
A,Molecule type: mRNA
A,Residues: 251-358 «EDL»
A,Residues: 251-358 «EDL»
A,Experimental source: melanoma cells
R,Pohl, G; Kallstrom, M; Bergadorf, N.; Wallen, P.; Jornvall, H.
Biochemistry 23, 3701-3707, 1984
A,Title: Tissue plasminogen activator: peptide analyses confirm an indirectly derived am)
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A,Reference number: A90488; MUID:85000468; PMID:6433976
A,Contents: annotation; melanoma cells, partial sequence of residues 36-562, active and 1 R,Fohl, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jornvall, H.
A,Fohl, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jornvall, H.
A,Title: Differences between uterine and melanoma forms of tissue plasminogen activator. A,Reference number: A91322; MUID:84158956; PMID:6538514
A,Rolecule type: protein
A,Residues: 33-45,311-320 <POH>
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Aj Experimental source: uterus
Aj Note: in the uterus, cleavage of the activation peptide may also occur after 38-Gln
R; van Zonneveld, A.J.; Veerman, H.; Pannekoek, H.
Biol. Chem. 261, 14214-14218, 1986
A; Reference number: A37567; MUID: 87033611; PMID: 3021732
Aj Contents: annotation; fibrin binding site
R; Verbeijen, J. H.; Caspers, M.P. M.; Chang, G.T.G.; de Munk, G.A.W.; Pouwels, P.H.; Enger-
EMBO J. 5, 3525-3530, 1986
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A;Reference number: A23529; MUID:86196143; PMID:3009482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
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A, Residues: 1-379, K., 381-559 «NYT»
A, Residues: 1-379, K., 381-559 «NYT»
A, Residues: 1-379, K., 381-559 «NYT»
A, Residues: 1-379, K., 381-559 (NID:g530159; PIDN:AAA41812.1; PID:g530160
C, Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom C, Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-17/Domain: signal sequence #status predicted «RG»
F;18-29/Domain: propeptide #status predicted «RAT»
F;30-308/Product: t-plasminogen activator fstatus predicted «AGH»
F;38-75/Domain: EGF homology «EGF»
F;38-75/Domain: EGF homology «ERR»
F;124-205/Domain: kringle homology «KR2»
F;213-294/Domain: kringle homology «KR2»
F;309-553/Domain: kringle homology «KR2»
F;309-553/Domain: kringle homology «FR2»
F;309-553/Domain: kringle homology «FR2»
F;309-553/Domain: kringle homology «FR2»
F;309-553/Domain: krypsin homology «FR2»
F;308-66.66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,297-4
F;319-68,66-75,83-94,88-105,107-116,124-205,145-187,185,48-105,107-116,124-205,145-187,185,48-105,107-116,135,145-187,185,48-105,107-116,135-149,481/Binding site: Arg-11e (Apashin, trypsin) #status predicted
F;355,404,510/Active site: His, Asp, Ser #status predicted
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                                                                             t-plasminogen activator (BC 3.4.21.68) precursor - rat
C;Species: Rattus norregicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A35029; A31597
R;Feng, P.; Ohlsson, M.; Ny, T.
B BJOL. Chem. 265, 2022-2027, 1990
A;Title: The structure of the TATA-less rat tissue-type plasminogen activator gene. Spec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-559 <FENS
Kross-references: UNIPROT:P19637; GB:M31197; NID:g207429; PIDN:AAA42261.1; PID:g207431
R;Ny, T.; Leonardsson, G.; Hsueh, A.J.W.
DNA 7, 671-677, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: Cloning and characterization of a cDNA for rat tissue-type plasminogen activato
A,Reference number: A31597, MUID:89170114, PMID:3148445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      700 GAIGCCIGCCAGGGIGAITCIGGGGGCCCCCTGGIGIGI 738
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Matches:
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Best Local Similarity:
Query Match:
DB:
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A, Status: preliminary
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Codgulation factor XIIa (EC 3.4.21.38) precursor - bovine (fragment)
N.Alternate names: Hageman factor (activated)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: S45201; A61329
R;Shibuya, Y.; Semba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
Biochim: Biophys. Acta 1206, 63-70, 1994
A;Title: Primary structure of bovine Hageman factor (blood coagulation factor XII): compt
A;Reference number: S45201; MuID:94242702; PMID:8186251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P98140; GB:S70164
A;Cross-references: UNIPROT:P98140; GB:S70164
A;Note: the authors translated the codon GAG for residue 23 as Val, GAG for residue 70 as 8 pro, CTC for residue 203 as Phe, GTG for residue 286 as Glr is, and ATC for residue 505 as Leu
R;Fujikawa, K.; Walsh, K.A.; Davie, E.W.
Biochemistry 16, 2270-2278, 1977
A;Fitle: Isolation and characterization of bovine factor XII (Hageman factor).
A;Reference number: A61329; MUID:77182112; PMID:861210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Molecule type: protein
A; Meaddues: 10-16, X'.18-19;525-550 <FUJ>
C; Superfamily: Coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C; Superfamily: Coagulation; fibrinolysis; glycoprotein; hydrolase; monomer; plasma; st
F; 37-78/Domain: fibronectin type II repeat homology <IF2>
F; 88-120/Domain: EGF homology <EGF>
F; 125-160/Domain: fibronectin type I repeat homology <FEB1>
F; 207-287/Domain: kingle homology <KRG>
F; 207-287/Domain: typein homology <TRY>
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N.Alternate names: Hageman factor
C.Species: Cavia porcellus (guinea pig)
C.Species: Cavia porcellus (guinea pig)
C.Species: Cavia porcellus (guinea pig)
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A;Residues: 1-603 <SEM>
A;Cross-references: UNIPROT:Q04962; EMBL:X68615; NID:g49578; PIDN:CAA48600.1; PID:g49579
C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C;Keywords: hydrolase; serine proteinase
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;134-169/Domain: fibronectin type I repeat homology <FB1>
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1216-294/Domain: kringle homology «KRG>
1359-597/Domain: trypsin homology «TRY>
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A; Residues: 1-593 <SHI>
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A; Rosidues: 1-36 < REZ.

A; Cross-references: GB:M1890; NID:g339837; PIDN:AAA61213.1; PID:g339839

C; Comment: Cleavage by plasmin or trypain produces two chains held together by a single C; Comment: t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val bond. It C; Comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I repeat. C; Genetics: GB:PD:PD:PD:A. PD:A. PD:A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-562 < HAR.
A; Residues: 1-562 < HAR.
A; Cross-references: GB:M15518; NID:g190031; PIDN:AAA60111.1; PID:g190032
A; Note: parts of this sequence were confirmed by peptide sequencing
R; Reddy, V.B.; Garramone, A.J.; Sasak, H.; Wei, C.
NA 6, 461-472, 1987
A; Title: Expression of human uterine tissue-type plasminogen activator in mouse cells us
A; Reference number: 160110; MUID:88054470; PMID:2824147
                                         R; Dodd, I.; Nunn, B.; Robinson, J.H.
Thromb. Haemost. 59, 523-528, 1988
A; Title: Isolation, identification and pharmacokinetic properties of human tissue-type p. A; Reference number: A60902; MUID:89044681; PMID:3142086
A; Contents: amnotation; novel forms of expressed recombinant t.PA
R; Harris, T.J.R.; Patel, T.; Marston, F.A.O.; Little, S.; Emtage, J.S.; Opdenakker, G.; Mol. Biol. Med. 3, 279-292, 1986
A; Title: Cloning of CDNA coding for human tissue-type plasminogen activator and its expra A; Reference number: A54645; MUID:86284200; PMID:3090401
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A; Contents: annotation; fibrin binding site R; Dodd, I.; Nunn. R · Paki---
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A,Cross-references: GDB:119892; OMIM:234000
*Map position: 5494-5qer
A;Introns: 19/3; 39/1; 72/2; 96/1; 133/1; 177/1; 212/1; 267/2; 340/1; 417/2; 463/1; 511/1.
C;Complex: factor XII, prekallikrein, and HMW kininogen form a complex bound to anionic f
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C,Superfamily: tryosin related polyprotein; trypsin homology
                                                                                                                                                                                                                                                              Typethway: blood coagulation, fibrinolysis

Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
Superfamily: load coagulation; fibrinolysis; glycoptotein; hydrolase; kringle; plasma; set;
1-13/Domain: signal sequence #status predicted <SIG>
120-372,773-615/Product: coagulation factor XIIa, alpha form #status experimental <AI2>
130-372,773-615/Product: coagulation factor XIIa, alpha form #status experimental <AI2>
1318-130/Domain: EdF homology <EG1>
1318-230/Domain: EGF homology <EG2>
1317-255/Domain: EGF homology <EG2>
1217-255/Domain: kringle homology <EG2>
1234-356,373-656/Product: coagulation factor XIIa, beta form #status experimental <B12>
133-409/Domain: trypsin homology <ERX>
133-610,000-119,121-130,135-163,161-170,178-189,183-198,200-209,217-295,238-277,266-290,
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R; Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
Bubmitted to the EMBL Data Library, March 1998
A; Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from Xer
A; Reference number: Z20829
                                                                                                                                                                                                       A; Description: factor XIIa catalyzes the proteolytic activation of plasminogen, plasma p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;109/Binding site: carbohydrate (Thr) (covalent) #status experimental F;249,433/Binding site: carbohydrate (Asn) (covalent) #status experimental F;299,305,328,329,337/Binding site: carbohydrate (Thr) (covalent) #status predicted F;308/Binding site: carbohydrate (Ser) (covalent) #status predicted F;412,461,563/Active site: His, Asp, Ser #status predicted
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C,Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
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A;Molecule type: mRNA
A;Residues: 1-1524 <YAN>
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A, Residues: 14-332, 'S', 334-615 <CO2>
A, Wolecule type: mRNA
A, Residues: 14-32, 'S', 334-615 <CO2>
A, Wolecule type: mRNA
A, Residues: 14-32, 'S', 334-615 <CO2>
A, Cross-references: GB: MI1723; NID: G180358; PIDN: AAA51986.1; PID: G180359
B, Godemsistry 25, 1552-1528; J1986
A, Title: Characterization of a CDNA coding for human factor XII (Hageman factor).
A, Reference number: A25191; MUID: 86216049; PMID: 3011063
A, Molecule type: mRNA
A, Residues: GB: MI3147; NID: G180360; PIDN: AAA70224.1; PID: G180361
A, Wollecule type: mRNA
A, Residues: GB: MI3147; NID: G180360; PIDN: AAA70224.1; PID: G180361
A, Fitle: Amino acid sequence of the heavy chain of human alpha-factor XIIa (activated Ha A, Rocession: A2248; MUID: 85182674; PMID: 386654
A, Rocession: A2248; MUID: B5182674; PMID: 386654
A, Rocession: A2248; MUID: B324-10933, 1983
A, Fitle: Amino acid sequence of human beta-factor XIIa.
A, Wollecule type: protein
A, Rocession: A21037; MUID: 33291041; PMID: 6604055
A, Residues: 354-3621373-615 < FOUS
A, Title: Amino acid sequence of human beta-factor MNW.
J. Biol. Chem. 267, 5102-5107, 1992
A, Title: O-linked fucose is present in the first epidermal growth factor domain of facto A, Reference number: A4606; MUID: 32184750; PMID: 544894
A, Concente: annotation; carbohydrate binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coagulation factor XIIa (EC 3.4.21.38) precursor [validated] - human
NiAlternate names: Hageman factor (activated)
C;Species: Homo sapiens (man)
C;Date: 27-Nov-1985 Hsequence revision 30-Jun-1991 #text change 09-Jul-2004
C;Accession: A29411; A26814; A00930; A25191; A22248; A21037
C;Accession: A29411; A26814; A00930; A25191; A22248; A21037
A;Col., D.E.; MacGillivray, R.T.A.
J. Biol. Chem. 262, 13662-13673, 1987
A;Title: Characterization of the human blood coagulation factor XII gene. Intron/exon ge
A;Reference number: A29411; MUID:88007593; PMID:2888762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 4-615 <TRL>
A; Residues: 4-615 <TRL>
A; Ccol, D. B.; Edgell, C. J. S.; Louie, G. V.; Zoller, M. J.; Brayer, G. D.; MacGillivray, R. T.
B; Cool, D. E.; Edgell, C. J. S.; Louie, G. V.; Zoller, M. J.; Brayer, G. D.; MacGillivray, R. T.
J. Biol. Chem. 260, 13666-13676, 1985
A; Title: Characterization of human blood coagulation factor XII cDNA. Prediction of the
A; Reference number: A00930; MUID: 86033830; PMID: 3877053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-615 <COO>
A; Cross-references: UNIPROT: P00748; GB:M17466; GB:J02807; NID:g180355; PIDN: AABS9490.1;
A; Cross-references: UNIPROT: P00748; GB:M17466; GB:J02807; NID:g180355; PIDN: AABS9490.1;
B; Tripodi, M.; Citarella, F.; Guida, S.; Galeffi, P.; Fantoni, A.; Cortese, R.
Nucleic Acids Res. 14, 3146, 1986
A; Title: CDNA sequence coding for human coagulation factor XII (Hageman).
A; Reference number: A26814; MUID: 86176794; PMID: 3754331
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Search completed: March
Job time: 70 secs
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A;Molecule type: mRNA
A;Residues: 1-191 «NIC>
A;Residues: 1-191 «NIC>
A;Cross-references: UNIPROT:P51779; EMBL:Z49058; NID:g773264; PIDN:CAA88844.1; PID:g7732
C;Superfamily: trypsin; trypsin homology
C;Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
F;1-181/Domain: trypsin homology (fragment) <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trypsin-like proteinase (EC 3.4.21.-) precursor - flesh fly (Sarcophaga bullata)
C;Species: Sarcophaga bullata
C;Species: Jo-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 865465; 865403
R;Borovsky, D.; Janssen, I.; Vanden Broeck, J.; Huybrechts, R.; Verhaert, P.; de Bondt, Bur. J. Biochem. 237, 279-287, 1996
A;Title: Molecular sequencing and modeling of Neobellieria bullata trypsin. Evidence for A;Reference number: 865403; MuID:96203936; PMID:8620885
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A;Residues: 1-254 <BOR>
A;Cross-references: UNIPROT:P51588; EMBL:X94691; NID:g1177315; PIDN:CAA64354.1; PID:g117
                   Complement factor D (EC 3.4.21.46) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: 854115
R;Nicolas, N.
submitted to the EMBL Data Library, April 1995
A;Reference number: 854115
A;Reference number: 854115
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A;Residues: 27-36 < BDW>
A;Note: 27-Leu, 35-Leu were also found
C;Superfamily: trypsin; trypsin homology
C;Superfamily: trypsin; trypsin extense proteinase
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-26/Domain: propeptide #status predicted <PRO>
F;27-254/Product: trypsin #status experimental <AMT>
F;27-274/Product: trypsin homology <FRV>
F;57-274/Domain: trypsin homology <FRV>
F;53-69,154-158,195-238,204-228/Disulfide bonds: #status predicted
F;68,113,208/Active site: His, Asp, Ser #status predicted
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-G-CGNZ_1/USFPO Spool_p/US10015385/runat_05005_173711_18178/app_query.fasta_1.1287
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Grimwood J. Gordon L.A., Olsen A.S., Terry A., Schmutz J.,

Atherr T. M., Altherr W., Balar B.,

Acrimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,

Antherr M., Altherr W., Balar B.,

Caenepeel S., Carrano A.V., Caolle C., Chan Y.M., Christensen M.,

Caenepeel S., Carrano A.V., Caolle C., Chan Y.M., Christensen M.,

Caenepeel S., Copeland A., Dalin B., Dehal P., Denys M., Detter J.C.,

Becobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,

Advin T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,

Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,

Kobayashi A., Larionov V., Leem S.-H., Loper F., Lowry S.,

Malfatti S., Martinez D., McTeady P.M., Medina C., Morgan J.,

Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,

Popkie A.P., Predki P., Ocharenko I., Pitluck S., Pollard M.,

Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustazewska A.,

Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Duchak I.,

Rubin E.M., Lucas S.M.,

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Rubin E.M., Stabbs L., Rokhsar D.S., Myers R.M.,

Rubin E.M., Lucas S. (2004)
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Vi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A., "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: Dioinformatics assessment."; Genome Res. 13:2265-2270(2003).
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GO; GO:000526; F:serine-type endopeptidase activity; NAS.

GO; GO:0004252; F:serine-type endopeptidase activity; NAS.

R GO; GO:0006508; P:proteolygis and peptidolygis; NAS.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001254; Peptidase_S1.

R PRIMTS; PR00722; CHYMOTYPEIN.

R PRIMTS; PR00722; CHYMOTYPEIN.

R PRART; SM00020; Tryp_SPC; 1.

R PROSITE; PS50240; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN HIS; 1.

R PROSITE; PS00134; TRYPSIN HIS; 1.

R Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=2;
IsoId=Q9UKRO-2; Sequence=VSP 005403;
SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
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EMBL; AF135025; AAF06065.1; --
EMBL; AF23521; AAG33365.1; --
EMBL; AX356524; AAG8888.1; --
EMBL; AC011473; AAG23258.1; --
MESOP, BOOT60; IEZX.
MEROPS; SO1.020; --
Genew; HGNC:6360; KLK12.
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Potential. Kallikrein 12. Charge relay system (By similarity).

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library, clone:2310008B01 product:similar to KALLIKREIN 12 3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (KLK-L5) (Fragment).
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STRAIN=C57BL/6J; TISSUE=Tongue;
The FANTOM Consortium,
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STRAIN=C57BL/6J; TISSUE=Tongue;
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                                                                 Mus musculus (Mouse)
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Name=Klk12;
  240
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R GO; GO:0008233; F:Peptidase activity; IEA. GO; GO:0006209; F:repptidase activity; IEA. GO; GO:0006509; P:proteolysis and peptidolysis; IEA. RILE-Pro; IPR001254; Peptidase 3.1.

R InterPro; IPR001254; Peptidase 3.1.

R InterPro; IPR0010254; Peptidase 3.1.

R PROSITE; PS00103; Trypsin. 1.

R PROSITE; PS00103; Trypsin. 1.

R PROSITE; PS00103; Trypsin. 1.

R PROSITE; PS00104; TRYPSIN. HIS; UNKNOWN_1.

W Hydrolase; Protease; Serine protease.

O SEQUENCE 111 AA; 11984 MW; 3E8BAB4295635D8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGGGCTCAGCATCTTTTTGCTCCTGTGTGTTTCTTGGGCTCAGCCAGGCAGCCACCACCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGGCACCAGCCTGCGCTGCGGGGGTGTCCTTATTGACCACAGGTGGGTCCTCACAGCG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetGlyLeuSerIlePheLeuLeuCysValLeuGlyLeuSerGlnAlaAlaThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGATTTTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluGlyThrSerLeuArgCysGlyGlyValLeuIleAspHisArgTrpValLeuThrAla
                                                                                                                                                                                                                                                                                                                                                                                            Yousef G.M., Luo L., Diamandis E.P., "Identification of novel human kallikrein-like genes on chromosome
                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male tongue cDNA, RIKEN full-length enriched
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65
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Xallikrein-like protein 5-related protein 2.
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Matches:
Conservative:
Mismatches:
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841 ATCCGGATGATCATGAGGAACAAC 864
                      241 IleArgMetIleMetArgAsnAsn 248
                                                                                                                                                                                                                                                                                                                                                                                                                                       19q13.3-q13.4.";
Anticancer Res. 79:2843-2852(1999).
                                                                                                                                 PRT;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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09 UKR2
10 09 UKR2
AC 09 UKR
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DT 01 - M
DT 01 - M
DE KAII
OC EUKA:
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Adachi J. Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Puruno M.,
A Arakawa T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Kato H.,
A Maxai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Sakai C., Saaki Y.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Pojima Y., Toya T., Yanamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
C -i - Shilaki Y., Shinagawa A., Shiraki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
C -i - Shilaki Y., Bab26143.1; -
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=C57BL/GJ; TISSUB=Tongue;

MEDLINE=C57BL/GJ; TISSUB=Tongue;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Rujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAB to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; IISSUE=Tongue;
MEDLINE=99279273; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carnino: P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ECFBL/60; TISSUE=Tongue;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTIUM;
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MGD; MG1:1916761; Klk12.
GO; GO:0004263; F:chymotrypsin activity; IEA.
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InterPro; IPR001314; Peptidase S1A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCysGlyGlyValLeuGlnGlyLeu 199
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Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matsusita A., Takahashi M.,
Matsushita M., Fujita T.;
"Origin of mannose-binding lectin-associated serine protease (WASP)-1
and MASP-3 involved in the lectin complement pathway traced back to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Hyperoartia,
Petromyzontiformes, Petromyzontidae, Lethenteron.
GO, GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001214; Peptidase S1A.
PRMT; PR00122; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS000134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN LOM; UNKNOWN 1.
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0008233; F:epeptidase activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004235; F:peptidase activity; IEA.
GO; GO:0006529; F:urypsin activity; IEA.
GO; GO:0006529; F:crypsin activity; IEA.
GO; GO:0006509; F:croteclysis and peptidolysis; IEA.
InterPro; IPR001086; Aldehyd_dehydrog.
InterPro; IPR001086; Aldehyd_dehydrog.
InterPro; IPR001081; EGF.Ca.
InterPro; IPR001081; EGF.Ca.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mannose-binding lectin associated serine protesse-1.
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Matches:
Conservative:
Mismatches:
Indels:
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J. Immunol. 170:4701-4707(2003).
-!- SIMILARITY: Belongs to peptidase family S1.
BEL; ABO89265; BAC75884.1;
-- HSSP; Q9JJS8; INTO.
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31.00
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Best Local Similarity:
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Pred. No.:
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O72T70
O97T70

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R InterPro; IPRO11361; Pept S1 Comp. Act.

R InterPro; IPR010361; Pept S1 Comp. Act.

R InterPro; IPR000436; Sushī_SCR_CCP.

R InterPro; IPR000436; Sushī_SCR_CCP.

R Pfam; PP000441; CUB; 2.

R Pfam; PP000445; EGF CA; 1.

R PRO0024; EARDOOS I TYPESIN.

R RINIS; PR00022; CUHMOTRYPSIN.

R SMART; SM00042; CUB; 2.

SMART; SM00042; CUB; 2.

SMART; SM00042; CUB; 2.

R SMART; SM00042; CUB; 2.

R SMART; SM00042; TYP BCF I.

R SMART; SM00042; TYP BCF I.

R PROSITE; PS00010; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.

R PROSITE; PS01080; CUB; 2.

R PROSITE; PS01180; CUB; 2.

R PROSITE; PS01180; CUB; 3.

R PROSITE; PS01180; CUB; 1.

R PROSITE; PS01180; CUB; 2.

R PROSITE; PS01180; CUB; 2.

R PROSITE; PS01180; EGF CA; UNKNOWN_1.

R PROSITE; PS01180; EGF CA; UNKNOWN_1.

R PROSITE; PS01181; TRYPSIN DOM; 1.

R PROSITE; PS01181; TRYPSIN LSS; UNKNOWN_1.

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; SOL1.06; ...
MGD; MGI:1920586; 1700036D21Rik.
MGD; MGI:1920586; 1700036D21Rik.
MGD; MG:0004263; F:chymocrypsin activity; IEA.
GG; GG:0008233; F:chypsin activity; IEA.
GG; GG:0006508; P:proteolysis and peptidolysis; IEA.
GG; GG:0006508; P:proteolysis and peptidolysis; IEA.
FEAM; PRO0722; CHYMOTRYPSIN.
FRINTS; PRO0722; CHYMOTRYPSIN.
SWART; SM00020; Tryp SPC; 1.
FROSITE; PS50240; TRYPSIN DOM; 1.
FROSITE; PS50240; TRYPSIN DOM; 1.
FROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 200 AA; 22135 MW; 972959E4686EF603 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mateni H., Takahashi T.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-i- SintlarITY: Belongs to peptidase family S1.
EMBL; AB047758; BaB63919.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          694 GGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            622 GlyGlnAspAlaCysGlnGlyAspSerGlyGlyProLeuVal 635
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-015-385A-193 (1-1091) x Q7ZT70 (1-681)
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14.00
100.00%
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3.92%
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine protease-like 1. Name=1700036D21Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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No.:

Q6FHW3 RESULT 6 Q6FHW3

8

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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Schamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heisteh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Caarninci P., Prange C.,
A. Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
A. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McZwan P.J., McKernan R.J., Mallek J.A., Gunazatne P.H.,
A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A. Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
M. Hilton B.K., Cimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.B.,
J
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                           MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: Belongs to peptidase family S1.
REMBL; BC034529; AR434529.1; --:
RSP; PC0746; 1BIO.
GO; GO:0006233; F:Chymotrypsin activity; IEA.
GO; GO:0006239; F:peptidase activity; IEA.
R GO; GO:0006239; F:peptidase activity; IEA.
R GO; GO:0006239; F:peptidase activity; IEA.
R GO; GO:0004295; F:rrypsin activity; IEA.
R InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR00909; Pept Ser Cys.
R Pfam; PR00089; Trypsin; 1.
R PRINTS; PR00722; CHYMOTRYPSIN.
R PRANT; SM00020; Tryp SPC; 1.
R PROSITE; PS50240; TRYPSIN DOM; 1.
R PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 235 AA; 25110 MW; 9DEF67A48D5913F6 CRC64
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-015-385A-193 (1-1091) x Q8N4E0 (1-235)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase, Protease, Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q80VS4 PRELIMINARY;
Q80VS4;
01-JUN-2003 (TEMBLrel. 24,
01-JUN-2003 (TEMBLrel. 26,
01-MAR-2004 (TEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.00
100.00%
100.00%
3.64%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                              FROM N.A.
                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Skin;
                                                                                              SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
Q80VS4
ID Q80V6
AC Q80V6
DT 01-JI
DT 01-M2
  Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S., A Meubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W., Koubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W., Koun B., Zubmitted (July 2004) to the EMBL/Genbank/DDBJ databases.

- I- SIMILARITY: Belongs to peptidase family SI.

R EMBL, CR53675; CAG38B12.1; -.

R GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:chymotrypsin activity; IEA.

R GO; GO:0006295; F:chymotrypsin activity; IEA.

R GO; GO:0006295; F:chymotrypsin activity; IEA.

R GO; GO:0006295; F:chymotrypsin activity; IEA.

R InterPro; IPR001314; Peptidase SI.

R InterPro; IPR001314; Peptidase SIA.

R InterPro; IPR001314; Peptidase SIA.

R PFOMPT; SM00020; Trypsin; I.

R RRINTS; PR00722; CHYMOTRYPSIN.

R SWART; SM00020; Trypsin; I.

R PROSITE; PS00134; TRYPSIN INS; UNKNOWN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Protease; Seri<u>n</u>e protease.
SEQUENCE    228 AA; 24423 MW; B1B9EA3B73E802C5 CRC64;
                     200
113
0
0
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113
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                                                                                                                                                                                                                                                        712 GGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGGAGTCCTT 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                           Gaps:
                                                                                                                                                                                    (1-200)
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                                                                                                                                                                                    US-10-015-385A-193 (1-1091) x Q924U6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26, DF protein (Fragment). Homo sapiens (Human).
                     0.00463
13.00
100.00$
100.00$
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13.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
Pred. No.:
Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DF protein.
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Q8N4E0;
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DB:
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RESULT 7

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Created)
Last sequence update)
Last annotation update)

243 AA.

PRT;

PRELIMINARY;

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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Nausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
An Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Stapleton M., Soarsa M.B., Bonaldo M.E., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malk J.A., Gunarance P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                     TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                01-0TM-2003 (TrEMBLrel. 24, 01-0TM-2003 (TrEMBLrel. 24, 01-MR-2004 (TrEMBLrel. 26, DF protein (Fragment). Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
   Q86VJ5,
Q86VJ5;
   HIDDEN SOCIAL SERVICE STREET S
                                                                                                                                                                                         STRAIL=NORI; TISSUE=Mammary tumor;

STRAIL=NORI; TISSUE=Mammary tumor;

MEDLINE=223825; PubMed=1247932; DOI=10.1073/pnas.242603899;

Astraubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. Buetow K.H., Schnefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schnefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Astapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                     Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=NMRI, TISSUE-Mammary tumor;
Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
-1 - SINILARITY: Belongs to peptidase family S1.
EMBL; BCO447756; AAH44756.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 AA; 26059 MW; A3F8A624DE481D36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; SOL.029; ...
MGD; MGI:2447564; KIK14.
GO; GO:0004253; F:chymotypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008235; F:trypsin activity; IEA.
GO; GO:0006296; F:trypsin activity; IEA.
InterPro; IPR001254; Peptidase SI.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR001314; Peptidase SIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN HIS; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Protease; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00089; Trypsin; 1
PRINTS; PR00722; CHYMOTRY
Klk14 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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SEQUENCE 243 AA; 25809 MW; 67F02995119490BC CRC64;
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113
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GO; GO:0008233; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR011254; Peptidase_S1.
InterPro; IPR010314; Peptidase_S1A.
InterPro; IPR090031; Peptidase_S1A.
PITTERPO; IPR0090031; Peptidase_S1A.
PFG00089; Trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   712 GGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGGAGTCCTT 750
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0722; CHYMOTRYBSIN.
SMART; SMO020; Tryp SPc; 1.
PROSITE; PSS0240; TRYPSIN DOM; 1.
PROSITE; PS00114; TRYPSIN HIS; UNKNOWN_1.
PROSITE; PS001135; TRYPSIN HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Protease; Serine protease.
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                                                     SEQUENCE FROM N.A.
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                                                                        rissum=Spleen;
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Length:
Matches:
Conservative:
Mismatches:
Indels:

13.00 100.00% 100.00% 3.64%

Best Local Similarity: Query Match: DB: Percent Similarity:

Score:

0.00454

Gaps:

TGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGGA 744

904 191

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RESULT 9

US-10-015-385A-193 (1-1091) x Q80VS4 (1-242)

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SEQUENCE FROM N.A.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Best Local Similarity:
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                                                                                               Trypsinogen.
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                                                    25-OCT-2004
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                           066PG9
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RESULT 11
              Q66PG9
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                                                                                                                                                                                                               MEDLINE-20219148; Pubmed-10753908; DOI=10.1074/jbc.275.15.11050; Matsui H., Kimura A., Yamashiki N., Moriyama A., Kaya M., Yoshida I., Takagi N., Takahashi T.;
                                                                                                                                                                                                                                                             "Molecular and biochemical characterization of a serine proteinase predominantly expressed in the medulla oblongata and cerebellar white
                                                                                                                                                                                                                                                                                                                                           STRAIN=Balb/c; TISSUE=Skin;
MEDLINE=995-62106; PubMed=10329394; DOI=10.1006/bbrc.1999.0600;
Meier N., Dear T.N., Boehm T.;
"A novel serine protease overexpressed in the hair follicles of nude
                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGJI1343120; FLEEL.

GG; GG:00055137; C:Cytcoplasm; ISS.
GG; GO:0005515; C:Cytcoplasm; ISS.
GG; GO:0005515; F:protein binding; ISS.
GG; GO:0042982; P:amyloid precuresor protein metabolism; ISS.
GG; GO:0007417; P:central nervous system development; ISS.
GG; GO:00042445; P:myloid precuresor protein metabolism; ISS.
GG; GO:0042545; P:myelination; ISS.
GG; GO:0042545; P:myelination; ISS.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR0010903; Pept_Ser_Gys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27496 MW; E20C080087139B63 CRC64;
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                                                                  Last sequence update)
Last annotation update)
(BSSP).
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                                                                                                                                                                                                                                                                                                                                                                                                    mice.";
Biochem. Biophys. Res. Commun. 258:374-378(1999)
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to peptidase family SI.
EMBL; AB015206; BAA28895.1; -.
EMBL; Y18723; CAA77269.1; -.
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Indels:
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HS; UNKNOWN 1.

PROSITE; PS00135; TRYPSIN HS; UNKNOWN 1.

Hydrolase; Protease; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-015-385A-193 (1-1091) x O88301 (1-246)
                                                                                                                                                                                                                                                                                        matter of mouse brain.";
J. Biol. Chem. 275:11050-11057(2000).
                                                       Created)
                             PRT;
                                                   01-NOV-1998 (TrEMBLrel. 08, Creat 01-NOV-1998 (TrEMBLrel. 08, Last 05-JUL-2004 (TrEMBLrel. 27, Last Brain Serine protease (BSP) (BSS) Name=Prss18; Synonyms=BSP, mbsp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB032402; BAA84544.1; -. HSSP; P00746; IFDP. MEROPS; S01.236; -. MGD; MGI:1343166; Pr8818.
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SEQUENCE FROM N.A.
STRAIN=C57BL; TISSUE=Brain;
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13.00
100.00%
100.00%
3.64%
                             PRELIMINARY;
                                                                                                                          Mus musculus (Mouse).
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Best Local Similarity:
Query Match:
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                                                                                                                                                               NCBI_TaxID=10090;
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193 CysGlnGlyAspSerGlyGlyProLeuValCysGlyGly 205

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TISSUE-Pancreas;
MEDLINE=2160773; PubMed=11742759; DOI=10.1016/S1096-4959(01)00487-0;
Suzuki T., Srivastava A.S., Kurokawa T.;
Suzuki T., Srivastava A.S., Kurokawa T.;
"CDNA cloning and phylogenetic analysis of pancreatic serine proteases from Japanese flounder, Paralichthys olivaceus.";
Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 131:63-70(2002).
-I. SIMILARITY: Belongs to peptidase family S1.
EMBI, AB029752; BAA82364.2; -.
HSSP; P00760; IEZX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Muteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                             Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Takifugu.
                                                                                                                                                                                                                                                                                                                        Roach J.C.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family Sl.
EMBL; AY661445; AAUG6120.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EB6EFDC9060F4552 CRC64;
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113
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        700 GAIGCCIGCCAGGGIGATICIGGGGGCCCCCTGGIGIGI
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001254; Peptidase S1.
InterPro; IPR001354; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR009003; Pept Ser Cys.
PEm; PR00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYBSIN.
SWART; SMO0020; Tryp Spc; 1.
PROSITE; PS00120; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DIM; I.
PROSITE; PS00135; TRYPSIN ERR; 1.
  247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 AA
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Paralichthys olivaceus (Japanese flounder)
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                                               Created)
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PRELIMINARY;
                                               (TrEMBLrel.
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Indels:

3.64%

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Percent Similarity:
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    Query Match:
DB:
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054854
                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                    QBCGR5
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
105-JUL-2004 (TrEMBLrel. 27, Last annotation update)
10-Sequent trypsin 5 precursor (EC 3.4.21.4).
10-Sepophtheirus salmonis (salmon louse).
10-Sepophtheirus salmonis (salmon louse).
10-Sepophtheirus (Copepoda; Siphonostomatoida; Caligidae; Lepeophtheirus.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro: IPR001254; Peptidase S1.
InterPro: IPR001314; Peptidase S1A.
InterPro: IPR001314; Peptidase S1A.
InterPro: IPR001314; Peptidase S1A.
InterPro: IPR001317; Peptidase S1A.
InterPro: IPR001317; Peptidase S1A.
InterPro: IPR001314; Trypsin, 1.
PRINTS; PR00122; CHYMOTRYPSIN.
SMART; SN00120; TryPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN SER; I.
Hydrolase; Protease; Serine protease.
SEQUENCE 247 AA; 26948 MW; DC486471179DDD972 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GG; GO:0004263; F:chymotrypsin activity; IEA.
GG; GO:0008233; F:chymotrypsin activity; IEA.
GG; GO:0008233; F:trypsin activity; IEA.
GG; GO:0006289; F:trypsin activity; IEA.
GG; GO:0006589; F:trypsin activity; IEA.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR00131; Peptidase_S1A.
PRINTS; PR00722; CHYMOTRYPSIN.
SNART; SM00020; Tryp_SPC; 1.
PROSITE; PS50024; TRYPSIN_DOM; 1.
PROSITE; PS50024; TRYPSIN_DOM; 1.
PROSITE; PS50024; TRYPSIN_ERR; 1.
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58C604D819043096 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
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Matches:
Conservative:
Mismatches:
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Indels:
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05-JUL-2004 (TrEMBLrel. 27, Last sec
05-JUL-2004 (TrEMBLrel. 27, Last ann
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13.00
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                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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DB:
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SEQUENCE FROM N.A.
MEDLINE=22325484; PubMed=12437987; DOI=10.1016/S0006-291X(02)02629-3; Olsson A.Y., Lundwall A.; Olsson A.Y., Lundwall A.; "Organization and evolution of the glandular kallikrein locus in Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCD; MCJ:244764; KIk14:

MCD; MCJ:2247654; KIk14:

GO; GO:0004263; F:chymotrypain activity; IEA.

GO; GO:0004203; F:peptidase activity; IEA.

GO; GO:0004203; F:peptidase activity; IEA.

GO; GO:0006508; F:trypain activity; IEA.

GO; GO:0006508; F:trypain activity; IEA.

InterPro; IPR00124; Peptidase_S1A.

InterPro; IPR00134; Peptidase_S1A.

InterPro; IPR00134; Peptidase_S1A.

InterPro; IPR00103; Peptidase_S1A.

INTERPRO; IPR00103; PEPTISIN_OF.

FRONTE; PR00125; CHYMOTRYPSIN.

SMART; SM00020; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.

HYDROJIES; PS00134; TRYPSIN HIS; UNKNOWN 1.

HYDROJIES; PS00135; TRYPSIN HIS; UNKNOWN 2.

HYDROJIES; PS00135; TRYPSIN HIS; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Adams M., Mural R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                           700 GATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGT 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250
0
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                                                                                                                    199 AspAlaCysGlnGlyAspSerGlyGlyProLeuValCys 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        706 TGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGGA 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 CysGlnGlyAspSerGlyGlyProLeuValCysGlyGly 211
                                                                                                                                                                                                                                                                                                01-WAR-2003 (TrEMBLrel. 23, Created)
(1-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Glandular kallikrein KLK14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 299:305-311(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SIMILARITY: Belongs to peptidase family Sl.
EMBL, AY152433, AAN78421.1; -.
HSSP, P00760; 1EZX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
US-10-015-385A-193 (1-1091) x Q6QX59 (1-249)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; S01.029; -
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DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
OS Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OC Rattus Natural.
OC Rattus norvegicus (Rat).
OC Rattus norvegicus (Rattus).
OC Rattus (Rattus).
OLO Rattus (Rattus).
OC Ra
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Search completed: March 5, 2005, 23:56:35 Job time: 240.5 secs

US-10-015-385A-193 (1-1091) x O54854 (1-251)

8 8

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Protein of the invention #54. WO200078961-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC18063 standard;
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4: genescap2000s:*
5: genescap2002s:*
6: genescap2003as:*
7: genescap2003bs:*
8: genescap2003bs:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description
                                                      (without alignments)
574.351 Million cell updates/sec
                                                                                                                           .....GUYTYICKYVDWIRMIMRNN 248
GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 5, 2005, 20:42:45 ; Search time 167 Seconds
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                                                                                                                                                                                                 2105692
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Human PRO1303 (UNQ669) amino acid sequence SEQ ID NO:194
WO200012708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9-MAR-2000.
(GETH ) GENENTECH INC.
(GETH MAtch 100.0%; Score 1374; DB 3;
ery Match 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 100.0%; Score 1374; DB 3; Local Similarity 100.0%; Pred. No. 5e-98;
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Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 4
                                                                                                                                                       Searched:
2105622 seds, 386760381 residues
210562 seds, 386760381 residues
210562 seds, 386760381 residues
Cotal number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Macch 100%
Listing first 1500 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO1303 protein; 248 AA.
WO20003221-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO1303 protein sequence SEQ ID NO:33. WO200053750-A1. 14-SEP-2000. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human EST encoded protein; 248 AA. WO200154477-A2.
                                                                                                                           1 MGLSIFLLLCVLGLSQAATP...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB21304 standard; protein; 248 AA.
Human KLK-LS protein #4.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB66142 standard; protein; 248 AA
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                                                                                                                                                                                                                                                                                                          A Geneseq 16Dec04:*
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geneseqp1990s:*
                                                                                       US-10-015-385A-194
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(MOUN ) MOUNT SINAI HOSPITAL.
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(GETH ) GENENTECH INC.
                                                                                                                                           BLOSUM62
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Best Local Similarity
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(HYSE-) HYSEQ INC.
                                                                                                                         Sequence:
Scoring table:
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Perfect score:
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RESULT 2
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Length 248;
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                                                                                 ABOUSJ635 Standard; protein; 248 AA.
Novel human secreted and transmembrane protein PRO1303.05202073130-A1.
                                                                                                                                                                                                                                                                                                                                                   ABO33512 standard; protein; 248 AA.
Novel human secreted and transmembrane protein PRO1303
US2003073129-A1.
17-APR-2003
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(GETH ) GENENTECH INC.
1ry Match 100.0%; Score 1374; DB 7;
                                                                                                                                      (GETH) GENENTECH INC.

(GETH) GENENTECH INC.

(GETH) ALCh

100.0%; Score 1374; DB 6;
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Pred. No. 5e-98;
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Pred. No. 5e-98;
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(GETH ) GENENTECH INC.
ry Match 100.0%; Score 1374; DB
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Pred. No. 5e-98;
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Pred. No. 5e-98;
                                                 Score 1374; DB
Pred. No. 5e-98;
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US2003054406-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD38353 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003096955-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                       ABO44488 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303
US2003044841-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD70709 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303
US2003099625-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD39786 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303
US2003083462-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD39309 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 248 AA
WO2000,000
28-DEC-2000,
(GETH ) GENENTECH INC.
100.0%;
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(GETH OGENENTECH INC.
Query Match
100.0%;
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US2003064925-A1.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                   Best Local Similarity RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                Query Match
Best Local Similarity
RESULT 7
                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 9
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Query Match
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                                                                     Query Match
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Louis (1917) 248 AA.

Louis (1917) 240.

Louis (1917) 240
                        CZ-MAY-2003.
(GETH) GENENTECH INC.
ery Match 100.0%; Score 1374; DB 7; Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE20096 standard; protein; 248 AA.

Human secreted/transmembrane protein PRO1303.

US2003092883-A1.

15-MAY-2003.

GETH ) GENENTECH INC.

100.0%; Score 1374; DB 7; Length 248; st Local Similarity 100.0%; Pred. No. 5e-98;
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(GETH ) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
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(GETH) GENENTECH INC.

ery Match

100.0%; Score 1374; DB 7;

ery Match

100.0%; Pred. No. 5e-98;
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Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 24
                                                                                                                                                                                                                             ADD38832 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003092061-A1.
15-MAY-2003.
(GETH) GENENTECH INC.
(GETH) GENENTECH 100.0%; Score 1374; DB 7;
Sty Match
the Local Similarity 100.0%; Pred. No. 5e-98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSCACATOR OF THE TOTAL OF STORE 1374; DB CETY MATCH 100.0%; Score 1374; DB CETY MATCH 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE21565 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003082628-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADF55883 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003204054-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE50007 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003082626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADF29990 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003204053-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH99187 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003065142-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD40263 standard, protein, 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003082627-A1.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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US2003096954-A1.
                                                                                                                      Query Match
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GETH ) GENENTECH INC. (GETH ) GENENTECH INC. (GETH ) GENENTECH INC. 100.0%; Score 1374; DB 8; Length 248; Pred. No. Se-98;
03-APR-2003.
(GETH ) GENENTECH INC.
ery Match 100.0%; Score 1374; DB 7; Length 248;
                                                                                                                                                                                        8; Length 248;
                                                                                                                                                                                                                                                                                                                                    DB 8; Length 248;
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(GETH ) GENENTECH INC.

LIO.0%; Score 1374; DB

ery Match

'imilarity 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                             PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB Best Local Similarity 100.0%; Pred. No. 5e-98; RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1374; DB 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1374; DB
Pred. No. 5e-98;
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Pred. No. 5e-98;
                                                                                                                                                                                      100.0%; Score 1374; DB 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1374; DB 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted/transmembrane protein PRO1303. US200321652-A1.
                                                                                           ADE96567 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003195347-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                       APE24777 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003198993-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted/transmembrane protein PRO1303.
US2003203401-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted/transmembrane protein PRO1303. US2003195334-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADH04036 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303
US2003220471-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH04513 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303
US2004005626-A1.
08-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADH03559 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303
US2003224478-A1.
                                                                                                                                                                                                                                           ADP25878 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303
US2003199675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADF29513 standard; protein; 248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE97044 standard; protein; 248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                     Best Local Similarity RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 31
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Best Local Similarity
RESULT 33
                                                                                                                                                                                                       Best Local Similarity RESULT 26
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Length 254;

Length 162;

us-10-015-385a-194.rag.spdi

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PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 45.9%; Score 630.5; DB 3; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 45.9%; Score 630.5; DB 3; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHIO/) SHIOZAKA S. (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK. (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK. 45.9%; Score 630.5; DB 3; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.9%; Score 630.5; DB 2; Length 260; 50.2%; Pred. No. 1.1e-40;
                                                                                                                              PA (MOUN) MOUNT SINAI HOSPITAL.

Query Match 74.2%; Score 1019; DB 3; Length 184;

Best Local Similarity 100.0%; Pred. No. 8.5e-71;

RESULT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB44300 standard; protein; 260 AA.
AMBH4300 standard; protein sequence SEQ ID NO:395.
WO200053756-A2.
        94.7%; Score 1301; DB 8; 100.0%; Pred. No. 2.2e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 45.9%; Score 630.5; DB 2
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 48
                                                                                                                                                                                                                                                                                                                              SCI INC.
59.0%; Score 811; DB 2;
64.1%; Pred. No. 8.1e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 630.5; DB 2
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                         AAY28642 standard; protein; 162 AA.
Human secreted protein from cDNA clone HKAFV61
WO9940183-A1.
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 64.1%; Pred. No. RESULT 45
ID AAV32852 standard; protein; 260 AA. DE Human serine protease protein sequence PN JP11225765-A.
                                                                    AAB21301 standard; protein; 184 AA.
Human KLK-L5 protein #1.
WO200053776-A2.
14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU12369 standard; protein; 260 AA.
Human PRO322 polypeptide sequence.
WO200140466-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY41744 standard; protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB21322 standard; protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO322 protein sequence. WO9946281-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 45.9%;
Best Local Similarity 50.2%;
RESULT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY51131 standard; prote.
Human neuropsin protein.
JP11318461-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1999.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-1999.
(UYAR-) UNIV ARKANSAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-2000.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-2001.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                              12-AUG-1999.
(HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-AUG-1999.
(SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 46
        Query Match
Best Local Similarity
RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human neuropsin.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
(GETH ) GENENTECH INC.
100.0%; Score 1374; DB 8; Length 248;
** 1.07.1 Similarity 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                             ADN10927 standard; protein; 248 AA.

Human kallikrein 12, marker of endocrine cancer.

WO2004029285-A2.

OW-ARP-2004.

OWOUN ) MOUNT SINAI HOSPITAL.

100.0%; Score 1374; DB 8; Length 248;

St. Local Similarity 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vuery Match
100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 37
                                                                                                                                                                                                      Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 254;
                                                                                                                                                                                      Description 100.0%; Score 1374; DB 8; Best Local Similarity 100.0%; Pred. No. 5e-98; RESULT 35

ID ADN10927 standard; protein; 248 AA.

DE Human kallikrein 12, marker of endocrine cancer. PD 08-APR-22004.

PD 08-APR-22004.

PD 08-APR-22004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB21303 standard; protein; 254 AA.

Human KLK-L5 protein #3.

W0200033776-A2.

H4-SEP-2000.

WOUNT SINAI HOSPITAL.

BY MAtch

St. Local Similarity 100.0%; Pred. No. 2.2e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-2003.

(MILL-) MILLENNIUM PHARM INC.

(MILL-) MILLENNIUM 99.5%; Score 1367; DB 6;

ery Match 99.6%; Pred. No. 1.7e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.7%; Score 1301; DB 5; 100.0%; Pred. No. 2.2e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.7%; Score 1301; DB 8; 100.0%; Pred. No. 2.2e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN10926 standard; protein; 254 AA.
Human kallikrein 12, marker of endocrine cancer.
WO2004029285-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ery Match 100.0%; Score 1374; DB ery Match 100.0%; Score 1374; DB ery Match 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                       ...... standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2004073015-A1.
                                                                                           ADH61514 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303
US2004014130-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP56174 standard; protein; 254 AA.
Human PRO protein sequence SEQ ID NO:2150.
WAZV-2004.
13-MAY-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human kallikrein-like protein; 248 AA.
Homan kallikrein-like protein 5 (18817).
HOSO03039475-AZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG66676 standard; protein; 254 AA.
Human novel polypeptide #11.
WO200244340-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADT94373 standard; protein; 248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOUN ) MOUNT SINAI HOSPITAL. Query Match
                                                                                                                                                       22-JAN-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-APR-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO1303 protein.
AU2003259607-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                            Best Local Similarity RESULT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-2002.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-APR-2004
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                                 Query Match
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Length 260;

DB 2; Length 260;

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19-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                      10-APR-2003
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RESULT 59
                                                                                                                                                                                                                                                                                                                                RESULT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 63
                                                                                                                                                                                                                    Score 630.5; DB 4; Length 260; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 630.5; DB 5; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 630.5; DB 6; Length 260; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                Score 630.5; DB 5; Length 260; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.9%; Score 630.5; DB 5; Length 260;
Score 630.5; DB 4; Length 260;
Pred. No. 1.1e-40;
                                                                                                          Score 630.5; DB 4; Length 260;
Pred. No. 1.1e-40;
                  Human angiogenesis-associated protein PR0322, SEQ ID NO:127. W020053753-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB95458 standard; protein; 260 AA.
Human angiogenesis related protein PRO322 SEQ ID NO: 72.
WO200208284-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human secreted and transmembrane protein PRO322. US2003032156-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 630.5; DB 5;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                            ABB64852 standard; protein; 260 AA.
Human PRO322 protein sequence SEQ ID NO:72.
WO200200690-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADI17076 standard; protein; 260 AA.
Human NOVX protein homologue SegID 612.
WO200268649-A2.
                                                                                                                                                  ABG23373 standard; protein; 260 AA.
Novel human diagnostic protein #23364.
WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                       AAU81959 standard; protein; 260 AA.
Human PRO322.
WO200109327-A2.
(G8-FEB-2001.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-2003.
(GETH) GENENTECH INC.
QUETY MATCH 45.9%;
45.9%;
                                                                                                          45.9%;
                                                                                                                                                                                                                      45.9%;
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Local Similarity 50.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAKER K P.
FERRARA N.
GERBER H.
GERLITSEN M E.
GODDARD A.
GODDAKI P J.
GURNEY A L.
HILLIAN K J.
MARSTERS S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PANJ)) PAN J.
(PAON)) PAONI N F.
(STEP, STEPHAN J F.
(WAILA)) WALLABBE C K.
(WILL) WILLIAMS P M.
(WOOD)) WOOD W I.
                                                                                                                                                                                                                                                                                                       03-JAN-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENENTECH INC.
                                                                                             (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-2002.
(CURA-) CURAGEN CORP.
       Best Local Similarity
RESULT 52
ID AAB53087 standard; pr
DE Human angiogenesis-as
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                Best Local Similarity RESULT 54
                                                                                                                    Best Local Similarity RESULT 53
                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                          11-OCT-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                       Query Match
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Query Match
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Length 260;
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                                                                                                                                                                                                                            DB 6; Length 260;
                                                                                     Length 260;
ABO25246 standard, protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003050239-A1.
                                                                                                                                                                                                                                                                              ABU72252 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6;
                                                                                    Score 630.5; DB 6;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                    Score 630.5; DB 6;
Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU84932 standard; protein; 260 AA.
Human secreted and transmembrane PRO polypeptide
US2002177553-A1.
28-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABO25038 standard; protein; 260 AA.
Human secreted/transmembrane protein (PRO) #198.
US2003036179-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABUS9848 standard; protein; 260 AA.
Novel secreted and transmembrane protein PRO322.
US2003017563-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 630.5; DB 6
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                                                                            45.9%; Score 630.5; DB 6 50.2%; Pred. No. 1.1e-40;
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14-Nov.
                                                                                                                                                                                                                                                                                                                                                                                                                   ADA05702 standard; protein; 260 AA.
Human NOV11h protein SEQ ID NO:62.
WO2003029424-A2.
                                                                                                                                     ABU81067 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003004311-A1.
02-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU66767 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003036180-A1.
                                                                                                                                                                                                                                                                                                                                                                     45.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                    13-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC
                                                                                                                                                                                                            (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 66
                                                                                Query Match
Best Local Similarity
RESULT 60
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Best Local Similarity
RESULT 65
                                                                                                                                                                                                                                       Best Local Similarity RESULT 61
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Best Local Similarity
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Best Local Similarity
RESULT 68
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us-10-015-385a-194.rag.spdi

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USZUCZ-
08-MAZ-2003.
(GETH ) GENENTECH INC.
MALCh '7-rity 50.2%;
 Human PRO polypeptide #198.
US2003087350-A1.
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                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                   Length 260;
                                                                                                                                                                                                                                                                                                                                                     Score 630.5; DB 6; Length 260;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                  ADA45915 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003022328-A1.
                                                                                                                                ABU67043 standard; protein; 260 AA.
Human secreted/transmembrane, PRO, protein SEQ ID 396.
US2003032155-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMASSA14 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US203082111-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB19404 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003068796-A1.
10-APR-2003.
(GETH ) GENENTECH INC.
                                                                                   Score 630.5; DB 6;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 630.5; DB 6;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
ABU80399 standard; protein; 260 AA.
Human secreted/transmembrane protein PRO322.
US2003004102-A1.
                                                                                                                                                                                                                                                                                                                                                                                                       protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB27945 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003082704-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB15988 standard; protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA61619 standard; protein; 260 AA
                                                                                                                                                                 US200302.
13-FEB-2003.
(GETH) GENENTECH INC.
45.9%; S
                               US2003003,
02-07M-2003,
(GETH ) GENENTECH INC.
45.9%;
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 50.2%;
RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA18996 standard; protein; Human PRO polypeptide #198. US20003054517.Al. C20-MAR-2003 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.2%;
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Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                    ADA76346 standard; protein;
Human PRO polypeptide #198.
US2003073212-A1.
                                                                                                                                                                                                                                                                                                                    30-JAN-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                             Query Match
Best Local Similarity
RESULT 69
                                                                                                                                                                                                                                 Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
US2003049816-A1.
                                                                                                                                                                                                                      Query Match
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ID ADA61
DE Homo
PN US200
PD 13-MP
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Length 260;
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Pred. No. 1.1e-40;
 Length 260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                ADA85872 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003082693-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human secreted and transmembrane protein PRO322. US2003087345-A1.
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Novel human secreted and transmembrane protein PRO322.
 Score 630.5; DB 6;
Pred. No. 1.1e-40;
                                                                                                                          Score 630.5; DB 6;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                       45.9%; Score 630.5; DB 6; 50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                           ADA47774 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003073215-A1.
                                                                                                                                                                       ADA67569 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003068795-A1.
                                                                                                                                                                                                                                                                                                    ADB30576 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003068794-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB16729 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003087349-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 AA
                                                                              PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.9%;
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Human PRO polypeptide #198.
US2003082763-A1.
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Human PRO polypeptide #198.
US2003082705-A1.
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Best Local Similarity 5
RESULT 84
ID ADA87527 stand?
DE Novel humar
PN US20030.
PD 08-
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                      10-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Query Match
Best Local Similarity
RESULT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 83
                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 80
                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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ADA75794 standard; protein; 260 AA.
Human PRO polypeptide #198.
01-MXY-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 17-APR-2003.

PA (GETH ) GENENTECH INC.

QUETY MATCh 45.9%;

Best Local Similarity 50.2%;

RESULT 100
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                                                                                                                                                                                                                                                            24-APR-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                           10-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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               GENENTECH INC
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                                Query Match
Best Local Similarity
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RESULT 103
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RESULT 102
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20-MAR-2003
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                                                              RESULT 96
                                                                                                                                                                                                                                                                                                             Score 630.5; DB 6; Length 260;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                 DB 6; Length 260;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABO19701 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003050240-A1.
13-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                             Novel human secreted and transmembrane protein PRO322.
USJ003073211-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABO43346 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003044945-A1.
                                                                                                                                                                                                                            ADA24934 standard, protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003050241-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB19956 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003082691-A1.
                                                                                                                                                                                Score 630.5; DB 6;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA12595 standard; protein; 260 AA.
Human secreted/transmembrane polypeptide PRO322.
US2003055216-A1.
                                             Score 630.5; DB 6
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB13268 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003082710-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                   Human PRO polypeptide #198. US2003087351-Al. (APMY-2003)
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24-APR-2003.
(GETH ) GENENTECH INC.
Match '7-rity 50.2%;
                                               45.9%;
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RESULT 88
                                                                                                                                                                                                                                                                                                             45.9%;
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RESULT 93
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(GETH ) GENENTECH INC.
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                                 GENENTECH INC.
                                                           Best Local Similarity
RESULT 87
ID ADB14884 standard, pi
DE Human PRO polypeptide
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 90
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 US2003082694-A1.
                01-MAY-2003
(GETH ) GEN
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Best Local Si
RESULT 89
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y Match 45.9%; Score 630.5; DB 6; Length 260; Local Similarity 50.2%; Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Length 260;
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Pred. No. 1.1e-40;
Length 260;
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Novel human secreted and transmembrane protein PRO322.
US2003082695-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA84768 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003082708-A1.
45.9%; Score 630.5; DB 6; 50.2%; Pred. No. 1.1e-40;
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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US2003077713-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA80552 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003082761-A1.
                                                           ADA74522 standard, protein, 260 AA.
Human PRO polypeptide #198.
US2003068798-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA82279 standard, protein, 260 AA.
Human PRO polypeptide #198.
US2003082701-A1.
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Human PRO polypeptide #198.
US2003073216-A1.
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Human.PRO polypeptide #198.
US2003073214-A1.
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Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
     Length 260;
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Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secreted and transmembrane polypeptide #60.13-M03049633-A1.
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Novel human secreted and transmembrane protein PRO322.
US2003082765-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jan 2007 9 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003082700-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Japase Standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003082709-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA46467 standard; protein; 260 AA. Novel human secreted and transmembrane protein PRO322
   45.9%; Score 630.5; DB 6; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                          Score 630.5; DB 6;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                    ADA95980 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003082759-A1.
(GETH ) GENENTECH INC.
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1052003077710-A1.
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Human PRO polypeptide #198.
US2003068797-A1.
                                                                                                                                                                                                   260 AA
                                                                                                                                             45.9%;
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                                                                                                                                                                                           Human PRO polypeptide #198. US2003082760-Al.
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Best Local Similarity 50.2%;
RESULT 120
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 119
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   Query Match
Best Local Similarity
RESULT 114
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                                                                                                                                                                                RESULT 115
ID ADB26289 standard;
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20-MAR-2003.
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                  Score 630.5; DB 6; Length 260;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                                                              ADB25315 standard; protein; 260 AA.
Human PRO polypeptide SEQ ID NO 396
US2003077715-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB24203 standard; protein; 260 AA. Human PRO polypeptide SEQ ID NO 396 US2003077714-A1.
                                                             Human PRO polypeptide #198, US2003073210-A1.
                                                                                                                                                                                                                                                                                                                                                          ADA33491 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003077721-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 260 AA.
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Human PRO polypeptide #198.
US2003082702-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID ADB2641 standard; protein; 26
DE Human PRO polypeptide #198.
PN US203092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
QUERY MATCh
Best Local Similarity 50.2%; P1
RESULT 109
              Best Local Similarity 50.2%;
RESULT 105
                                                                                                                                                            Query Match
Best Local Similarity 50.2%;
RESULT 106
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Best Local Similarity 50.2%;
RESULT 107
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Best Local Similarity 50.2%;
RESULT 108
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Best Local Similarity 50.2%;
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Human PRO polypeptide #198.
US2003096386-A1.
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US2003082690-Al.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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US2003049817-A1.
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08-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                           (GETH ) GENENTECH INC.
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                                    GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                               Best Local Similarity RESULT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 138
 US2003077712-A1.
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                    24-APR-2003
                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                    Query Match
                                                                                                       Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADABB631 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003073213-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB22326 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003087344-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 630.5; DB 7;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                Score 630.5; DB 7
Pred. No. 1.1e-40;
                ADB28497 standard; protein; 260 AA. Human PRO Polypeptide #198. US2003082699-A1. O1-MAY-2003. (GETH ) GENENTECH INC. 45 9%; Score 63 User Local Similarity 50.2%; Pred. Nc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB23651 standard; protein; 260 AA.
Human PRO polypeptide SEQ ID NO 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO polypeptide #198.
10S2003077711-A1.
                                                                                                                                                                                                                                                                                                 ADA77001 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003059909-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB27393 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003022239-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA67017 standard, protein, 260 AA.
Human PRO polypeptide #198.
US2003068793-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 260 AA.
                                                                                                                                                            protein; 260 AA
                                                                                                                                                                                               US20050.
01-MAY-2003.
(GETH ) GENENTECH INC.
MATCh .-1 arity 50.2%;
                                                                                                                                                                                                                                                                                                                                    US2003022.
27-MMR-2003.
(GETH ) GENENTECH INC.
11-ch 12-14: 45.9%;
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Query March
Best Local Similarity 50.2%;
RESULT 127
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Local Similarity 50.2%;
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Best Local Similarity 50.2%;
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US2003082686-A1.
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US2003082706-A1.
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(GETH ) GENENTECH INC.
RESULT 123

ID ADB28497 standard; p
DE Human PRO polypeptid
PN US200308269-A1.
PD 01-WAY-2003.
PA (GETH ) GENENTECH IN
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                                                                                                                    Best Local Similarity RESULT 124
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                            ADB29049 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-2003.
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                                                                                                         Query Match
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Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                           Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.9%; Score 630.5; DB 7; Length 260; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.9%; Score 630.5; DB 7; Length 260; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                             Aubsie88 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003082766-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB30136 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087347-A1.
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Novel human secreted and transmembrane protein PRO322.
US2003082764-A1.
                                                                 ADA92373 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003082712-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB66608 standard, protein; 260 AA.
Abbed human secreted and transmembrane protein PRO322 US2003082689-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 630.5; DB 7;
Pred. No. 1.1e-40;
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27-DEC-2002.
(EOSB-) EOS BIOTECHNOLOGY INC.
(EOSB-) EOS BIOTECHNOLOGY INC.
ery Match 45.9%; Score 630.5; DB 7
ery Match 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 630.5; DB 7
Pred. No. 1.1e-40;
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                                                                                                                                                                                                                          RESULT 134
ID ADB15436 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087352-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADBB9688 standard, protein, 260 AA.
Human PRO polypeptide #198.
US2003082698-A1.
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                                                                                                                                                                                                                                                                                                                                                                45.9%;
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PA (GETH) GENENTECH INC.

QUETY MATCh

BEST Local Similarity 50.2%;

RESULT 136
  45.9%;
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Best Local Similarity 50.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB90420 standard; protein;
Human PRO polypeptide #198.
US2003082762-A1.
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Length 260;

Length 260;

Length 260;

DB 7;

Length 260;

7;

Length 260;

Length 260;

DB 7;

Length 260;

DB 7;

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45.9%; Score 630.5; DB 7; Length 260; 50.2%; Pred. No. 1.1e-40;
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                     45.9%; Score 630.5; DB 7; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                       Score 630.5; DB 7;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                            ADC44043 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003054986-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC66867 standard; protein; 260 AA.
Aman secreted/transmembrane protein, PRO322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC61803 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003049684-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC68991 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003064407-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC63051 standard, protein, 260 AA.
Human secreted/transmembrane protein, PR0322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted/transmembrane protein, PRO322. US2003054405-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC68116 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003069178-A1.
                                                                            ADB36169 standard; protein; 260 AA. Human PRO polypeptide SEQ ID NO 396. US2003077720-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC63767 standard; protein; 260 AA
                                                                                                                                                                     45.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
 (GETH ) GENENTECH INC.
                                                                                                                                    24-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 156
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Best Local Similarity
RESULT 153
 PA (GETH ) GENENTECH IN
Query Match
Best Local Similarity
RESULT 151
                                                                                                                                                                                       Best Local Similarity
RESULT 152
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Best Local Similarity
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Best Local Similarity
RESULT 159
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                                   Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 45.9%; Score 630.5; DB 7; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 149
                                                                                                                                                                                         Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D ADB77356 standard; protein; 260 AA.

E Novel human secreted and transmembrane protein PR0322.

N US2003082656-A1.

D 01-MAY-2003.

A (GEMAY-2003.

Query Match
                                                                                                                                                                                                                                          ADB47144 standard; protein; 260 AA. Novel human secreted and transmembrane protein PRO322. US2003082687-A1.
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(GETH ) GENENTECH INC.
(ery Match 45.9%; Score 630.5; DB 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB35617 standard; protein; 260 AA.
Human PRO polypeptide SEQ ID NO 396.
US2003077719-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO polypeptide SEQ ID NO 396.
US200307716-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB35065 standard; protein; 260 AA.
Human PRO polypeptide SEQ ID NO 396.
US2003077718-A1.
24-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AbB76617 standard; protein; 260 AA.
Human PRO polypeptide #60.
US2003083248-A1.
                                                                                       ADB73901 standard; protein; 260 AA
Human PRO polypeptide #60.
US2003045462-A1.
                                                                                                                                                                                                                                                                                                                                                                                                protein; 260 AA.
                               Best Local Similarity 50.2%;
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Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                       45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
QUETY MATCH 45.9%;
Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.9%;
                                                                                                                                                                                                                                                                                                                                                                                            ADB86751 standard; protein;
Human PRO polypeptide #198.
US2003082697-A1.
                                                                                                                                              06-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                  01-MAY-2003.
(GETH ) GENENTECH INC.
01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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50.2%; Pred. No. 1.1e-40;

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Best Local Similarity RESULT 169
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(GETH ) GENENTECH INC.
45.9%; Score 630.5; DB 7; Length 260;
 Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
                                                                                                                                          Length 260;
                                                                                                                                                                                                                                                                                DB 7; Length 260;
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Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Length 260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC52970 standard; protein; 260 AA.
Novel human secreted and transmembrane protein Seg ID396
US2003087365-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC57324 standard, protein; 260 AA.
Novel human secreted and transmembrane protein Seg ID396.
US2003087366-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human secreted and transmembrane protein PRO322. US2003092106-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUC/1984 Standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003092107-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC59963 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003092105-A1.
                                                                                                                                          Score 630.5; DB 7;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 630.5; DB 7;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                  ADC41436 standard; protein; 260 AA.
Human secreted/transmembrane protein, PR0322.
US2003072745-A1.
17-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                     ADCG7491 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003073131-A1.
                                                                                                                                                                                                                                                                                                                                ADC62427 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003073624-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC42060 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003104998-A1.
                                                                                                                                                                                                                           US20030,2003,
17-APR-2003,
(GETH ) GENENTECH INC.
45.9%; St
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-2003.
) GENENTECH INC.
45.9%; Sr
     45.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                        Query Match
Best Local Similarity
RESULT 161
ID ADC67491 standard, pi
DE Human secreted/transf
PN US2003073131-41.
PD 17-ARR-2003.
PA (GETH ) GENENTECH IN
 Query Match
Best Local Similarity
RESULT 160
                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 162
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DB 7; Length 260;
                                                                                                                                                                                                                            Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human secreted and transmembrane protein Seq ID396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC59999 standard; protein; 260 AA.
Novel human secreted and transmembrane protein Seg ID396.
US2003087359-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC55977 standard, protein, 260 AA.
Novel human secreted and transmembrane protein Seg ID396.
US2003087360-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC56547 standard; protein; 260 AA.
Novel human secreted and transmembrane protein Seg ID396.
US2003087346-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC54615 standard; protein; 260 AA.
Novel human secreted and transmembrane protein Seg ID396
US2003087363-A1.
ADC60515 standard; protein; 260 AA. Novel human secreted and transmembrane protein PRO322. US2003087367-A1.
                                                                                                                                        ADC50990 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087361-A1.
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Novel human secreted and transmembrane protein PRO322
US2003092104-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 630.5; DB 7;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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                                                                                      45.9%; Score 630.5; DB 7 50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                     Human PRO polypeptide #198.
US2003087362-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                    08-MAY-2003.
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 177
                                                                                                      Best Local Similarity
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Best Local Similarity
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RESULT 171
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ADC47969 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003194771-A1.
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                                                      16-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                 Query Match
Best Local Similarity
RESULT 188
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Best Local Similarity
RESULT 192
                                                                                                                                                                                                                                        Best Local Similarity
RESULT 189
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     ADD09498 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2003
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                                                                                                                                                                                                                                            Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
                                                                                                      Length 260;
                                                                                                                                                                                                                                                                                                                                                                                   Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 260;
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Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.9%; Score 630.5; DB 7; Length 260; 50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
          ADC90213 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087348-A1.
08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human secreted and transmembrane protein PRO322. US2003087354-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human secreted and transmembrane protein PRO322. US-1889.
                                                                                                   Score 630.5; DB 7;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 630.5; DB 7;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Human secreted/transmembrane PRO polypeptide #36
US2003105011-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD09100 standard; protein; 260 AA.
Human kallikrein 8 protein SEQ ID NO:2.
WO2003085404-A1.
                                                                                                                                                                                                                                                                                              ADC48521 standard, protein, 260 AA.
Human PRO polypeptide #198.
US2003194773-A1.
                                                                                                                                                         protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD10050 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003194776-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDI1088 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003194774-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003101.
05-JUN-2003.
(GETH ) GENENTECH INC.
45.9%; SC
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(MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                     45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 45.9%;
Local Similarity 50.2%;
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Local Similarity 50.2%;
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Best Local Similarity 50.2%;
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Best Local Similarity 50.2%;
                                                                                                                                                                       Human PRO polypeptide #198.
US2003194770-A1.
                                                                                                                                                                                                          16-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                    (GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 187
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Best Local Similarity
RESULT 185
                                                                                                                     Best Local Similarity
                                                                                                                                                       ADC69632 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                      Query Match
RESULT 178
ID ADC902
DE Novel
PN US2003
PD 08-MAY
                                                                                                                                                                                                                                                                                RESULT 180
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Query Match 45.9%; Score 630.5; DB 7; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 260;
 Length 260;
                                                                                                                                               Length 260;
                                                                                                                                                                                                                                                                                              DB 7; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 260;
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                                                  ADC80029 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087358-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD53642 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003203437-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD41211 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003203438-A1.
45.9%; Score 630.5; DB 7; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                             45.9%; Score 630.5; DB 7; 50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7;
                                                                                                                                                                                                 ADD11321 standard; protein; 260 AA.
Human secreted/transmembrane PRO polypeptide #36.
US2003105013-A1.
05-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD37114 standard; protein; 260 AA.
Human secreted/transmembrane PRO polypeptide #36.
US2003105012-A1.
                                                                                                                                                                                                                                                                US-UUM-200..
(GETH) GENENTECH INC.
ry Match Gimilarity 50.2%; Score 630.5; DB 7;
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Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 630.5; DB 7
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO polypeptide #198.
US2003194792-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD52350 standard, protein; 260 AA.
Human PRO polypeptide #198.
US2003194769-A1.
                                                                                                                                                                                                                                                                                                                                                  protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       45.9%;
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RESULT 194
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US2003194775-A1.
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PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                         08-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                        16-OCT-2003. (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                        Query Match
Best Local Similarity
RESULT 207
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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RESULT 209
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      US2003194765-A1.
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(GETH ) GEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
                                                                     Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
                                                                                                                                                                                                           7; Length 260;
                                                                                                                                                                                                                                                                                                                                           Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Length 260;
Human tumour antigen derived gene-14 (TADG-14) protein.
US2002037581-A1.
28-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE32337 standard; protein; 260 AA. Novel human secreted and transmembrane protein PRO322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD54213 standard, protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003203432-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 630.5; DB 7 Pred. No. 1.1e-40;
                                                                                                                                                                                                           Score 630.5; DB 7
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE49429 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003096744-A1.
                                                                                                                                                                                                                                                                                                                                                                                          ADD02031 standard, protein, 260 AA.
Human PRO polypeptide #198.
US2003203430-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDO2530 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199030-A1.
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US2003199055-A1.
                                                                                                                      ADD51798 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003194779-A1.
                                                                                                                                                                                                                                                             protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 260 AA
                                                                                                                                                                                                                                                                                              US20052.
30-007-2003.
(GETH ) GENENTECH INC.
Match '12rity 50.2%;
                                                                        45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.9%;
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                                                                                                                                                              PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 50.2%;
RESULT 198
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Local Similarity 50.2%;
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Best Local Similarity 50.2%;
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US2003199057-A1.
                                                                                                                                                                                                                                                                           Human PRO polypeptide #198
US2003203431-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                         (UABR-) UAB RES FOUND.
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                                                                       Query Match
Best Local Similarity
RESULT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                           ADD02597 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                              30-OCT-2003
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Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                               DB 7; Length 260;
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   DB 7; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7; Length 260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE33441 standard; protein; 260 AA.
Novel human serreted and transmembrane protein PRO322.
US2003194767-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 630.5; DB 7;
Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 45.9%; Score 630.5; DB 7
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 214
   Score 630.5; DB 7
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                 Score 630.5; DB 7
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                 45.9%; Score 630.5; DB 7
50.2%; Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                             ADE35483 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003203434-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE16597 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003203435-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADD73212 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003203436-A1.
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US2003199053-Al.
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US2003199023-A1.
                                          Human PRO polypeptide #198.
US2003199056-A1.
                                                                                                                                                                                         ADD79493 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003203428-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE42029 standard, protein, 260 AA.
Human PRO polypeptide #198.
US2003194772-A1.
                                                                                                                                                                                                                                                                               45.9%;
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RESULT 212
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Best Local Similarity 50.2%;
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Length 260;

Length 260;

Length 260;

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Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
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                                                                                                                                                                                                   אר 260 AA.
Novel human secreted and transmembrane protein PRO322.
USSO03194766-AI.
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Best Local Similarity 50.2%; Score 630.5; DB 7;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
REGULT 231
ID ADE04708 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US20031999034-A1.
PD 23-0CT-2003.
PA (GETH ) GENENTECH INC.
                Score 630.5; DB 7;
Pred. No. 1.1e-40;
                                                                                                                                                             Score 630.5; DB 7;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE17221 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003203433-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO polypeptide #198.
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(922003199031-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO polypeptide #198.
1052003194777-Al.
                                                                                                                                                                                                                                                                                                                                                     Lucat Brandard; protein; 260 AA. Human PRO polypeptide #198.
                                                                     ADD78939 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003203429-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD89625 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199028-A1.
                45.9%;
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Best Local Similarity 50.2%;
RESULT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                         30-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
PA (GETH ) GENENTECH INC.

Query Match
Best Local Similarity 5
RESULT 224
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
SULT 228
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Best Local Similarity
RESULT 230
                                                                                                                                                                                               RESULT 225
ID ADB32889 standard; F
DE Novel human secretee
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
RESULT 232
                                                                                                                                                                                                                                                                                                              Query Match
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PA (GETH) GENENTECH INC.

Query Match

45.9%; Score 630.5; DB 7; Length 260;

Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 220
                                                                                                                                                                                  Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                 Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                           Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                    ADE33993 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003194791-A1.
16-OCT--2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD72570 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003194781-A1.
                                                                                                                                                                                                                                                                                                                                                                    Human PRO polypeptide #198. ' 1052003194768-A1.
                                                                                                                                                                                                                                 ADD80045 standard; protein; 260 AA. Human PRO polypeptide #198. US2003207417-A1. Ge-NOV-2003. (GETH.) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE19502 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199025-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE22821 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199064-A1.
23-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 221

D. ADBA91146 standard; protein; 260 AA.
DB Human PRO polypeptide #198.
PN US2003199033-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 260 AA
                                   Query Match 45.9%;
Best Local Similarity 50.2%;
                                                                                                                                                                            Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.9%;
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) 23-OCT-2003.
A (GETH ) GENENTECH INC.
Query Match 45.9%;
Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.2%; RESULT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 16-OCT-2003.

A (GETH) GENENTECH INC.

A (GETH) 45.94;

Best Local Similarity 50.24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Are 1950 standard; protein;
Human PRO polypeptide #198.
US2003199026-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD95935 standard; protein;
Human PRO polypeptide #198.
US2003199059-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2003.
(GETH ) GENENTECH INC.
16-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2003.
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 219
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Length 260;

Length 260;

50.2%; Pred. No. 1.1e-40;

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Best Local Similarity RESULT 242
                                                                                                                                                                                                                                                                                      Query
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(GETH ) GENENTECH INC.
45.9%; Score 630.5; DB 7; Length 260;
                                                                                             Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                            Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
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Novel human secreted and transmembrane protein PRO322.
US2003207381-A1.
                                                                                                                                                                                                                                                                                                                                                                                         ADG21546 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003207355-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADG23187 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003207384-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 630.5; DB 7;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 630.5; DB 7;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                       ADF47235 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
182001195333-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG52992 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
20.00V-2003.
CGETH ) GENENTECH INC.
19 Aston                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG60312 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003206915-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO polypeptide #198.
US2003207372-A1.
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US2003207373-A1.
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US2003207370-A1.
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06-NOV-2003.
(GETH ) GENENTECH INC.
45.9%; S'
                                                                                             45.9%;
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Local Similarity 50.2%;
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Local Similarity 50.2%;
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Local Similarity 50.2%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
LY Match
Best Local Similarity
RESULT 233
ID ADP47235 stand>
DE Human secre'
PN US20031
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Best Local Similarity
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Best Local Similarity
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AUN39182 standard, protein; 260 AA.
Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:500.
WO2003042661-A2.
                                                                                                    DB 7; Length 260;
                                                                                                                                                                                                                                                                Length 260;
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Query Match
45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.9%; Score 630.5; DB 7; Length 260; 50.2%; Pred. No. 1.1e-40;
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ADH55878 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207379-A1.
                                                                                                                                                                                                                                                                                                                            ADI64097 standard, protein, 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207385-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADH81959 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322. US2003207388-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADHB1407 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207377-A1.
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Novel human secreted and transmembrane protein PRO322.
US2003087355-A1.
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Novel human secreted and transmembrane protein PRO322.
US2003087353-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADNI6604 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087385-A1.
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                                                                                                                                                                                                                                                                  Score 630.5; DB 7;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7;
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 249
                                                                                                  45.9%; Score 630.5; DB 7 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 630.5; DB 7
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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                                                                                                                                                              ADIG1072 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003077700-A1.
                                                                                                                                                                                                                                                                  45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  45.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                 (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
RESULT 250
                                                                                                                 Best Local Similarity RESULT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 244
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                                                             06-NOV-2003
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                                                                                                                                                                                                                                                                    Query Match
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23-OCT-2003
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                       BBBBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                vuery Match
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.9%; Score 630.5; DB 7; Length 260; 50.2%; Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                                                               Length 260;
                                               ADNI5423 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087356-A1.
                                                                                                                                                                                                                                                                                                       ADNI4871 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087357-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Movel human secreted and transmembrane protein PRO322.
US2032207387-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADI65046 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207386-AI.
USCOW-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC81133 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003092115-A1.
                                                                                                                                                                                                            Score 630.5; DB 7;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO polypeptide #198. US200302113-A1.
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Human PRO polypeptide #198.
US2003211571-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 AA
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...ard; protein,
...an Secreted and tr.
...an GETH ) GENENTECH INC.
...an GETH ) GENENTECH INC.
...an GETH ) GENENTECH INC.
...an GENENT 252
...an Secreted and Secreted 
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50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.2%;
RESULT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 50.2%;
RESULT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD76581 standard; protein;
Human PRO polypeptide #198.
US2003100087-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 45.9%;
Best Local Similarity 50.2%;
RESULT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 45.9%;
Local Similarity 50.2%;
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US2003203440-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADD86349 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Best Local Similarity 50.2%; Score 630.5; DB 8; Length 260; RESULT 269
ID ADBRORAN ALCA
                                                                                       8; Length 260;
                                                                                                                                                                                                                                                                                                                                                                             45.9%; Score 630.5; DB 8; Length 260; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 45.9%; Score 630.5; DB 8; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 267 ID ADE18398 standard; protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 260;
                                                                                                                                                                                                                                 Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 630.5; DB 8;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.9%; Score 630.5; DB 8; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 8;
                                                                                                                                                                                                                               45.9%; Score 630.5; DB 8; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.9%; Score 630.5; DB 8; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                      ADE41322 standard; protein; 260 AA.
Human secreted/transmembrane PRO polypeptide #36
US200140497-A1.
29-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 630.5; DB 8
Pred. No. 1.1e-40;
                                                                                       Score 630.5; DB 8
Pred. No. 1.1e-40;
ADE48729 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003104536-A1.
                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.2%; Pred. No RESULT 262
DE Human PRO polypeptide #198.
PM US2003022108-A1.
PM (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                               ADE23925 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003092110-A1.
15-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE24568 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003092111-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD87393 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003203439-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.9%;
                                                                                   Query Match
Best Local Similarity 50.2%;
RESULT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO polypeptide #198. US2003194794-Al.
                                                                                                                                                                                                                                                                                                                                                                                             50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE88707 standard; protein;
Human PRO polypeptide #198.
US2003199054-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE89259 standard; protein;
Human PRO polypeptide #198.
US2003199062-A1.
                                                  05-JUN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-OCT-2003,
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 265
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 264
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Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.9%; Score 630.5; DB 8; Length 260; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 260;
                                                                                                                                                                                                          Length 260;
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                                                                                                                                                                                                                                                                                            PD 30-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match

45.9%; Score 630.5; DB 8;

Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 282
ID ADF27180 standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PRO322.
PN US2003199436-A1.
                                                                                                                                                                                                            Score 630.5; DB 8;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 630.5; DB 8 Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.9%; Score 630.5; DB 8 50.2%; Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                           مدون الم 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003199021-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apr23730 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003203402-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                         ADP24354 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003204055-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADF33713 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003194780-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADF27816 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003199437-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Auris 4970 standard; protein; 260 AA. Human PRO polypeptide #198. US2003199029-A1. 23-CGT-2003. GCTH J GENENTECH INC.
ADE95279 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199052-A1.
                                                                                                                           ADE93389 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199060-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE92285 standard; protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 45.9%;
Best Local Similarity 50.2%;
RESULT 284
                                                                              45.9%;
                                                                                                                                                                                                        Query Match
Best Local Similarity 50.2%;
RESULT 277
                                                                                                                                                                          23-OCT-2003.
(GETH ) GENENTECH INC.
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                                              23-OCT-2003.
(GETH ) GENENTECH INC.
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                                                                                          Best Local Similarity RESULT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 279
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Best Local Similarity
RESULT 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                Query Match
   BBBBB
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.9%; Score 630.5; DB 8; Length 260; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 45.9%; Score 630.5; DB 8; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADF61470 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003195345-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               אס אס איניביאים brotein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003195148-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF41162 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003198994-A1.
 Human secreted/transmembrane protein, PRO322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PRO polypeptide #198.
032003199027-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE91138 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199061-A1.
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PA (GETH) GENENTECH INC.
Ouery Match 45.9%;
Best Local Similarity 50.2%;
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Best Local Similarity 50.2%;
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Best Local Similarity 50.2%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                             GERBER H.
GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-2003. (GETH ) GENENTECH INC.
                                             ASHKENAZI A J.
                                                            BAKER K P.
BOTSTEIN D.
DESNOYERS L.
EATON D L.
FERRARA N.
FILVAROFF E.
FONG S.
                                                                                                                                                                                                                                                                                                                                                      PAN J.
PAONI N F.
ROY M A.
SHELTON D L.
STEWART T A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (TUMA/) TUMAS D.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
                                                                                                                                                                                                                                           GODOWSKI P J. GIRMALDI J C.
                                                                                                                                                                                                                                                                                                             KLJAVIN I J
                                                                                                                                                                                                                                                                                                                            KUO S S.
NAPIER M A.
                                                                                                                                                                                                                                                                           GURNEY A L.
HILLAN K J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                              GODDARD A.
                JS2003130181-A1.
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BOTS/)
DESN/)
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ROYM/)
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NAPI/
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US2003207352-A1
 Query Match
 Query Match
 Query Match
 Query Match
 13.NOV-2003.
(GETH) GENENTECH INC.
ery Match 45.9%; Score 630.5; DB 8; Length 260;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40;
 Length 260;
 Length 260;
 Length 260
 Length 260;
 Length 260;
 Length 260
 ADE91733 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003199058-A1.
Novel human secreted and transmembrane protein PRO322. US2003199051-A1.
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 RESULT 291

ID ADP46582 standard; protein; 260 AA.

DE Human secreted/transmembrane protein, PR0322.

PN US2003195344-A1.

PD 16-OCT-2003.

PA (GETH) GENENTECH INC.
 ADF33089 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003211091-A1.
 ADF25455 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003211092-A1.
 ADF41410 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003199435-A1.
 ADF26556 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003199674-A1.
 ADF34345 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003194410-A1.
 ADE90586 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199063-A1.
 ADG02312 standard; protein; 260 AA.
Human PRO polypeptide #198.
 Best Local Similarity 50.2%; Pre-RESUT 286
ID ADF41410 standard; pro-PN US200319947
 , GENENTECH INC.

, GENENTECH INC.

Best Local Similarity 50.2%; Pre RESULT 292
ID ADE91733 standard; pro DE Novel human Rec
 USZUCZ-2003.
23-007-2003.
(GETH) GENENTECH INC.
AECh -- 1arity 50.2%;
 45.9%;
 Match
Local Similarity 50.2%;
 Query Match
Best Local Similarity 50.2%;
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Best Local Similarity 50.2%;
 Query Match
Best Local Similarity 50.2%;
 23-OCT-2003.
(GETH) GENENTECH INC.
 13-NOV-2003.
(GETH) GENENTECH INC.
 16-OCT-2003.
(GETH) GENENTECH INC.
 23-OCT-2003.
(GETH) GENENTECH INC.
 Best Local Similarity RESULT 287
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
RESULT 285
 Query Match
 Query Match
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Length 260;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 45.9%; Score 630.5; DB 8; Length 260; 50.2%; Pred. No. 1.1e-40;
 Length 260;
 Length 260;
 Length 260;
 Length 260;
 Length 260;
 Length 260;
 ADG24291 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207426-A1.
 Novel human secreted and transmembrane protein PRO322 US2003207360-A1.
 PD 06-NOV-2003.

PA (GETH) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 8;

Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 295
 45.9%; Score 630.5; DB 8; 50.2%; Pred. No. 1.1e-40;
 45.9%; Score 630.5; DB 8; 50.2%; Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 DB 8;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 45.9%; Score 630.5; DB 8 50.2%; Pred. No. 1.1e-40;
 ADF98074 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003207422-A1.
(G6-NOV-2003.
 ADF98645 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003208055-A1.
 ADG20168 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003207376-A1.
 ADG03476 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003207351-A1.
 ADG16782 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003207359-A1.
 ADG05241 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003207375-A1.
 protein; 260 AA
 260 AA
 45.9%;
 45.9%;
 45.9%;
 Query Match
Best Local Similarity 50.2%;
RESULT 294
 Best Local Similarity 50.2%;
RESULT 300
 ADF99197 standard; protein;
Human PRO polypeptide #198.
US2003207353-A1.
 50.2%;
06-NOV-2003.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
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 06-NOV-2003.
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 06-NOV-2003.
(GETH) GENENTECH INC.
 Best Local Similarity RESULT 298
 Query Match
Best Local Similarity
RESULT 299
 Best Local Similarity RESULT 296
 Best Local Similarity SSULT 301
 ** Ouery Match
Best Local Similarity
RESULT 302
 Best Local Similarity RESULT 297
 ADG22098 standard;
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Length 260;

Length 260;

Length 260;

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DB 8; Length 260;
 DB 8; Length 260;
 ADG62041 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207428-A1.
 ADGS6929 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207364-A1.
 ADG55825 standard; protein; 260 AA.

Novel human secreted and transmembrane protein PRO322.
US2003207365-A1.
(G6-NOV-2001)
(GETH) GENENTECH INC.
 ADG07226 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003207350-A1.
 ADG07778 standard; protein; 260 AA.
Novel human serreted and transmembrane protein PRO322.
US2003207356-A1.
 ADG55273 standard; protein; 260 AA.

Novel human secreted and transmembrane protein PRO322.
US2003194778-A1.
 Novel human secreted and transmembrane protein PRO322. US2003207362-A1.
 Novel human secreted and transmembrane protein PRO322 US2003207390-A1.
 PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 312
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; \ DB 8; Pred. No. 1.1e-40;
 DB 8;
 DB 8;
 DB 8;
 Score 630.5; DB 8 Pred. No. 1.1e-40;
 45.9%; Score 630.5; DB 8 50.2%; Pred. No. 1.1e-40;
 Score 630.5; DB 8 Pred. No. 1.1e-40;
 45.9%; Score 630.5; DB 8 50.2%; Pred. No. 1.1e-40;
 Score 630.5; DB 8
Pred. No. 1.1e-40;
 45.9%; Score 630.5; DB 8 50.2%; Pred. No. 1.1e-40;
 ADG82242 standard, protein, 260 AA.
Human PRO polypeptide #198.
US2003207358-A1.
 45.9%;
 45.9%;
 45.9%;
 45.9%;
 Query Match 45.9%;
Best Local Similarity 50.2%;
RESULT 317
 06-NOV-2003.
(GETH) GENENTECH INC.
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 06-NOV-2003.
(GETH) GENENTECH INC.
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 Query Match
Best Local Similarity
 Best Local Similarity RESULT 318
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 Best Local Similarity RESULT 313
 Query Match
Best Local Similarity
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RESULT 319
 06-NOV-2003
 06-NOV-2003
 06-NOV-2003
 06-NOV-200
 Ouery Match
 Ouery Match
 Query Match
 RESULT 314
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 303
 Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40;
 Length 260;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 45.9%; Score 630.5; DB 8; Length 260; 50.2%; Pred. No. 1.1e-40;
 Length 260;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 Length 260;
 Length 260;
 Novel human secreted and transmembrane protein PRO322.06-NOV-2003.
 ADG00402 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003207424-A1.
 ADG23739 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207389-A1.
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 AUGIS572 standard; protein; 260 AA. Human PRO polypeptide #198. US2003219885-A1. 27-NOV-2003. CAP. GENENTECH INC.
 Human PRO polypeptide #198.
US2003207371-A1.
 ADG19508 standard; protein; 260 AA. Human PRO polypeptide #198.
US2003207425-A1.
 ADG13345 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003207357-Al.
 260 AA.
 ADG04028 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003207423-A1.
 45.9%;
 45.9%;
 Best Local Similarity 50.2%;
 45.9%;
 45.9%;
 ADG06155 standard; protein;
Human PRO polypeptide #198.
US2003207374-A1.
 Query Match 45.9%;
Best Local Similarity 50.2%;
 Match 45.9%;
Local Similarity 50.2%;
 06-NOV-2003.
(GETH) GENENTECH INC.
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 Local Similarity
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 Local Similarity
 06-NOV-2003
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 06-NOV-2003
 Query Match
 Query Match
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RESULT 307

Length 260;

Length 260;

Length 260;

8;

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RESULT 336
 RESULT 331
 Length 260;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 Match 45.9%; Score 630.5; DB 8; Length 260; Local Similarity 50.2%; Pred. No. 1.1e-40;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 Length 260;
 Length 260;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 Length 260;
 Length 260;
 Novel human secreted and transmembrane protein PRO322.
US2003207415-A1.
 ADDIZULY Standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207419-A1.
 ADG55858 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322 US2003207368-A1.
 ADG70951 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
 Novel human secreted and transmembrane protein PRO322. US2003207363-A1.
 ADG71503 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207421-A1.
Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB.8;
Pred. No. 1.1e-40;
 ADG50568 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003207803-A1.
 Human PRO polypeptide #198.
US2003207805-A1.
 ADH30652 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003077723-A1.
 protein; 260 AA
 US200320...
06-NOV-2003.
(GETH) GENENTECH INC.
45.9%; S'
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(GETH) GENENTECH INC.
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Local Similarity 50.2%;
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(GETH) GENENTECH INC.
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(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 24-APR-2003.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
 Best Local Similarity RESULT 328
 Query Match
Best Local Similarity
 Best Local Similarity
 ADG58033 standard;
 Best Local Similarity
 US2003207420-A1.
 06-NOV-2003.
 Query Match
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Length 260;
 Length 260;
 Length 260;
 Length 260;
 Length 260;
 Length 260;
 Length 260;
 Length 260;
 Length 260;
 Aunicos standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207378-A1.
 ADG54169 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207416-A1.
 ADG56377 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003207366-A1.
 ADG52441 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003207414-A1.
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
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 Score 630.5; DB 8;
 DB 8;
 Score 630.5; DB 8
Pred. No. 1.1e-40;
 Score 630.5; DB 8 Pred. No. 1.1e-40;
 Pred. No. 1.1e-40;
 Score 630.5; DB 8 Pred. No. 1.1e-40;
ADG49944 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003215905-A1.
(GETH) GENENTECH INC.
 Human secreted/transmembrane protein, PRO322.
US2003215908-A1.
 Human secreted/transmembrane protein, PRO322.
US203216560-A1.
 Human secreted/transmembrane protein, PRO322 US2003216305-A1.
 Human PRO polypeptide #198.
16-0003194793-A1.
 ADG51816 standard; protein; 260 AA
 260 AA
 45.9%;
 45.9%;
 45.9%;
 45.9%;
 45.9%;
 45.9%;
 45.9%;
 45.9%;
 45.9%;
 50.2%;
 protein;
 16-OCT-2003.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
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(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 20-NOV-2003.
(GETH) GENENTECH INC.
 Query Match
Best Local Similarity
RESULT 337
 Query Match
Best Local Similarity
RESULT 332
 Query Match
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Best Local Similarity
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Best Local Similarity
RESULT 333
 Best Local Similarity
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
RESULT 339
 Best Local Similarity
 ADG49320 standard;
 20-NOV-2003
 20-NOV-2003
 Query Match
 Query Match
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Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 DB 8; Length 260;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40;
 Length 260;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 Novel human secreted and transmembrane protein PRO322. US2003207429-A1.
 ADG54721 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207367-A1.
 ADG59761 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207369-A1.
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 Score 630.5; DB 8 Pred. No. 1.1e-40;
 ADG51192 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2004005312-A1.
 ADG59136 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2004005657-A1.
 Human secreted/transmembrane protein, PRO322.
US_204006219-A1.
 ADH43505 standard, protein, 260 AA.
Human PRO polypeptide #36.
US2003224984-A1.
 ADH28576 standard, protein, 260 AA.
Human PRO polypeptide #198.
US2003022331-Al.
 ADI81185 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003207361-A1.
 ADI39730 standard; protein; 260 AA.
protein; 260 AA
 US2005.2003.
06-NOV-2003.
(GETH) GENENTECH INC.
45.9%; S'
 USZUCZUZ
30-JDN-2003.
(GETH) GENENTECH INC.
*** MATCh ''1arity 50.2%;
 USZUOZZOGO OG-NOV-ZOOJ. (GETH) GENENTECH INC. 45.9%;
 45.9%;
 45.9%;
 Best Local Similarity 50.2%;
 (GETH) GENENTECH INC.
ry.Match
t Local Similarity 50.2%;
 Query Match
Best Local Similarity 50.2%;
RESULT 348
 Query Match
Best Local Similarity 50.2%;
 08-JAN-2004.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 04-DEC-2003.
(GETH) GENENTECH INC.
 08-JAN-2004.
(GETH) GENENTECH INC.
 RESULT 346
ID ADG62592 standard; p.
DE Human secreted/transi
PN US2004006219-A1.
PD 08-JAW-2004.
PA (GETH) GENENTECH IN
 Query.Match
Best Local Similarity
RESULT 341
 Best Local Similarity RESULT 342
ADG61489 standard;
 Local Similarity
 Best Local Similarity
 Local Similarity
 08-JAN-2004
 Query Match
 Query / Match
 Query Match
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.
ADH25617 standard, protein; 260 AA.
Human neurotrimin homologue related protein sequence SEQ ID NO:395.
EP1386931-A1.
 Query Match 45.9%; Score 630.5; DB 8; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 351
 Query Match 45.9%; Score 630.5; DB 8; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 352
 45.9%; Score 630.5; DB 8; Length 260; 50.2%; Pred. No. 1.1e-40;
 Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40;
 45.9%; Score 630.5; DB 8; Length 260; 50.2%; Pred. No. 1.1e-40;
 DB 8; Length 260;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 Length 260;
 Length 260,
 ADJ63607 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
26-FEB-2004.
 ADI14731 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207383-A1.
 ADG09928 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2004009548-A1.
 ADI15399 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003207382-A1.
 ADG09276 standard; protein; 260 AA.
ADG091 human secreted and transmembrane protein PRO322.
US2004009547-A1.
 ADI18326 standard, protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003207349-A1.
 Query Match 45.9%; Score 630.5; DB 8; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 349
 45.9%; Score 630.5; DB 8; 50.2%; Pred. No. 1.1e-40;
 vuery Match 45.9%; Score 630.5; DB 8
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 356
 Query Match
Best Local Similarity 50.2%; Pred.
RESULT 3554
ID AD137154 standard; protein; 260 AA.
DE Human TADG-14 protein.
PN US2003199010-A1.
 ADJ77502 standard; protein; 260 AA.
Human PRO polypeptide #198.
Human TADG-14 protein.
04-NOV-2003.
(UYAR-) UNIV ARKANSAS MEDICAL SCI.
 45.9%;
 45.9%;
 04-FEB-2004.
(GETH) GENENTECH INC.
 15-JAN-2004.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 23-OCT-2003.
(UYAR-) UNIV ARKANSAS.
 GENENTECH INC
 (GETH) GENENTECH INC
 Query Match
Best Local Similarity
RESULT 354
 Query Match
Best Local Similarity
 Best Local Similarity RESULT 350
 Local Similarity
 06-NOV-2003
(GETH) GEN
 Query Match
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CATT/)
JIWW/)
 RESULT 370
 RESULT 37:
 Query Match
Query Match
A5.9%; Score 630.5; DB 8; Length 260;
BESULT 361
ID ADM17394 standard; protein; 260 AA.
DE Human secreted/transmembrane nervices of the protein of
 (GETH) GENENTECH INC.

TY Match 45.9%; Score 630.5; DB 8; Length 260;

t Local Similarity 50.2%; Pred. No. 1.1e-40;
 Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40;
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40;
 Length 260,
 Score 630.5; DB 8; Length 260;
Pred. No. 1.1e-40;
 PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 360
 ADL07228 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2004063921-A1.
 ADM42484 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2004058424-A1.
GE-MAR-2004.
(GETH) GENENTECH INC.
 ADJ65624 standard, protein, 260 AA.
Human PRO polypeptide #198.
US2004038335-A1.
 protein; 260 AA
 ADN62866 standard; protein; 260 AA
 45.9%;
 45.9%;
 45.9%;
 PD 04-MAR-2004.

PA (GETH) GENENTECH INC.

QUELY MATCH 45.9%;

Best Local Similarity 50.2%;

RESULT 359
 Human PRO polypeptide #36.
US2004043927-A1.
US2004038336-A1.
26-FEB-2004.
(GETH) GENENTECH INC.
 GUO X.
PATTURAJAN M.
SPYTEK K A.
EDINGER S R.
 (GETH) GENENTECH INC.
 MALYANKAR U M.
 ZERHUSEN B D.
 ELLERMAN K.
 SMITHSON G.
 Query Match
Best Local Similarity
RESULT 358
 Local Similarity
 Local Similarity
 ADK82850 standard;
 MILLET I.
PEYMAN J 7
KEKUDA R.
 ORT T.
GORMAN L.
 Human NOV11h.
US2004038223-A1.
 01-APR-2004
 Query Match
 (GORM/)
(ZERH/)
 SMIT/)
 MILL/)
 PEYM/)
 Best Loca
RESULT 3 64
ID ADNGS98
DE HUMBUN 192 100
PN UGS2004
PN (SETE)
PA (SMILL/PA (MILL/PA KEKU/
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```
ADR72883 standard; protein; 260 AA.
Human ovarian cancer-related tumour marker kallikrein 8 (hK8) protein.
WO2004075713-A2.
 Length 260;
 Length 260;
 DB 8; Length 260;
 Length 260;
 Length 260;
 45.9%; Score 630.5; DB 8; Length 260; 50.2%; Pred. No. 1.1e-40;
 Length 305;
 AAB37985 standard; protein; 306 AA.
Human secreted protein encoded by gene 2 clone HWJAE49.
WO200055371-A1.
 ADI96380 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207354-A1.
 vuery Match 45.9%; Score 630.5; DB 8;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 365
 (MOUN) MOUNT SINAI HOSPITAL.

ry Match
t Local Similarity, 50.2%; Pred. No. 1.1e-40;
 Score 630.5; DB 8;
Pred. No. 1.1e-40;
 45.9%; Score 630.5; DB 8; 50.2%; Pred. No. 1.1e-40;
 45.9%; Score 630.5; DB 8 50.2%; Pred. No. 1.1e-40;
 45.6%; Score 627; DB 2; 50.9%; Pred. No. 2.4e-40;
 AAY32853 standard; protein; 305 AA.
Human serine protease protein sequence.
JP11225765-A.
 ADN04214 standard; protein; 260 AA. Antipsoriatic protein sequence #302 WO2004028479-A2.
 Human PRO polypeptide #198.
24-808
 ADM28346 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2004077064-A1.
 Query Match
Best Local Similarity 50.2%;
RESULT 366
 50.2%;
 STON/) STONE D. D. STONE D. D. SHENA/) PENA C E A. (SHEN/) SHENDY S G (SHIM/) SHIMKETS R A. (KOTH/) LACH M. D. (LEAC/) LEACH M. D. (AGER/) AGEE M. L. (BERG/) BERGHS C. (BERG/) BERGHS C. (BELSE/) ELSEN A. (GANG/) GANGOLLI E A. (RIES/) RIEGER D K. (RIES/) SPADDERNA S K. 45
 08-APR-2004.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC
 (GETH) GENENTECH INC
 Query Match
Best Local Similarity
RESULT 369
CATTERTON E.
 (SUNR) SUNTORY LID.
 Best Local Similarity RESULT 367
 Query Match
 Best Local Similarity RESULT 368
 Query Match
Best Local Similarity
 MILLER C RASTELLI
 10-SEP-2004
 22-APR-2004
 24-APR-2003
 Query Match
 Query Match
 (MILL/)
(RAST/)
(STON/)
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Length 250;

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45.3%; Score 622.5; DB 8; Length 260; 49.0%; Pred. No. 4.5e-40;
 Query Match 45.0%; Score 618.5; DB 4; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 386
 45.0%; Score 618.5; DB 4; Length 250; 48.2%; Pred. No. 8.7e-40;
 (HUMA-) HUMAN GENOME SCI INC.
ry Match
t Local Similarity 48.2%; Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 5; Length 250; 48.2%; Pred. No. 8.7e-40;
 45.3%; Score 622.5; DB 8; Length 260; 49.0%; Pred. No. 4.5e-40;
 45.0%; Score 618.5; DB 3; Length 250; 48.2%; Pred. No. 8.7e-40;
 AAY99390 standard; protein; 250 AA.
Human PRO1279 (UNQ649) amino acid sequence SEQ ID NO:170.
WO200012708-A2.
 ABBS0479 standard; protein; 250 AA.
Human secreted protein encoded by gene 179 SEQ ID NO:427.
WO200162891-A2.
 45.0%; Score 618.5; DB 3; 48.2%; Pred. No. 8.7e-40;
 45.2%; Score 621.5; DB 5; 48.6%; Pred. No. 5.3e-40;
 ABG61816 standard; protein; 250 AA.
Prostate cancer-associated protein #17.
WQ200<u>2</u>30268-A2.
 ADI17074 standard; protein; 260 AA.
Rat NOVX protein homologue SeqID 610.
WO200268649-A2.
06-SEP-2002.
 AAU83684 standard; protein; 250 AA.
Human PRO protein, Seq ID No 186.
WO200208288-A2.
 ADI37155 standard; protein; 260 AA.
Mouse neuropsin.
US2003199010-A1.
 AAB21325 standard; protein; 250 AA.
Human TLSP.
WOZDO053776-A2.
(MOUN) MOUNT SINAI HOSPITAL.
 AAB66139 standard, protein; 250 AA. Protein of the invention #51. WO200078961-A1.
 AdU12424 standard; protein; 250 AA.
Human PRO1279 polypeptide sequence.
WO200140466-A2.
(UYAR-) UNIV ARKANSAS MEDICAL SCI.
 (EOSB-) EOS BIOTECHNOLOGY INC.
 09-MAR-2000.
(GETH) GENENTECH INC.
 28-DEC-2000.
(GETH) GENENTECH INC.
 07-JUN-2001.
(GETH) GENENTECH INC.
 (UYAR-) UNIV ARKANSAS
 (GETH) GENENTECH INC
 (CURA-) CURAGEN CORP
 Best Local Similarity RESULT 385
 Best Local Similarity RESULT 384
 Query Match
Best Local Similarity
RESULT 383
 Query Match
Best Local Similarity
RESULT 389
 Best Local Similarity RESULT 382
 Best Local Similarity RESULT 387
 Best Local Similarity RESULT 388
 Best Local Similarity RESULT 381
 31-JAN-2002
 23-OCT-2003
 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
 ABB57219 standard; protein; 260 AA.
Mouse ischaemic condition related protein sequence SEQ ID NO:533.
WO200188188-A2.
22-NOV-2001.
 LYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

17 Match 45.3%; Score 622.5; DB 5; Length 260; t Local Similarity 49.0%; Pred. No. 4.5e-40;
 Score 622.5; DB 5; Length 260; Pred. No. 4.5e-40;
 (SMIK) SMITHKLINE BEECHAM PLC.
Query Match
45.6%; Score 626.5; DB 2; Length 260;
Best Local Similarity 50.4%; Pred. No. 2.2e-40;
 (MOUN) MOUNT SINAI HOSPITAL.

17. Match

45.6%; Score 626.5; DB 3; Length 275; t Local Similarity 50.4%; Pred. No. 2.3e-40;
 24-SEP-1996.
(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
ery Match 45.3%; Score 622.5; DB 2; Length 260;
ery match 49.0%; Pred. No. 4.5e-40;
 Score 622.5; DB 2; Length 260;
Pred. No. 4.5e-40;
 Score 622.5; DB 2; Length 260; Pred. No. 4.5e-40;
 Length 306;
 Length 315;
 AAW10694 standard; protein; 260 AA.
Human recombinant neuropsin, used for antibody production.
2708245700-A.
 WCACULO
03-JAN-2002.
(HUMA-) HUMAN GENOME SCI INC.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 45.6%; Score 627; DB 5;
 45.6%; Score 627; DB 3; 50.9%; Pred. No. 2.4e-40;
 ABP41332 standard; protein; 315 AA.
Human ovarian antigen HCOQP78, SEQ ID NO:2464
WO200200677-A1.
 AAW87703 standard; protein; 260 AA.
A human serine protease designated HGBAB90.
EP887414-A2.
30-DEC-1998
(SMIK) SMITHKLINE BEECHAM PLC.
 ADI17073 standard; protein; 260 AA.
Murine NOVX protein homologue SeqID 609.
WO200268649-A2.
 AAY06438 standard; protein; 260 AA.
 ADI39731 standard; protein; 260 AA. Mouse neuropsin protein. US6642013-B1. 04-NOV-2003.
 protein; 260 AA
 AAB21311 standard; protein; 275 AA
21-SEP-2000.
(HUMA-) HUMAN GENOME SCI INC.
 45.3%;
 45.3%;
 45.3%;
 22-JUL-1999.
(INCY-) INCYTE PHARM INC
 Mouse neuropsin protein. JP08311099-A.
 Human protease HUPM-7. W09936550-A2.
 (CURA-) CURAGEN CORP
 Best Local Similarity RESULT 372
 Query Match
Best Local Similarity
RESULT 376
 26-NOV-1996.
(SHIO/) SHIOZAKA S.
 Query Match
Best Local Similarity
 AAW12393 standard;
 Local Similarity
 Local Similarity
 Human neuropsin.
WO200053776-A2.
14-SEP-2000.
 Query Match
Best Local Si
RESULT 373
 Query Match
 Query Match
 Query Match
```

```
RESULT 404
 31-OCT-2002.
(EOSB-) EOS BIOTECHNOLOGY INC.
(EY Match 45.0%; Score 618.5; DB 6; Length 250;
ery Match 48.2%; Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 5; Length 250; 48.2%; Pred. No. 8.7e-40;
 Query Match
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 393
 Length 250;
 Score 618.5; DB 5; Length 250;
Pred. No. 8.7e-40;
 Length 250;
 Score 618.5; DB 6; Length 250; Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 6; Length 250; 48.2%; Pred. No. 8.7e-40;
 ABB95526 standard; protein; 250 AA.
Human angiogenesis related protein PRO1279 SEQ ID NO: 208
WO200208284-A2.
 Novel human secreted and transmembrane protein PRO1279. US200332156-A1.
 AB033797 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003045687-A1.
 Score 618.5; DB 5;
Pred. No. 8.7e-40;
 Score 618.5; DB 6;
Pred. No. 8.7e-40;
 ABB84920 standard; protein; 250 AA.
Human PRO1279 protein sequence SEQ ID NO:208.
WO200200690-A2.
 Lung cancer-associated polypeptide #332.
 Human PRO polypeptide #93.
105200303635-A1.
 ABU81122 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003004311-A1.
 W02002000
03-ChV-2002.
(GETH) GENENTECH INC.
45.0%;
 45.0%;
 45.0%;
 / Match 45.0%;
Local Similarity 48.2%;
 Best Local Similarity 48.2%;
 GURNEY A L.
HILLAN K J.
MARSTERS S A.
 13-FEB-2003.
(GETH) GENENTECH INC.
 20-FEB-2003.
(GETH) GENENTECH INC.
 06-MAR-2003.
(GETH) GENENTECH INC.
 02-JAN-2003.
(GETH) GENENTECH INC.
 (PANJ/) PAN J.
(PAON/) PAONI N F.
(STEP/) STEPHAN J F.
(WATA/) WATANABE C K.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
 GENENTECH INC.
 GERRITSEN M E.
 GODOWSKI P J.
 BAKER K P.
FERRARA N.
 Query Match
Best Local Similarity
RESULT 395
Query Match
Best Local Similarity
 GODDARD A.
 Local Similarity
 Best Local Similarity
 GERBER H.
 11-JAN-2002
 Query Match
 Query Match
 Query Match
 Query Match
 (GETH)
 GURN/
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Length 250;
 Length 250;
 Length 250;
 Length 250;
 Length 250;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 Length 250;
 Length 250;
 Length 250;
 ABU82140 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003088063-A1.
 Novel human secreted and transmembrane protein PRO1279. 39-74N-2003.
 ABUG7098 standard; protein; 250 AA.
Human secreted/transmembrane, PRO, protein SEQ ID
US2003032155-A1.
 ,
9
 Score 618.5; DB 6;
Pred. No. 8.7e-40;
 Score 618.5; DB 6;
Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 6; 48.2%; Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 6; 48.2%; Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 6; 48.2%; Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 6; 48.2%; Pred. No. 8.7e-40;
 DB 6;
 ABUS9903 standard; protein; 250 AA.

Novel secreted and transmembrane protein PRO1279.
US2003017563-A1.
 ABO25093 standard; protein; 250 AA.
Human secreted/transmembrane protein (PRO) #253
US2003036179-A1.
 Score 618.5; DB 6
Pred. No. 8.7e-40;
 Score 618.5; DB 6
Pred. No. 8.7e-40;
RESULT 397

ID ABU66822 standard; protein; 250 AA.

DE Human PRO polypeptide #253.

PN US2003036180-Ai.

PD 20-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match

A5.0%; Score 61
 ADA19106 standard; protein; 250 AA. Human PRO polypeptide #253. US2003054517-A1.
 ADA76456 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003073212-A1.
 protein; 250 AA
 45.0%;
 US200305-2-20-MAR-2003.
(GETH) GENENTECH INC.
45.0%;
 45.0%;
 Query Match
Best Local Similarity 48.2%;
RESULT 405
 17-APR-2003.
(GETH) GENENTECH INC.
 20-FEB-2003.
(GETH) GENENTECH INC.
 13-FEB-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 Human PR01279 protein.
US2003050448-A1.
 13-MAR-2003.
(GETH) GENENTECH INC.
 Best Local Similarity RESULT 403
 Query Match
Best Local Similarity
RESULT 401
 Query Match
Best Local Similarity
 Best Local Similarity
 Best Local Similarity RESULT 398
 Best Local Similarity RESULT 399
 Query Match
Best Local Similarity
RESULT 400
 Query Match
Best Local Similarity
RESULT 406
 ABJ72320 standard;
 23-JAN-2003
 08-MAY-2003
 Query Match
 Query Match
 Query Match
```

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Human PRO polypeptide #253.
US2003068794-Al.
 Query Match
 Query Match
 Query Match
 Ouerv Match
 Score 618.5; DB 6; Length 250; Pred. No. 8.7e-40;
 Query Match 45.0%; Score 618.5; DB 6; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 6; Length 250; Pred. No. 8.7e-40;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 Length 250;
 Query Match 45.0%; Score 618.5; DB 6; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 ABO33632 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003073130-A1.
17-APR-2003.
(GETH) GENENTECH INC.
 ADA86534 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082711-A1.
01-MAY-2003.
 ADB19514 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003068796-A1.
 Score 618.5; DB 6;
Pred. No. 8.7e-40;
 Novel human secreted protein; 250 AA. US2003065160-A1.
 Human PRO polypeptide #253.
10-2003068795-A1.
 ADB16098 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003087350-A1.
 ADA47884 standard, protein, 250 AA.
Human PRO polypeptide #253.
US2003073215-Al.
 protein; 250 AA.
 ADB30686 standard; protein; 250 AA
 ADA61729 standard; protein; 250 AA
 (HUMA-) HUMAN GENOME SCI INC.
 US20050---
13-MAR-2003.
(GETH) GENENTECH INC.
"a+ch '....try 48.2%;
 45.0%;
 Best Local Similarity 48.2%;
RESULT 414
 Watch 45.0%;
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 45.0%;
Best Local Similarity 48.2%;
RESULT 415
 Match 45.0%;
Local Similarity 48.2%;
 ADE28055 standard; protein.
Human PRO polypeptide #253
US2003082704-Al.
 01-MAY-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 Query Match
Best Local Similarity
RESULT 407
 Best Local Similarity RESULT 408
 Best Local Similarity RESULT 410
 Homo sapiens.
US2003049816-A1.
 08-MAY-2003
 17-APR-2003
 Query Match
 Query Match
 Query Match
 Query Match
```

```
45.0%; Score 618.5; DB 6; Length 250; 48.2%; Pred. No. 8.7e-40;
 Length 250;
 Length 250;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 DB 6; Length 250;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 DB 6; Length 250;
 Length 250;
 DB 6; Length 250;
 AUBIB955 Btandard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
17.300.073211-A1.
 ADA85982 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082693-A1.
 ADAG7637 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003087345-A1.
 ADA91931 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082694-A1.
 Score 618.5; DB 6;
Pred. No. 8.7e-40;
 Score 618.5; DB 6;
Pred. No. 8.7e-40;
 DB 6;
 Query Match 45.0%; Score 618.5; DB 6
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 421
 Score 618.5; DB 6
Pred. No. 8.7e-40;
 Score 618.5; DB 6
Pred, No. 8.7e-40;
 45.0%; Score 618.5; DB 6
48.2%; Pred. No. 8.7e-40;
 Human PRO polypeptide #253.
US2003082763-A1.
 ADA97194 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082705-A1.
 ADBI6839 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003087349-A1.
 אס 350 אם. Human PRO polypeptide #253.
 250 AA
 45.0%;
 45.0%;
 45.0%;
 Ouery Match 45.0%;
Best Local Similarity 48.2%;
RESULT 417
 PD 01-MAY-2003.

PA (GETH) GENENTECH INC.

QUERY MATCh

BEST Local Similarity 48.2%;

RESULT 418
 Best Local Similarity 48.2%;
RESULT 423
 Query Match 45.0%;
Best Local Similarity 48.2%;
 ADB14994 standard; protein;
Human PRO polypeptide #253.
US2003087351-A1.
10-APR-2003.
(GETH) GENENTECH INC.
 01-MAY-2003.
(GETH) GENENTECH INC.
 GENENTECH INC.
 08-MAY-2003.
(GETH) GENENTECH INC.
 01-MAY-2003.
(GETH) GENENTECH INC.
 01-MAY-2003.
(GETH) GENENTECH INC.
 08-MAY-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 Best Local Similarity RESULT 419
 Query Match
Best Local Similarity
RESULT 416
 Best Local Similarity
 Best Local Similarity RESULT 420
```

Length 250;

DB 6;

Length 250;

Length 250;

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vuery Match 45.0%; Score 618.5; DB 6; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 436
 PD 17-APR-2203.
PA (GETH) GENENTECH INC.
QUECY MAtch
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 6;
Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 6; 48.2%; Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 6; 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 6
Pred. No. 8.7e-40;
 Score 618.5; DB 6 Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 6
48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 6
Pred. No. 8.7e-40;
 ADB25425 standard; protein; 250 AA. Human PRO polypeptide SEQ ID NO 506 US2003077715-A1.
 ADB30134 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003073214-Al.
 DAP433601 standard; protein; 250 AA. Human PRO polypeptide #253.
US2003077721-A1.
 ADB31238 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003096386-AI.
 ADA75904 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082703-A1.
 ADA47129 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003073210-A1.
 ADB26951 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003092147-A1.
 ABJ72448 standard; protein; 250 AA.
Human PRO1279 protein.
US2003027988-A1.
 250 AA
 Query Match
Best Local Similarity 48.2%;
RESULT 439
 Query Match
Best Local Similarity 48.2%;
RESULT 434
 Query Match
Best Local Similarity 48.2%;
RESULT 435
 ADA80662 standard; protein;
Human PRO polypeptide #253.
US2003082761-A1.
 Query Match 45.0%;
Best Local Similarity 48.2%;
 48.2%;
 01-MAY-2003.
(GETH) GENENTECH INC.
 01-MAY-2003.
(GETH) GENENTECH INC.
 17-APR-2003.
(GETH) GENENTECH INC.
 24-APR-2003.
(GETH) GENENTECH INC.
 24-APR-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 15-MAY-2003.
(GETH) GENENTECH INC.
 22-MAY-2003.
(GETH) GENENTECH INC.
 Best Local Similarity RESULT 440
 Best Local Similarity RESULT 441
 Local Similarity
 01-MAY-2003
 Query Match
 Query Match
 Query Match
 RESULT 437
 RESULT 442
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 6; Length 250;
 Query Match 45.0%; Score 618.5; DB 6; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 DB 6; Length 250;
 Score 618.5; DB 6; Length 250; Pred. No. 8.7e-40;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 6; Length 250;
 Novel human secreted and transmembrane protein PRO1279. US2003808291-A1.
 ABO43401 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003044945-A1.
 ADA84878 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082708-A1.
 ADA85430 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003082695-A1.
 Score 618.5; DB 6 Pred. No. 8.7e-40;
 Score 618.5; DB 6
Pred. No. 8.7e-40;
 Score 618.5; DB 6
Pred. No. 8.7e-40;
 ADB24865 standard, protein; 250 AA.
Human PRO polypeptide SEQ ID NO 506
US2003077713-A1.
 ADA74632 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003068798-A1.
 ADA75352 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003073216-A1.
 ADBI3378 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082710-A1.
 ADA82389 standard; protein; 250 AA.
 ...and; protein,
...an secreted and tr.
...03044945-A1.

06-MAR-2003.

PA (GETH) GENENTECH INC.
QUETY MATCh
Best Local Similarity 48.2%; Pre
RESULT 428
ID ADA74632 standard; prorbe Human PRO polyper.
PD Human PRO polyper.
PD 10-APP
 Query Match 45.0%;
Best Local Similarity 48.2%;
RESULT 426
 45.0%;
 Query Match 45.0%;
Best Local Similarity 48.2%;
 Query Match
Best Local Similarity 48.2%;
 45.0%;
 45.0%;
 Watch 45.0%;
Local Similarity 48.2%;
 Best Local Similarity 48.2%;
RESULT 431
 Human PRO polypeptide #253.
US2003082701-A1.
 24-APR-2003.
(GETH) GENENTECH INC.
 01-MAY-2003.
(GETH) GENENTECH INC.
 01-MAY-2003.
(GETH) GENENTECH INC.
 24-APR-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 17-APR-2003.
(GETH) GENENTECH INC.
 01-MAY-2003.
(GETH) GENENTECH INC.
 Local Similarity
 Best Local Similarity RESULT 432
US2003077722-A1.
 01-MAY-2003
 Query Match
 Query Match
 Query Match
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Length 250;

DB 6;

Length 250;

DB 6; Length 250;

Length 250;

7; Length 250;

Length 250;

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SS-FEB-2003.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 45.0%; Score 618.5; DB 7; Length 250;
 45.0%; Score 618.5; DB 7; Length 250; 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 7; Length 250;
Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 7; Length 250; 48.2%; Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 7; Length 250;
 DB 7; Length 250;
 DB 7; Length 250;
 ADA87086 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
(01-MAY-2003)
 ADA45577 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003054516-A1.
 льный ветапрата, protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082700-A1.
 RESULT 459
ID ABO26216 standard; protein; 250 AA.
DE Human protein from novel secreted protein gene 179
PN US6522174-B1.
 DB 7;
 DB 7;
45.0%; Score 618.5; DB 7 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 7
Pred. No. 8.7e-40;
 Score 618.5; DB 7
Pred. No. 8.7e-40;
 Score 618.5; DB 7
Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 7 48.2%; Pred. No. 8.7e-40;
 ABO44485 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003044841-A1.
 Human PRO polypeptide #253.
US2003077710-Al.
24-APR-2003.
(GETH) GENENTECH INC.
RY Match
 Human PRO polypeptide #253.
US2003082699-Al.
 ADB29159 standard; protein; 250 AA. Human PRO polypeptide #253. US2003082706-A1.
 ADA77111 standard, protein; 250 AA.
Human PRO polypeptide #253.
US2003059909-A1.
 45.0%;
 45.0%;
 Query Match
Best Local Similarity 48.2%;
 Query Match
Best Local Similarity 48.2%;
RESULT 458
 01-MAY-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 01-MAY-2003.
(GETH) GENENTECH INC.
 01-MAY-2003.
(GETH) GENENTECH INC.
 27-MAR-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 Best Local Similarity
RESULT 452
ID ADB18402
BE Human PRO polypeptide
PD 24-APR-2003.
PA (GETH) GENENTECH INC
 GENENTECH INC
 Query Match
Best Local Similarity
 Best Local Similarity RESULT 457
 Best Local Similarity
RESULT 454
 Query Match
Best Local Similarity
RESULT 455
 Best Local Similarity RESULT 453
 Best Local Similarity RESULT 460
 20-MAR-2003
 06-MAR-2003
 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
 Score 618.5; DB 6; Length 250; Pred. No. 8.7e-40;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 OI-MAY-2003.
(GETH) GENENTECH INC.
ery Match 45.0%; Score 618.5; DB 6; Length 250;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 DB 6; Length 250;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
 Query Match 45.0%; Score 618.5; DB 6; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 ADB21884 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082765-A1.
 78034343 standard; protein; 250 AA.
Human secreted/transmembrane polypeptide PRO 1279
 Score 618.5; DB 6
Pred. No. 8.7e-40;
 Human PRO polypeptide SEQ ID NO 506.
US2003077714-A1.
 Human PRO polypeptide #253.
102003068797-A1.
 ADA96642 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082690-A1.
 Human PRO polypeptide #253. US2003082702-A1.
 Human PRO polypeptide #253.
01-May.
 protein; 250 AA
 ADB26399 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082760-A1.
 US200304202.
13-MAR-2003.
(GETH) GENENTECH INC.
45.0%; SC
 45.0%;
 45.0%;
 Best Local Similarity 48.2%;
RESULT 447
 45.0%;
 Best Local Similarity 48.2%;
RESULT 451
 / Match 45.0%;
Local Similarity 48.2%;
 01-MAY-2003.
(GETH) GENENTECH INC.
 01-MAY-2003.
(GETH) GENENTECH INC.
 10-APR-2003.
(GETH) GENENTECH INC.
 01-MAY-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 (GETH) GENENTECH INC
 Best Local Similarity RESULT 443
 Best Local Similarity RESULT 444
 Local Similarity
 Query Match
Best Local Similarity
 ADA61166 standard;
 Homo sapiens.
US2003049817-A1.
 24-APR-2003
 01-MAY-200
 Query Match
 Query Match
 Query Match
 Query Match
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Length 250;

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ADB85053 standard; protein
Human PRO polypeptide #93.
 GENENTECH INC
 (GETH) GENENTECH INC
 Query Match
Best Local Similarity
RESULT 476
 Query Match
Best Local Similarity
 Best Local Similarity RESULT 472
 Best Local Similarity RESULT 473
 Best Local Similarity RESULT 474
 Best Local Similarity RESULT 475
 Best Local Similarity RESULT 479
 01-MAY-2003.
(GETH) GENENTECH
 22-MAY-2003
 Query Match
 Query Match
 Query Match
 Query Match
 Ouery Match
 Query Match
 ABJ72150 standard; protein; 250 AA.
Human membrane bound receptor/protein PRO1279 amino acid sequence.
US2003065147-A1.
 Score 618.5; DB 7; Length 250; Pred. No. 8.7e-40;
 Length 250;
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Novel human secreted and transmembrane protein PRO1279.
US2003073129-A1.
 ADA88741 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003073213-A1.
 ADB22436 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003087344-A1.
08-MAY-2003.
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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48.2%; Pred. No. 8.7e-40;
 Human PRO polypeptide SEQ ID NO 506. US2003077712-A1.
 Human PRO polypeptide #253.
01-Mav.c.
 ADA67127 standard; protein; 250 AA. Human PRO polypeptide #253.
US2003068793-AI.
10-AER-2003.
(GETH) GENENTECH INC.
 Human PRO polypeptide #253.
192003077711-A1.
 ADB27503 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003022239-A1.
 ADA92483 standard; protein; 250 AA
 17-ARR-2003.
(GFTH.) GENENIECH INC.
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(GETH) GENENTECH INC.
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RESULT 470
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Local Similarity 48.2%;
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Local Similarity 48.2%;
 24-APR-2003.
(GETH) GENENTECH INC.
 24-APR-2003.
(GETH) GENENTECH INC.
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 01-MAY-2003.
(GETH) GENENTECH INC.
 Best Local Similarity
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DB 7; Length 250;
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 Novel human secreted and transmembrane protein PRO1279. US2003073814-A1. I7-APR-2003. (GTH) GENENTECH INC.
 Novel human secreted and transmembrane protein PRO1279. US200387347-A1.
 ADB66718 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082689-A1.
Novel human secreted and transmembrane protein PRO1279. US2003082712-A1.
 ADBB0782 standard, protein, 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003088068-A1.
 ADB73323 standard, protein, 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003096968-A1.
 ADB78405 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003092889-A1.
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Novel human secreted and transmembrane protein PRO1279
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 ADBI5546 standard, protein, 250 AA.
Human PRO polypeptide #253.
US2003087352-A1.
 protein; 250 AA
 45.0%;
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 Query Match 45.0%;
Best Local Similarity 48.2%;
RESULT 471
 45.0%;
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RESULT 478
 (GETH) GENENTECH INC.
 08-MAY-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 15-MAY-2003.
(GETH) GENENTECH INC.
 08-MAY-2003.
(GETH) GENENTECH INC.
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 Best Local Similarity RESULT 494
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10-APR-2003
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 24-APR-2003
 24-APR-200
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 ADB39631 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082764-A1.
01-MAY-2003.
GERTH) GENENTECH INC.
45.0%; Score 618.5; DB 7; Length 250;
st Local Similarity 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Novel human secreted and transmembrane protein PRO1279.
US2003092886-A1.
 ADB47254 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082687-A1.
01-MAY-2003.
(GETH) GENENTECH INC.
 איסים באפנים (Protein; 250 AA. Novel human secreted and transmembrane protein PRO1279.
US2003069397-Al.
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27-DEC-2002.
(EOSB-) EOS BIOTECHNOLOGY INC.
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48.2%; Pred. No. 8.7e-40;
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 Score 618.5; DB 7
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 _____ Brandard; protein; 250 AA.
Ovarian cancer-associated protein #81.
27.nnc....
 Human PRO polypeptide #93. US2003092890-A1.
 Human PRO polypeptide #93. US2003088067-A1.
 Human PRO polypeptide #253.
01-Mav-2003082698-Al.
 ADB90530 standard; protein; 250 AA. Human PRO polypeptide #253. US2003082762-A1. 01-MAY-2003. (GETH.) GENENTECH INC.
 US200302-15-WAY-2003.
15-WAY-2003.
(GETH) GENENTECH INC.
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 17-APR-2003.
(GETH) GENENTECH INC.
 Best Local Similarity RESULT 482
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 US2003073817-A1.
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Novel human secreted and transmembrane protein PRO1279.
US2003082696-A1.
 ADB73077 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003092887-A1.
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ery Match
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 491
Score 618.5; DB 7
Pred. No. 8.7e-40;
 Score 618.5; DB 7
Pred. No. 8.7e-40;
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 Human PRO polypeptide SEQ ID NO 506. US2003077719-Al.
 ADB34071 standard; protein; 250 AA. Human PRO polypeptide SEQ ID NO 506. US2003077716-A1.
 ADB35175 standard; protein; 250 AA. Human PRO polypeptide SEQ ID NO 506 US2003077718-A1.
 ADB36279 standard; protein; 250 AA.
Human PRO polypeptide SEQ ID NO 506
US2003077720-A1.
 Prostate cancer marker protein, 250 AA. W02003009814-A2.
 ADB34623 standard; protein; 250 AA.
Human PRO polypeptide SEQ ID NO 506
US2003077717-A1.
 ADB86861 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082697-A1.
45.0%;
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 15-MAY-2003.
(GETH) GENENTECH INC.
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Query Match

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ADC53686 standard; protein; 250 AA.
Novel human secreted and transmembrane protein Seq ID506.
US2003087364-A1.
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 AUCS/434 standard; protein; 250 AA.
Novel human secreted and transmembrane protein Seg ID506.
US2003087366-A1.
 ADC53080 standard; protein; 250 AA.
Novel human secreted and transmembrane protein Seg ID506.
US2003087365-A1.
 protein; 250 AA.
ed and transmembrane protein Seg ID506
 ADC49652 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003088071-A1.
08-MAY-2003.
(GETH) GENENTECH INC.
 Novel human secreted and transmembrane protein PRO1279.
US2003087367-A1.
 ADC51100 standard, protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003087361-A1.
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
 ADC65627 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003087362-A1.
 protein; 250 AA
 US200505
08-MAY-2003.
(GETH) GENENTECH INC.
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 ADC54725 standard; pr
Novel human secreted
US2003087363-A1.
08-MAY-2003.
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 ADC60625 standard;
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 Score 618.5; DB 7; Length 250; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
 ADC50547 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003092106-A1.
 ADC72094 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003092107-A1.
 ADC49936 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US200308064-A1.
08-MAY-2003.
 AUCA9115 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003088070-A1.
 ADB46674 standard; protein; 250 AA.
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US2003082692-A1.
 ADC60073 standard, protein, 250 AA.
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Pred. No. 8.7e-40;
 Human PRO polypeptide #51.
03-003064925-A1.
 ADC36915 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003088065-A1.
08-MAY-2003.
 protein; 250 AA
 Best Local Similarity 48.2%; Pr
RESULT 499
ID ADC18039 standard; protein; 250
DE Human PRO polypeptide #51.
PN US2000364925-A1.
PD 03-ARR-2003.
 US200302.
15-MXY-2003.
(GETH) GENENTECH INC.
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 Human PRO polypeptide #93.
US2003096969-Al.
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(GETH) GENENTECH INC.
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RESULT 534
 08-MAY-2003
 16-OCT-2003
 15-MAY-2003
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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 Novel human secreted and transmembrane protein Seg ID506.
US2003087359-Al.
 ADC56087 standard; protein; 250 AA. Novel human secreted and transmembrane protein Seg ID506 US2003087360-A1.
 ADD03331 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003092104-A1.
 ADC90323 standard, protein, 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003087348-A1.
 ADC47258 standard, protein, 250 AA.
Novel human secreted and transmembrane protein PRO1279
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Pred. No. 8.7e-40;
 Score 618.5; DB 7;
Pred. No. 8.7e-40;
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 Score 618.5; DB 7;
Pred. No. 8.7e-40;
 Score 618.5; DB 7
Pred. No. 8.7e-40;
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 Human PRO polypeptide #253.
US2003194770-Al.
 ADC48631 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003194773-A1.
 ADC59209 standard; protein; 250 AA
 US2005-C
08-MAY-2003.
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US2003096972-A1.
 AUC/7887 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
 ADC80139 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003087358-A1.
 ADD04735 standard; protein; 250 AA.

Novel human secreted and transmembrane protein PRO1279.
US2003087354-A1.
 ADC80691 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003092103-A1.
 ADD06368 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003073816-A1.
 ADD10497 standard; protein; 250 AA.
Human secreted/transmembrane PRO polypeptide #104
US2003105011-A1.
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Pred. No. 8.7e-40;
 Score 618.5; DB 7
Pred. No. 8.7e-40;
 Human PRO polypeptide #253.
182003194771-A1.
 ADD11198 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003194774-A1.
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 17-APR-2003.
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ADC48079 standard;
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Novel human secreted and transmembrane protein PRO1279.
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 ADD37250 standard; protein; 250 AA.
Human secreted/transmembrane PRO polypeptide #104
US2003105012-A1.
05-UDN-2003.
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Pred. No. 8.7e-40;
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
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 45.0%; Score 618.5; DB 7 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
 Score 618.5; DB 7
Pred. No. 8.7e-40;
 Human secreted/transmembrane protein PRO1279.
 ADD39285 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003096954-A1.
 ADD38329 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
 ADD51908 standard; protein; 250 AA. Human PRO polypeptide #253.
US2003194779-A1.
 ADD02707 standard; protein; 250 AA. Human PRO polypeptide #253.
US2003203431-A1.
 ADD50577 standard; protein; 250 AA Human PRO polypeptide #93.
US2003096971-A1.
 250 AA
 US2003201...
30-OCT-2003.
(GETH) GENENTECH INC.
45.0%;
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 Best Local Similarity 48.2%;
RESULT 551
 ADD02141 standard; protein;
Human PRO polypeptide #253.
US2003203430-A1.
 20-MAR-2003.
(GETH) GENENTECH INC.
 30-OCT-2003.
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 (GETH) GENENTECH INC.
 22-MAY-2003.
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 Best Local Similarity RESULT 545
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Novel human secreted and transmembrane protein PRO1279.
US2003105291-A1.
 ADD41321 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003203438-A1.
 ADD51096 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279,
US2003105290-A1.
05-UDN-2003.
ADD11457 standard; protein; 250 AA.
Human secreted/transmembrane PRO polypeptide #104.
US2003105013-A1.
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Pred. No. 8.7e-40;
 Score 618.5; DB 7
Pred. No. 8.7e-40;
 ADD70685 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003099625-A1.
 ADD39762 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003083462-A1.
 Human PRO polypeptide #253.
1052003194775-A1.
 ADD52460 standard, protein, 250 AA.
Human PRO polypeptide #253.
US2003194769-A1.
 Human PRO polypeptide #253.
182003194792-A1.
 ADD53752 standard; protein; 250 AA
 45.0%;
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 ADE33551 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003194767-A1.
 ADE34103 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003194791-A1.
 ADE32447 standard, protein, 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003194765-A1.
 45.0%; Score 618.5; DB 7; 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 7 48.2%; Pred. No: 8.7e-40;
 Human PRO polypeptide #253.
16-003194772-Al.
 ADD92088 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199053-Al.
 /T 563
ADE22379 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199056-A1.
 ADD79603 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003203428-A1.
 ADE17956 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199023-A1.
 ADD80155 standard; protein; 250 AA.
Human PRO polypeptide #253.
06-NOV-2003.
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 (GETH) GENENTECH INC.
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 / Match 48.0%; Score 618.5; DB 7; Length 250; Local Similarity 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 7; Length 250;
Pred. No. 8.7e-40;
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 Score 618.5; DB 7; Length 250;
Pred. No. 8.7e-40;
 AD51342 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003105289-A1.
05-JUN-2003.
(GETH) GENENTECH INC.
 Score 618.5; DB 7;
Pred. No. 8.7e-40;
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 Score 618.5; DB 7
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 Score 618.5; DB 7
Pred. No. 8.7e-40;
 ADD38808 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003092061-A1.
 ADD40239 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003082627-A1.
 ADE50460 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003069179-A1.
 ADE20072 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003092883-A1.
 ADD50331 standard; protein; 250 AA. Human PRO polypeptide #93. US203096970-A1. CAPAY-2003. (GETH.) GENENTECH INC.
 ADD92640 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199030-A1.
 ADD91536 standard, protein, 250 AA.
Human PRO polypeptide #253.
US2003199055-A1.
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 ADEOUS standard; protein;
Human PRO polypeptide #253.
US2003199057-A1.
 48.2%;
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ADD50331 standard;
US2003203432-A1.
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 ADE32999 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US200194766-A1.
16-OCT-2003.
 GETH GENENTECH INC.

Query Match
Best Local Similarity 48.2%; Score 618.5; DB 7;
RESULT 586
ID ADE92947 standard; protein; 250 AA.
DE Human PRO polypeptide #253
PD US2003194777-A1.
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 ADF55859 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003204054-A1.
 ADF29966 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003204053-A1.
 ADD89735 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199028-A1.
 ADE41019 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199031-A1.
 ADE42691 standard; protein; 250 AA. Human PRO polypeptide #253.
US2003199032-A1.
 ADD80707 standard; protein; 250 AA
Human PRO polypeptide #253.
US2003207418-A1.
 Best Local Similarity 48.2%;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
 Score 618.5; DB 7
Pred. No. 8.7e-40;
 ADE49983 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003082626-A1.
 ADE21541 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003082628-A1.
 Human PRO polypeptide #253.
1052003199059-A1.
 ADE19060 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199026-A1.
 Human PRO polypeptide #253.
US2003199033-A1.
 ADE22931 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199064-A1.
 Human PRO polypeptide #253.
 ADD93192 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003194768-A1.
 protein; 250 AA.
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US2003199025-A1.
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 ADE19612 standard;
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 US2003207377-A1.
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 RESULT 598
 DB 7; Length 250;
 Score 618.5; DB 7; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 7; Length 250; Pred. No. 8.7e-40;
 Length 250;
 Score 618.5; DB 7; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 7; Length 250;
Pred. No. 8.7e-40;
 Length 250;
 Score 618.5; DB 7; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 7; Length 250; Pred. No. 8.7e-40;
 ADG21656 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207355-A1.
 ADH55988 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207379-A1.
 ADG23297 standard, protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207384-A1.
 Novel human secreted and transmembrane protein PRO1279.
US2003207381-A1.
06-NOV-2003.
 Novel human secreted and transmembrane protein PRO1279.
US2003207385-A1.
 Score 618.5; DB 7 Pred. No. 8.7e-40;
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 Score 618.5; DB 7
Pred. No. 8.7e-40;
Best Local Similarity 48.2%; Fred. No. 8.7e-40;
RESULT 589
 ADH99363 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003065142-A1.
 ADF97632 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003207370-A1.
 Human PRO polypeptide #253.
US2003207372-A1.
 ADG80696 standard, protein, 250 AA.
Human PRO polypeptide #253.
US2003207373-A1.
 ADH55436 standard; protein; 250 AA
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 Best Local Similarity
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 ADI64207 standard;
 06-NOV-2003
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 Query Match
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SEQ ID NO:560
 Length 250;
 Score 618.5; DB 7; Length 250; Pred. No. 8.7e-40;
 DB 7; Length 250;
 Score 618.5; DB 7; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 7; Length 250;
Pred. No. 8.7e-40;
 Length 250;
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 Length 250,
ADI65156 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207386-A1.
 Novel human secreted and transmembrane protein PRO1279. US200387385-A1.
 ADN14981 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
 ADM82069 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207388-A1.
 ADM82686 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003087355-A1.
 Novel human secreted and transmembrane protein PRO1279 US2003087356-A1.
 ADH81517 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
 ADNI6085 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003087353-A1.
 ADN39242 standard; protein; 250 AA.
Cancer/angiogenesis/fibrosis-related polypeptide,
WO2003042661-A2.
 Score 618.5; DB 7;
Pred. No. 8.7e-40;
 Score 618.5; DB 7;
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 Best Local Similarity RESULT 604
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Novel human secreted and transmembrane protein PRO1279.
US2003100738-A1.
 22-MAY-2003
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 RESULT 622
 Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
 Score 618.5; DB 7; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
) LD-TRAIL EXUSECT INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
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 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Length 250;
 AUD75879 standard; protein; 250 AA.

Novel human secreted and transmembrane protein PRO1279.
US2003100717-A1.
29-MAY-2003.
(GETH) GENENTECH INC.
ADI63655 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207387-A1.
06-NOV-2003.
(GETH) GENENTECH INC.
15 Score 618.5; DB 7; Lengt
PRY Match 48.2%; Pred. NO. 8.7e-40;
 ADC48889 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003092888-A1.
 ADC81243 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003092115-A1.
 ADE21060 standard, protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100735-A1.
 Novel human secreted and transmembrane protein PRO1279, US2003100722-A1.
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 Human PRO polypeptide #93. US2003100728-A1.
 ADD75133 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100712-AI.
29-MAY-2003.
(GETH) GENENTECH INC.
 ADD86937 standard; protein; 250 AA
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29-WAY-2003.
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 (GETH) GENENTECH INC.
 29-MAY-2003.
(GETH) GENENTECH INC.
 Query Match
Best Local Similarity
RESULT 608
ID ADC48889 standard; px
DE Novel human secreted
PN USZO03092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC
 Best Local Similarity
RESULT 610
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Length 250;
 45.0%; Score 618.5; DB 8; Length 250; 48.2%; Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 8; Length 250; 48.2%; Pred. No. 8.7e-40;
 Length 250;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Length 250;
 Length 250;
 DB 8; Length 250;
 Length 250;
 ADE20814 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100734-A1.
29-MAY-2003.
(GETH) GENENTECH INC.
 ADD78483 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100737-A1.
 Novel human secreted and transmembrane protein PRO1279. US200396362-A1.
 Luery Match 45.0%; Score 618.5; DB 8;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 624
ID ADD78483 standard; protein; 250 AA.
DB Novel human secreted and trace DD 22003100737-A1.
PD 29-MAY-200.
 ADE41458 standard; protein; 250 AA.
Human secreted/transmembrane PRO polypeptide #104.
 DB 8;
 45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
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 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 Score 618.5; DB 8
Pred. No. 8.7e-40;
 ADD88055 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003092113-A1.
 ADD86459 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003203440-A1.
 ADE05658 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100727-A1.
 ADD73643 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100711-A1.
 Human PRO polypeptide #253.
US2003100.
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(GETH) GENENTECH INC.
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(GETH) GENENTECH INC
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 Query Match
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RESULT 641
 RESULT 636
ID ADE24678 standard;
 Local Similarity
 29-MAY-2003
 15-MAY-2003
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 RESULT 635
PN US2003100497-A1.
PD 29-MAY-2003.
A (GETH) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 626
 Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
 DB 8; Length 250;
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 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Length 250
 ADD85617 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100721-A1.
 ADD76125 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100718-A1.
29-MAY-2003.
(GETH) GENENTECH INC.
 ADE21306 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100736-Al.
 ADD77421 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100732-A1.
 ADE20568 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100733-A1.
29-MAY-2003.
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 Score 618.5; DB 8
Pred. No. 8.7e-40;
 Human PRO polypeptide #93.
US2003100064-A1.
 ADD74149 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100708-A1.
29-MAY-2003
(GETH) GENENTECH INC.
 ADD74395 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100709-A1.
 protein; 250 AA
 USZUCZ-
29-MVZ-2003.
(GETH) GENENTECH INC.
ATCh 45.0%;
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 Query Match
Best Local Similarity 48.2%;
RESULT 627
 PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
QUETY MATCh 45.0%;
Best Local Similarity 48.2%;
RESULT 628
 45.0%;
 45.0%;
 Query Match
Best Local Similarity 48.2%;
 Match 45.0%;
Local Similarity 48.2%;
 ADE23483 standard; protein;
Human PRO polypeptide #253.
US2003092108-A1.
 15-MAY-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC. Query Match 4
 29-MAY-2003. (GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 Best_Local Similarity
RESULT 629
 Local Similarity
 Local Similarity
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 29-MAY-2003
 Query Match
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 Query Match
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Length 250;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 DB 8; Length 250;
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 DB 8; Length 250;
 8; Length 250;
 DB 8; Length 250;
 8; Length 250;
 DB 8; Length 250;
 ADD78159 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100731-A1.
29-MAY-2003.
 ADD76923 standard, protein, 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100715-A1.
 ADD86691 standard, protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100719-A1.
 DB 8;
 Query Match 48.0%; Score 618.5; DB 8 Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 639
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 642
 Score 618.5; DB 8
Pred. No. 8.7e-40;
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 8 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 ADE05166 standard; protein; 250 AA. Human PRO polypeptide #93. US2003100726-A1. 29-MAY-2003. (GETH) GENENTECH INC.
 ADD87503 standard, protein, 250 AA.
Human PRO polypeptide #253.
US2003203439-A1.
 ADD75779 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100714-A1.
 ADE24035 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003092110-A1.
 250 AA
 250 AA
 45.0%;
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 45.0%;
 Human PRO polypeptide #253. US20033092111-A1.
 Best Local Similarity 48.2%;
RESULT 637
 Query Match 45.0%;
Best Local Similarity 48.2%;
RESULT 638
 ADE89369 standard; protein;
Human PRO polypeptide #253.
US2003199062-A1.
 30-OCT-2003.
(GETH) GENENTECH INC.
 15-MAY-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 23-OCT-2003.
(GETH) GENENTECH INC.
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Length 250;

Length 250;

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Length 250;

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(GETH) GENENTECH INC.
45.0%; Score 618.5; DB 8; Length 250;
 45.0%; Score 618.5; DB 8; Length 250; 48.2%; Pred. No. 8.7e-40;
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 Score 618.5; DB 8;
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Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 8 48.2%; Pred. No. 8.7e-40;
 Query Match
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 659
ID ADE95389 standard; protein; 250 AA.
 Score 618.5; DB 8
Pred. No. 8.7e-40;
 Score 618.5; DB 8
Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 8 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 8
Pred. No. 8.7e-40;
 ADF25854 standard; protein; 250 AA..
Human secreted/transmembrane protein PRO1279.
US2003199675-A1.
GENT) GENENTECH INC.
 ADE96543 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003195347-A1.
 ADP24753 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003198993-A1.
 Human PRO polypeptide #253.
US2003199052-Al.
 Human PRO polypeptide #253.
US2003199027-A1.
 ADE93499 standard; protein; 250 AA. Human PRO polypeptide #253. US2003199060-AI. CAST-2003. (GETH) GENENTECH INC.
 protein; 250 AA
 ADD74887 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100724-A1.
 ADE91248 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199061-A1.
 45.0%;
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 Query Match
Best Local Similarity 48.2%;
RESULT 657
 48.28;
 ADEO5412 standard; protein;
Human PRO polypeptide #93.
US2003100723-A1.
29-MAY-2003.
(GETH) GENENTECH INC.
 29-MAY-2003.
(GETH) GENENTECH INC.
 16-OCT-2003.
(GETH) GENENTECH INC.
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 Best Local Similarity RESULT 656
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 Score 618.5; DB 8; Length 250;
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Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Length 250
 ADD77667 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100729-A1.
 ADD77913 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100730-A1.
 ADD85371 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100725-A1.
 ADD77169 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100716-A1.
 ADD85863 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279, US2003100720-A1.
29-MAY-2003.
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 ADE88817 standard; protein; 250 AA. Human PRO polypeptide #253. US2003199054-A1. C3-OCT-2003. (GETH) GENENTECH INC.
 D ADD73903 standard; protein; 250 AA.
E Human PRO polypeptide #93.
N US2003100710-A1.
D 29-MAY-2003.
QUETH) GENENTECH INC.
A (GETH) GENENTECH INC.
 ADD74641 standard; protein; 250 AA. Human PRO polypeptide #93. US2003100713-A1. C9-WAY-2003. (GETH) GENENTECH INC.
 ADE18508 standard, protein, 250 AA. Human PRO polypeptide #253. US2003194794-A1. 16-OCT-2003. (GETH) GENENTECH INC.
 US200310.
29-MAY-2003.
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Query Match
Best Local Similarity
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Best Local Similarity
RESULT 646
 Query Match
Best Local Similarity
RESULT 647
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 Best Local Similarity RESULT 651
 Query Match
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Length 250;

Length 250;

Length 250;

Length 250;

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Query Match
Best Local Similarity
RESULT 680
 06-NOV-2003
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 Query Match
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 Query Match
RESULT 671
 Score 618.5; DB'8; Length 250;
Pred. No. 8.7e-40;
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 Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
 DB 8; Length 250;
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 Length 250;
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Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
 ADE91843 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003199058-A1.
23-OCT-2003.
(GETH.) GENENTECH INC.
 ADG05699 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003096959-A1.
 ADE92395 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003199051-A1.
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 Score 618.5; DB 8;
 (GETH) GENENTECH INC.

ry Match 45.0%; Score 618.5; DB 8; t Local Similarity 48.2%; Pred. No. 8.7e-40;
 Pred. No. 8.7e-40;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 ADE97020 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003195334-A1.
16-OCT-2003.
 ADF29489 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003203401-A1.
 ADF35080 standard, protein, 250 AA.
Human PRO polypeptide #253.
US2003199029-A1.
 ADE90696 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199063-A1.
 ADG27253 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003096962-A1.
 protein; 250 AA
 PD 30-OCT-2003.

PA (GETH) GENENTECH INC.

Query Match 45.0%;

Best Local Similarity 48.2%;

RESULT 663
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 Best Local Similarity, 48.2%;
RESULT 670
 Match 45.0%;
Local Similarity 48.2%;
 45.0%;
 Human PRO polypeptide #253
US2003207352-A1.
 23-OCT-2003.
(GETH) GENENTECH INC.
 23-OCT-2003.
(GETH) GENENTECH INC.
 22-MAY-2003.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
Query Match 4
 (GETH) GENENTECH INC.
 22-MAY-2003.
(GETH) GENENTECH INC.
 Local Similarity
 Best Local Similarity RESULT 668
 Query Match
Best Local Similarity
RESULT 669
 Local Similarity
 ADG02422 standard;
 Query Match
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 Ouery Match
 RESULT 662
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45.0%; Score 618.5; DB 8; Length 250; 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
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 DB 8; Length 250;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Length 250;
 DB 8; Length 250;
 Length 250;
ADG22208 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207360-A1.
 ADG24401 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207426-A1.
06-NOV-2003.
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 DB 8;
 Query Match 45.0%; Score 618.5; DB 8
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 673
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 8 48.2%; Pred. No. 8.7e-40;
 ADF98184 standard; protein; 250 AA. Human PRO polypeptide #253. US2003207422-A1. GENOV-2003. (GEH.) GENENTECH INC.
 Human PRO polypeptide #253.
US2003208055-A1.
 Human PRO polypeptide #253.
US2003207359-A1.
 ADG20278 standard; protein; 250 AA.
 ADG03586 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003207351-A1.
 ADF99307 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003207353-A1.
 ADG05351 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003207375-A1.
 45.0%;
 Best Local Similarity 48.2%;
RESULT 677
 Query Match
Best Local Similarity 48.2%;
RESULT 672
 45.0%;
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 Query Match 45.0%;
Best Local Similarity 48.2%;
RESULT 679
 48.2%;
 Human PRO polypeptide #253
US2003207376-A1.
 06-NOV-2003.
(GETH) GENENTECH INC.
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 Best Local Similarity RESULT 678
 Query Match
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Human PRO polypeptide #253.
US2003207423-A1.
06-NOV-2003.
(GENT) GENENTECH INC.
45.0%; Seet Local Similarity 48.2%; P
 Query Match
Best Local Similarity
RESULT 690
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 Length 250;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
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 DB 8; Length 250;
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Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 ADG23849 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207389-A1.
 ADG11316 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003045967-A1.
 ADGOB512 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207424-A1.
 ADG12095 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003096963-A1.
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 DB 8;
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 Score 618.5; DB 8
Pred. No. 8.7e-40;
 ADG19618 standard; protein; 250 AA. Human PRO Polypeptide #253. US2003207425-A1. 06-NOV-2003. (GETH) GENENTECH INC. DLTY MALCH ABLCH 45.0%; SCOTE 61 Poet Local Similarity 48.2%; Pred. No Poet North ADG15682 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003219885-A1.
 ADG13455 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003207357-Al.
 ADG06265 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003207374-A1.
 ADG04138 standard; protein; 250 AA
 protein; 250 AA
 US20032...
06-NOV-2003.
(GETH) GENENTECH INC.
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Best Local Similarity 48.2%;
 Human PRO polypeptide #253
US2003207371-A1.
06-NOV-2003.
(GETH) GENENTECH INC.
 22-MAY-2003.
(GETH) GENENTECH INC.
 27-NOV-2003.
(GETH) GENENTECH INC.
 GENENTECH INC.
 Best Local Similarity
RESULT 681
 Best Local Similarity RESULT 683
 Best Local Similarity RESULT 685
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 Query Match
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 ADF97080 standard;
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Length 250;
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 Length 250;
 Novel human secreted and transmembrane protein PRO1279. US20003207427-A1.
 ADG07336 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207350-A1.
 ADG55383 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003194778-A1.
 AUG61047 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
 Novel human secreted and transmembrane protein PRO1279 US2003207428-A1.
 Novel human secreted and transmembrane protein PRO1279 US2003096964-A1.
 ADG07888 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003207356-A1.
 45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Score 618.5; DB 8;
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Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
 ADH03058 standard; protein; 250 AA.
Human secreted/transmembrane protein PR01279
 ALMOND / 48 Standard; protein; 250 AA. Human PRO polypeptide #93. US2003096966-A1. 22-MAY-2003. C2-MAY-2003.
 protein; 250 AA
 ADG62151 standard; protein; 250 AA
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 06-NOV-2003.
(GETH) GENENTECH INC.
 O6-NOV-2003. (GETH) GENENTECH INC.
 16-OCT-2003.
(GETH) GENENTECH INC.
 22-MAY-2003.
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 (GETH) GENENTECH INC
 Query Match
Best Local Similarity
RESULT 693
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RESULT 691
 Query Match
Best Local Similarity
 Best Local Similarity
RESULT 696
 Query Match
Best Local Similarity
RESULT 697
 Best Local Similarity RESULT 692
 ADF94652 standard;
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45.0%;
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 45.0%;
 Ouery Match 45.0%;
Best Local Similarity 48.2%;
RESULT 713
 45.0%;
 48.28;
 Human PRO polypeptide #253
US2003077723-A1.
 (GETH) GENENTECH INC. Query Match 4
 24-APR-2003. (GETH) GENENTECH INC.
 GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
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 Query Match
Best Local Similarity
RESULT 714
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RESULT 709
 Best Local Similarity RESULT 712
 Local Similarity
 ADH30762 standard;
 US2003207416-A1.
 06-NOV-2003
 22-MAY-2003
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 Query Match
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 Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
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 Length 250
 Length 250;
 الا 250 AA.
Novel human secreted and transmembrane protein PRO1279.
VS2003264-A1.
 ADG55935 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207365-A1.
 ADG71061 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207420-A1.
 ADM39092 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003096965-A1.
 Novel human secreted and transmembrane protein PRO1279 US2003207362-A1.
 ADGS8695 standard, protein, 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207368-A1.
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
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 Score 618.5; DB 8
Pred. No. 8.7e-40;
 ADH03535 standard; protein; 250 AA.
Human secreted/transmembrane protein PR01279.
US200324478-A1.
GADG-2003.
GETH) GENENTECH INC.
 ADH04012 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003220471-A1.
 protein; 250 AA.
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06-NOV-2003.
(GETH) GENENTECH INC.
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th 45.0%;
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 Best Local Similarity 48.2%;
RESULT 705
 45.0%;
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Local Similarity 48.2%;
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 ADG82352 standard; protein;
Human PRO polypeptide #253.
US2003207358-A1.
 20-NOV-2003.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
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 27-NOV-2003
 Query Match
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Score 618.5; DB 8; Length 250;
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 Length 250;
 Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
 DB 8; Length 250;
 Length 250;
 DB 8; Length 250;
 8; Length 250;
 Length 250;
 ADG/88143 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207363-A1.
06-NOV-2003.
(GETH) GENENTECH INC.
 ADG53727 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207415-A1.
 ADH12129 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207419-A1.
 Movel human secreted and transmembrane protein PRO1279
US2003207421-A1.
 Novel human secreted and transmembrane protein PRO1279 US20037414-A1.
 ADG54279 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
 8;
 45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
 DB 8;
 vuery Match 45.0%; Score 618.5; DB 8
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 710
45.0%; Score 618.5; DB 8 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 8 48.2%; Pred. No. 8.7e-40;
 Human PRO polypeptide #253.
US2003207805-A1.
 ADG81248 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003194793-A1.
 protein; 250 AA
```

48.2%; Pred. No. 8.7e-40;

```
Best Local Similarity
RESULT 726
ID. ADTOC
 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
 (GETH)
 RESULT 729
 ADH04489 standard, protein, 250 AA.

Human secreted/transmembrane protein PRO1279.
US2004005628-A1.
08-JAN-2004.
(GETH) GENENTECH INC.
45.0%; Score 618.5; DB 8; Length 250;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
 ADG54831 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207367-A1.
06-NOV-2003.
(GETH.) GENENTECH INC.
 ADG34182 standard; protein; 250 AA.

Novel human secreted and transmembrane protein PRO1279.
US2004006206-A1.
US2004006206-A1.
US2004006206-A1.
US2004006206-A1.
US2004006206-A1.
US200406-A1.
US20040-A1.
US20040-A1.
US2040-A1.
US204
 ADG56487 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207366-A1.
06-NOV-2003.
 ADH12753 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003207378-A1.
 ADG61599 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207429-A1.
06-NOV-2003.
 Novel human secreted and transmembrane protein PRO1279 US2003207369-A1.
 AD426686 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003022331-A1.
 protein; 250 AA
 protein; 250 AA
 US2003.2.2.03.04-DEC-2003.
(GETH) GENENTECH INC.
"...t.ch '...ttv 48.2%;
 45.0%;
 45.0%;
 45.0%;
 45.0%;
 45.0%;
 45.0%;
 45.0%;
 ADH43641 standard; protein;
Human PRO polypeptide #104.
US2003224984-Al.
 30-JAN-2003.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 Best Local Similarity RESULT 717
 Best Local Similarity RESULT 718
 Best Local Similarity RESULT 721
 Best Local Similarity RESULT 722
 Query Match
Best Local Similarity
RESULT 723
 Query Match
Best Local Similarity
 Local Similarity
 Local Similarity
 ADG59871 standard;
 06-NOV-2003
 Query Match
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 Query Match
 Best Loca
RESULT 719
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Length 250;
 Length 250;
 Length 250;
 Length 250;
 Length 250;
 Length 250;
 Length 250;
 Length 250;
 Length 250;
 Novel human secreted and transmembrane protein PRO1279.
US2004009548-A1.
 Novel human secreted and transmembrane protein PRO1279. US2003207382-A1.
 AUGUSTANDE Standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2004009547-A1.
 Auliavi standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207383-AI.
 AULZYYU7 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2200196961-A1.
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 DB 8;
 45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
 .;
0
 45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
 DB 8;
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 8 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 Score 618.5; DB 8
Pred. No. 8.7e-40;
 ADH61490 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2004014130-A1.
 AD133652 standard, protein; 250 AA.
Human PRO polypeptide #93.
US2003096960-A1.
ADI81295 standard; protein; 250 AA. Human PRO polypeptide #253. US2003207361-A1.
 ADH69746 standard, protein, 250 AA. Human PRO polypeptide #93.
US2004019183-A1.
 45.0%;
 45.0%;
 45.0%;
 Best Local Similarity 48.2%;
RESULT 731
 45.0%;
 15-JAN-2004.
(GETH) GENENTECH INC.
 22-MAY-2003.
(GETH) GENENTECH INC.
 22-JAN-2004.
(GETH) GENENTECH INC.
 15-JAN-2004.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
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 (GETH) GENENTECH INC
 Query Match
Best Local Similarity
RESULT 733
 Best Local Similarity
RESULT 727
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
 Local Similarity
 Best Local Similarity RESULT 734
 Best Local Similarity
 Best Local Similarity
 22-MAY-2003
 29-JAN-2004
(GETH) GEN
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Human secreted/transmembrane protein PRO1279.
 ADL94689 standard; protein; 250 AA
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
 Length 250;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
 DB 8; Length 250;
 Length 250;
 DB 8; Length 250;
 nulleas6 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
 Novel human secreted and transmembrane protein PRO1279. US2004044179-A1.
 ADJ63717 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2004039164-A1.
 8
 Score 618.5; DB 8;
Pred. No. 8.7e-40;
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 Human PRO polypeptide #253.
11-Mao - 11-Mao
 protein; 250 AA.
 ADK82986 standard; protein; 250 AA.
 ADK6662 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2004044180-Al.
(4-MAR-2004)
(GETH) GENENTECH INC.
 Human PRO polypeptide #253. US2004038335-A1.
 Human PRO polypeptide #253.
US2004058424-Al.
 protein; 250 AA.
 US20040-20-2
25-WMR-2004.
(GETH) GENENTECH INC.
45.0%;
 45.0%;
 45.0%;
 PA (GETH) GENENTECH INC.
Query Match 45.0%;
Best Local Similarity 48.2%;
RESULT 739
 Best Local Similarity 48.2%;
RESULT 742
 45.0%;
 Query Match 45.0%;
Best Local Similarity 48.2%;
RESULT 737
 Match 45.0%;
Local Similarity 48.2%;
 Match 45.0%;
Local Similarity 48.2%;
 Human PRO polypeptide #104.
US2004043927-A1.
 ADJ77612 standard; protein.
Human PRO polypeptide #253
US2004038336-Al.
 06-NOV-2003.
(GETH) GENENTECH INC.
 04-MAR-2004.
(GETH) GENENTECH INC.
 04-MAR-2004.
(GETH) GENENTECH INC.
 26-FEB-2004.
(GETH) GENENTECH INC.
 11-MAR-2004.
(GETH) GENENTECH INC.
 26-FEB-2004.
(GETH) GENENTECH INC.
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
RESULT 744
 ADM27304 standard;
 Local Similarity
 Query Match
 Query Match
 Query Match
RESULT 735
ID ADI184
DE Novel
PN US2003
PD 06-NOV
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ADR72890 standard; protein; 250 AA.
Human ovarian cancer-related tumour marker kallikrein 11 (hK11) protein2.
WO2004075713-A2.
 ADR72632 standard; protein; 250 AA.
Human renal cell carcinoma-related kallikrein 11 (hKll) protein 2.
WO2004077060-A2.
10-SEP-2004.
 DB 8; Length 250;
 Length 250;
 Length 250;
 Query Match 45.0%; Score 618.5; DB 8; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 3; Length 282; Pred. No. 9.9e-40;
 Length 282;
 Length 250;
 Length 250
 Length 250
 AD196490 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207354-A1.
06-NOV-2003.
(GETH) GENENTECH INC.
 ADS34892 standard; protein; 250 AA.
Human autoimmue disease-related protein - SEQ ID 106.
WO2004083403-A2.
30-SEP-2004.
 8;
 45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
 DB 8;
 45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
 ;
;
 AAB11712 standard; protein; 282 AA.
Human serine protease BSSP6 (hBSSP6) SEQ ID NO:2
WO200031257-A1.
 US4CA-2APR-2003.
(GETH) GENENTECH INC.
(GETY Match 45.0%; Score 618.5; DB 8
(ery Match 48.2%; Pred. No. 8.7e-40;
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 Score 618.5; DB 8 Pred. No. 8.7e-40;
 45.0%; Score 618.5; DB 2 48.2%; Pred. No. 9.9e-40;
 (SMIK) SMITHKLINE BEECHAM BIOLOGICALS,
 AD195938 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003077659-A1.
 ADM28456 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2004077064-A1.
 AAY43636 standard; protein; 282 AA
 AAY42439 standard; protein; 282 AA
CASB12 amino acid sequence.
WO9949055-A1.
 10-SEP-2004.
(MOUN) MOUNT SINAI HOSPITAL.
 45.0%;
 (MOUN) MOUNT SINAI HOSPITAL.
 Query Match
Best Local Similarity 48.2%;
RESULT 746
 FUSO PHARM IND LTD.
h
Similarity 48.2%;
 22-APR-2004.
(GETH) GENENTECH INC.
US2004073015-A1.
15-APR-2004.
(GETH) GENENTECH INC.
 (APPL-) APPLERA CORP.
 Best Local Similarity RESULT 747
 PA , (MOUN) MOUNT SINAL
Query Match
Best Local Similarity
RESULT,750
 Best Local Similarity
SULT 745
 Best Local Similarity RESULT 748
 Local Similarity 752
 Best Local Similarity RESULT 749
 Best Local Similarity
RESULT 753
 30-SEP-1999
 02-JUN-2000
 Query Match
 Ouery Match
 Query Match
 Query Match
 (FUSO)
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AAB36483 standard; protein; 289 AA.
Fusion gene with human serine protease catalytic domain protein #14.
WO200066709-A2.
 Length 250;
 Length 250;
 Length 320;
 Length 320;
 Length 289
 Length 275;
 Length 225;
 Length 256;
 Length 256;
 AAB67543 standard; protein; 289 AA.
Amino acid sequence of catalytic domain in PFBK1-6XHIS-TAG
WO200116289-A2.
 31-JAN-2002.
(INOY-) INCYTE GENOMICS INC.
(ery Match 43.6%; Score 599.5; DB 5;
(ery Match 46.4%; Pred. No. 3.3e-38;
 43.8%; Score 601.5; DB 2; 47.4%; Pred. No. 1.8e-38;
 Score 601.5; DB 8;
Pred. No. 1.8e-38;
 (ORTH) ORTHO-MCNEIL PHARM RES INC.

43.6%; Score 598.5; DB 3;

tt Local Similarity 49.1%; Pred. No. 3.5e-38;
 AAB11714 standard; protein; 275 AA.
Human serine protease BSSP6 (hBSSP6) SEQ ID NO:6.
WO200031257-A1.
 43.6%; Score 599.5; DB 5;
46.4%; Pred. No. 3.3e-38;
 AAU82732 standard; protein; 320 AA.
Amino acid sequence of novel human protease #31
WO200200860-A2.
 ADNI0932 standard; protein; 256 AA.
Human kallikrein 15, marker of endocrine cancer
WO2004029285-A2.
 43.6%; Score 599; DB 5;
49.8%; Pred. No. 2.5e-38;
 Score 601; DB 3;
Pred. No. 2.1e-38;
 43.6%; Score 599; DB 5; 47.1%; Pred. No. 2.8e-38;
 43.6%; Score 599; DB 8; 47.1%; Pred. No. 2.8e-38;
 Murine NOVX protein, 225 AA.
Wozo0268649-AZ.
 AAE19166 standard; protein; 320 AA.
Human protease, PRTS-3 protein.
WO200208396-A2.
 protein; 250 AA.
 AAU79390 standard; protein; 256 AA.
Novel human kallikrein KLKIS.
WO200214485-A2.
21-FEB-2002.
 Human secreted polypeptide #252. US2004110939-A1.
 08-APR-2004.
(MOUN) MOUNT SINAI HOSPITAL.
 (MOUN) MOUNT SINAI HOSPITAL.
 43.8%;
 PD 02-JUN-2000
PA (FUSO) FUSO PHARM IND LTD.
Query Match 43.7%;
Best Local Similarity 44.2%;
RESULT 765
 "-2002.
"-2002.
"-2002.
"-4dry Match
Best Local Similarity 4, RESULT 767
ID AD117075 stand?
PD Murine NOV?
PN WO2002.
PD 06
PN W09931236-A2.
PD 24-JUN-1999.
PA, (GEST) GENSET.
Query Match
Best Local Similarity
RESULT 763
 Query Match
Best Local Similarity
RESULT 764
 Query Match
Best Local Similarity
RESULT 766
 Best Local Similarity RESULT 768
 Query Match
Best Local Similarity
RESULT 769
 Query Match
Best Local Similarity
RESULT 770
 Query Match
Best Local Similarity
 ADP19401 standard;
 10-JUN-2004.
(GEST) GENSET SA.
 03-JAN-2002.
(SUGE-) SUGEN INC.
 09-NOV-2000
 Query Match
 ADR72889 standard; protein; 282 AA.
Human ovarian cancer-related tumour-marker kallikrein 11 (hK11) protein1.
WO2004075713-A2.
 AAB35482 standard; protein; 288 AA.
Fusion gene with human serine protease catalytic domain protein #13.
WO200066709-A2.
 ADR72631 standard, protein, 282 AA.
Human renal cell carcinoma-related kallikrein 11 (hK11) protein 1.
WO2004077060-A2.
 AAY42440 standard; protein; 281 AA.
CASB12 polypeptide derived from Expressed Sequence Tag products.
WO9949055-A1.
 45.0%; Score 618.5; DB 8; Length 282; 48.2%; Pred. No. 9.9e-40;
 Length 282;
 45.0%; Score 618.5; DB 8; Length 282.48.2%; Pred. No. 9.9e-40;
 45.0%; Score 618.5; DB 8; Length 282.48.2%; Pred. No. 9.9e-40;
 Length 282;
 Length 281;
 DB 8; Length 282
 Length 288
 Length 288
 ADQ17587 standard, protein, 282 AA.
Human soft Lissue sarcoma-upregulated protein - SEQ ID 404.
WO20040489318-A2.
10-UNM-2004.
(PROT-) PROTEIN DESIGN LABS INC.
 мањ67542 standard; protein; 288 дА.
Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG
W02.00116289-A2.
 AAY36093 standard; protein; 250 AA.
Extended human secreted protein sequence, SEQ ID NO. 478
 ADS34893 standard; protein; 282 AA.
Human autoimmune disease-related protein - SEQ ID 107.
WO2004083403-A2.
A human prostate-associated serum protease (PRASP) W09941387-A2.
 / Match 45.0%; Score 618.5; DB 8; Local Similarity 48.2%; Pred. No. 9.9e-40;
 OS-NOV-2000.

(ORTH) ORTHO-MCNEIL PHARM RES INC.

ery Match
43.9%; Score 602.5; DB 3;

ery Match
71.1%; Pred. No. 1.7e-38;
 Score 618.5; DB 3;
Pred. No. 9.9e-40;
 43.9%; Score 602.5; DB 4; 51.1%; Pred. No. 1.7e-38;
 ADNI1125 standard; protein; 282 AA.
Human kallikrein-11, marker for prostate cancer.
WO2004029616-A2.
 45.0%; Score 618.5; DB 8 48.2%; Pred. No. 9.9e-40;
 (ORTH) ORTHO-MCNEIL PHARM INC.
 08-APR-2004.
(MOUN) MOUNT SINAI HOSPITAL.
 (MOUN) MOUNT SINAI HOSPITAL.
 (MOUN) MOUNT SINAI HOSPITAL.
 WOX3-2--
19-AUG-1999.
(INCY-) INCYTE PHARM INC.
orv Match '--'13rity 48.2%;
 (APPL-) APPLERA CORP.
 Best Local Similarity RESULT 755
 Best Local Similarity
RESULT 757
 Query Match
Best Local Similarity
RESULT 754
 Best Local Similarity
 Local Similarity
 Local Similarity
 10-SEP-2004
 30-SEP-2004
 10-SEP-2004
 Query Match
 Ouery Match
 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
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ADL/1094 standard; protein; 277 AA.
Human kallikrein 13 protein SEQ ID NO:1.
WO2004021009-A2.
11-MAR-2004.
 ABP64969 standard; protein; 250 AA.
Human protein SEQ ID 629.
WO200259260-A2.
 AB000554 standard; protéin; 277 AA.
Novel human polypeptide #141.
WO2003023013-A2.
 AAB21298 standard; protein; 250 AA.
Human KLK-L3 protein #2.
WO200053776-A2.
 AAB21300 standard; protein; 277 AA.
Human KLK-L4 protein #2.
WO200053776-A2.
 08-APR-2004.
(MOUN) MOUNT SINAI HOSPITAL.
 14-SEP-2000.
(MOUN) MOUNT SINAI HOSPITAL.
 MOUNT SINAI HOSPITAL.
 (MOUN) MOUNT SINAI HOSPITAL.
 41.3%;
 (INCY-) INCYTE GENOMICS INC.
 (GETH) GENENTECH INC
 Best Local Similarity
RESULT 782
 Best_Local Similarity RESULT 784
 Best Local Similarity
 Best Local Similarity RESULT 783
 Best Local Similarity RESULT 786
 Best Local Similarity
RESULT 788
 Best Local Similarity RESULT 789
 Best Local Similarity
 Query Match
Best Local Similarity
 01-AUG-2002.
(HYSE-) HYSEQ INC.
 (HYSE-) HYSEQ INC.
14-SEP-2000
(MOUN) MOUN
 03-JAN-2003
 14-SEP-2000
 20-MAR-2003
 Query Match
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 Query Match
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 Query Match
 Learity 48.6%; Pred. No. 7.7e-38;

Larity 48.6%; Pred. No. 7.7e-38;

Luman TLSP.

DE Human TLSP.

PN WO200033776-A2.

PA (MOUN) MOUNT SINAI HOSPITAL.

Query Match

Best Local Similarity 49.3%; Pred. No. 8.7e-38;

ID AAW08475 standard; protein; 247 AA.

DE POrcine trypainogen.

PD 03-JAN-1997.
 ORTHO-MCNEIL PHARM INC.
th
Similarity 49.1%; Pred. No. 3.5e-38;
 Score 597.5; DB 4; Length 248; Pred. No. 3.6e-38;
 Length 276;
 Score 593.5; DB 5; Length 260;
Pred. No. 7.7e-38;
 Length 247;
 . Match 41.7%; Score 573; DB 8; Length 247; Local Similarity 45.6%; Pred. No. 2.8e-36;
 Length 298;
 Length 247;
 Score 597.5; DB 3;
Pred. No. 4e-38;
 Mouse serine protease BSSP6 (mBSSP6) SEQ ID NO:4. Mouse serine protease BSSP6 (mBSSP6) SEQ ID NO:4. W0200031257-A1. 02-JUN-2000. (FUSO) FUSO PHARM IND LTD. 43.5%; Score 597.5; DB 3; sty Match 43.5%; Pred. No. 4e-38; st Local Similarity 47.0%; Pred. No. 4e-38;
 Human novel polypeptide sequence, SEQ ID NO:1471 WO2003029271-A2. 10-APR-2003. (HYSE-) HYSEQ INC.
 41.7%; Score 573; DB 2; 45.6%; Pred. No. 2.8e-36;
 OGENOUS TOCKE DIAGNOSTICS GMBH.
(HOFF) HOFFMANN LA ROCHE & CO AG F.
ry Match
t Local Similarity 45.6%; Pred. No. 2.8e-36;
 Score 595; DB 7;
Pred. No. 6.8e-38;
 Human NOVX protein homologue SeqID 613.
 AAE08017 standard; protein; 248 AA.
Human PS133 consensus protein sequence
US6232456-B1.
 ABB98258 standard; protein; 247 AA.
Pig trypsinogen SEQ ID NO 1.
WO200261064-A2.
08-AUG-2002.
 ADJ92132 standard; protein; 247 AA
 AAB21306 standard; protein; 251 AA Human KLK-L6 protein #2. W0200053776-A2.
 ADC31389 standard; protein; 298 AA
 Pig pro-trypsin.
0x200404345-Al.
04-MRR-2004.
(NOVO) NOVOZYMES BIOTECH INC.
 43.5%;
 43.3%;
 Best Local Similarity
RESULT 773
ID AABI1713 standard; pr
DE Mouse serine protease
PN WO200031257-A1.
PD 02-UUN-2000.
PA (FUSO) FUSO PHARM IN
 Query Match
Best Local Similarity
RESULT 775
ID AD117077 standard; p1
DE Human NOYX protein hc
PN W0200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
 15-MAY-2001.
(ABBO) ABBOTT LAB.
 Best Local Similarity
 Local Similarity
08-MAR-2001
(ORTH) ORTH
 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
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PADER

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ABJ26666 standard; protein; 267 AA.
Human protein modification + maintenance molecule protein SEQ ID No 20.
WO2003000844-A2.
 41.4%; Score 568.5; DB 3; Length 250; 46.7%; Pred. No. 6.2e-36;
41.4%; Score 569.5; DB 3; Length 251; 46.9%; Pred. No. 5.2e-36;
 41.4%; Score 569.5; DB 8; Length 251; 46.9%; Pred. No. 5.2e-36;
 41.4%; Score 568.5; DB 5; Length 250; 46.7%; Pred. No. 6.2e-36;
 DB 6; Length 250;
 8; Length 250;
 41.4%; Score 569.5; DB 6; Length 267 46.9%; Pred. No. 5.6e-36;
 Length 277;
 Length 277;
 ABR55400 standard; protein; 250 AA.
Amino acid sequence of human kallikrein 9 (hK9).
W020033131-A2.
24-ARR-2003.
(MOUN) MOUNT SINAI HOSPITAL.
 41.3%; Score 567; DB 3;
46.8%; Pred. No. 9e-36;
 ADN10930 standard; protein; 251 AA.
Human kallikrein 14, marker of endocrine cancer
WO2004029285-A2.
 41.4%; Score 568.5; DB 6 46.7%; Pred. No. 6.2e-36;
 41.4%; Score 568.5; DB 8 46.7%; Pred. No. 6.2e-36;
 Score 567; DB 6;
Pred. No. 9e-36;
 ADNO5516 standard; protein; 250 AA. Antipsoriatic protein sequence #924. W02004028419-A2. 08-APR-2004.
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us-10-015-385a-194.rag.spdi

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Query Match 41.1%; Score 564.5; DB 4; Length 293; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 801
 Ouery Match 41.1%; Score 564.5; DB 6; Length 293; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 805
 Query Match 41.1%; Score 564.5; DB 6; Length 293; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 807
 Length 293;
 Length 293;
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 Length 293;
 Length 293;
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 ABO17843 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003032156-A1.
 ABUS9142 standard; protein; 293 AA.
Novel human secreted or transmembrane protein PRO1132.
US2002132252-A1.
 AAB65249 standard; protein; 293 AA.
Human PRO1132 (UNQ570) protein sequence SEQ ID NO:309
WO200073454-A1.
 41.1%; Score 564.5; DB 3; 45.3%; Pred. No. 1.5e-35;
 (MOUN) MOUNT SINAI HOSPITAL.
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t Local Similarity 45.3%; Pred. No. 1.5e-35;
 Score 564.5; DB 5;
Pred. No. 1.5e-35;
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 Query Match 41.1%; Score 564.5; DB 4
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 802
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Pred. No. 1.5e-35;
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45.3%; Pred. No. 1.5e-35;
 ABU82654 standard; protein; 293 AA.
Human secreted/transmembrane protein PRO1132.
22003032023-A1.
13-FEB-2003.
 AAB21296 standard; protein; 293 AA.
Human KLK-L2 protein.
WG20053776-A2.
H4-SEP-2000.
 AAU12399 standard; protein; 293 AA. Human PRO132 polypeptide sequence. WO200140466-A2.
 ABU58064 standard; protein; 293 AA.
Human PRO polypeptide #96.
US2003027163-A1.
 A DAS7425 standard; protein; 293 AA. Human secreted protein #257. WO2002102994-A2. 27-DEC-2002. (HUMA-) HUMAN GENOME SCI INC.
 AAU81966 standard; protein; 293 AA
 41.1%;
 Query Match
Best Local Similarity 45.3%;
RESULT 803
 07-DEC-2000.
(GETH) GENENTECH INC.
 Human PRO1132.
WO200109327-A2.
08-FEB-2001.
(GETH) GENENTECH INC.
 19-SEP-2002.
(GETH) GENENTECH INC.
 13-FEB-2003.
(GETH) GENENTECH INC.
Query Match
Best Local Similarity
RESULT 799
 Best Local Similarity
RESULT 800
 Best Local Similarity RESULT 804
 Best Local Similarity RESULT 806
 Best Local Similarity
RESULT 808
 06-FEB-2003.
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 15-JUL-1999.
(HUMA.) HUMAN GENOME SCI INC.
11:19; Score 564.5; DB 2; Length 293;
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 4; Length 247;
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(MOUN) MOUNT SINAI HOSPITAL.

1.3%; Score 567; DB 8; Length 277; t Local Similarity 46.8%; Pred. No. 9e-36;
 Score 567; DB 8; Length 277;
Pred. No. 9e-36;
 ADRI4575 standard; protein; 277 AA.

Human NF-kappaB pathway-associated protein SeqID576.
WO2004065577-A2.
05-AUG-2004.
(BRIM) BRISTOL-MYERS SQUIBB CO.
 41.1%; Score 564.5; DB 2; 45.3%; Pred. No. 1.5e-35;
 02-AUG-2001.
(HUDA-) HUMAN GENOME SCI INC.
(HTDA HUTCH 41.1%; Score 564.5; DB 4;
ery Match 46.9%; Pred. No. 1.3e-35;
 AAY38426 standard; protein; 293 AA.
Human secreted protein encoded by gene No. 27.
WO9935158-A1.
 AAY38412 standard; protein; 293 AA.
Human secreted protein encoded by gene No. 27.
WO9935158-A1.
 AAU16971 standard; protein; 251 AA.
Human novel secreted protein, SEQ ID 212.
WO200155441-A2.
 protein; 293 AA.
derived protease (KDP)
 (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
 Antipsoriatic protein; 277 AA. WO2004028479-AZ. 08-APR-2004
 AAUZ3217 standard; protein; 247 AA. Novel human enzyme polypeptide #303.WO200155301-A2.
 -AAX30524 standard; protein; 293 AA.
Human PDSP-1 protein.
WO9946391-A2.
 AAY66726 standard; protein; 293 AA.
Membrane-bound protein PRO1132.
WO9963088-A2.
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Local Similarity 46.8%;
 15-APR-1999.
(PROC) PROCTER & GAMBLE CO.
 08-APR-2004.
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RESULT 793
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 AAY16777 standard;
Human keratinocyte
 Best Local Similarity
RESULT 797
 Best Local Similarity
 WO9918219-A1.
 09-DEC-1999
 16-SEP-1999
 Query Match
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RESULT 796
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RESULT 798
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Human secreted protein.
WO2002102993-A2.
27-DEC-2002.
(HUMA-) HUMAN GENOME SCI INC.
 23-JAN-2003.
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 Best Local Similarity RESULT 822
 Best Local Similarity RESULT 824
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 US2002127576-A1.
 30-JAN-2003.
 06-FEB-2003.
 20-FEB-2003
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ADA56974 standard; protein; 293 AA.

Human secreted protein #257.

WO2002102994-A2.

YO2002102994-A2.

(HUMA-) HUMAN GENOME SCI INC.

A1.1%; Score 564.5; DB 6; Length 293;

ELocal Similarity 45.3%; Pred. No. 1.5e-35;
 TO-DEC-2002.
(HUMA-) HUMAN GENOME SCI INC.
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41.1%; Score 564.5; DB 6; Length 293;
 ADA57428 standard; protein; 293 AA.

Human secreted protein #257.

WO2002102994-A2.

27-DEC-2002.

(HUMA-) HUWAN GENOME SCI INC.

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MAIL : Score 564.5; DB 6; Length 293;

FLocal Similarity 45.3%; Pred. No. 1.5e-35;
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US200300531-A1.
02-JAN-2003.
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 ABUGO573 standard; protein; 293 AA.
Human secreted/transmembrane protein, #130.
 Human secreted protein; 293 AA. WO2002102994-A2.
 ABU66797 standard; protein; 293 AA. Human PRO polypeptide #228. US2003036180-A1. 20-FEB-2003. G-FEB-2003.
 ABU13955 standard; protein; 293 AA.
Human PRO1132 polypeptide.
US2002103125-A1.
01-AUG-2002.
 ABUB1097 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003004311-A1.
 Human secreted protein; 293 AA. WO2002102993-A2.
 ADA41305 standard; protein; 293 AA.
 27-DEC-2002.
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 02-JAN-2003.
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 (GETH) GENENTECH INC.
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Best Local Similarity
RESULT 811
ID ABU60573 standard; pro
DE Human secreted/transme
PD 31-OCT-2002.
PA (GETH) GENENTECH INC
 (GETH) GENENTECH LTD.
 (GETH) GENENTECH INC.
 Best Local Similarity RESULT 816
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RESULT 810
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US2003022187-A1.
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Novel human secreted or transmembrane protein PRO1346.
US2003027985-A1.
 41.1%; Score 564.5; DB 6; 45.3%; Pred. No. 1.5e-35;
 WOLDEC-2002.
27-DEC-2002.
(HUMA-) HUMAN GENOME SCI INC.
(ery Match 41.1%; Score 564.5; DB 6; ery Match 6:milarity 45.3%; Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 6; 45.3%; Pred. No. 1.5e-35;
 ABUSS978 standard; protein; 293 AA.
Novel secreted and transmembrane protein PRO1132.
US2003017563-A1.
 ABO25068 standard; protein; 293 AA.
Human secreted/transmembrane protein (PRO) #228
US2003036179-A1.
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Human sectreted/transmembrane protein, #130.
US2002142961-A1.
 ABU59289 standard; protein; 293 AA.
Human secreted/transmembrane protein, #130.
US2003027162-A1.
UG-FEB-2003.
 ADA41306 standard; protein; 293 AA Human secreted protein. WO2002102993-A2.
 ABO25986 standard; protein; 293 AA.
Human PRO1132 polypeptide.
 ADA40825 standard; protein; 293 AA
Human secreted protein.
WO2002102993-A2.
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ADA61679 standard; protein; 293 AA.
Homo sapiens.
US2003049816-A1.
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Novel human secreted and transmembrane protein PRO1132.
US2003022328-A1.
 Novel human secreted and transmembrane protein PRO1132. US2003017476-A1.
 ABUGI662 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2002177164-A1.
 ABU88601 standard; protein; 293 AA.
Human secreted and transmembrane polypeptide PRO1132.
US2002197615-A1.
 ABUG7073 standard; protein; 293 AA.
Human secreted/transmembrane, PRO, protein SEQ ID
US2003032155-A1.
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US2003073212-A1.
 AUA19056 standard; protein; 293 AA. Human PRO polypeptide #228. US2003054517-A1. 20-MAR.2003.
 Human PRO polypeptide #96. US2002123463-A1.
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US2003017981-A1.
 30-JAN-2003.
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 28-NOV-2002.
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 26-DEC-2002.
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 17-APR-2003.
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 13-FEB-2003
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Novel human secreted and transmembrane protein PRO1132.
N22003068796-A1.
10-APR-2003.
 ADA86484 standard; protein; 293 AA.
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US2003082711-A1.
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Pred. No. 1.5e-35;
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US2003059831-A1.
 Human secreted/transmembrane protein PRO1132. US200308297-A1.
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Human PRO polypeptide #228.
US2003068795-A1.
 ADB28005 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003082704-A1.
 ADA47834 standard; protein; 293 AA.
Human PRO polypeptide #228.
UV22003073215-A1.
17-APR-2003.
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Human PRO polypeptide #228.
US2003087350-A1.
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 ADA10293 standard; protein; 293 AA
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 08-MAY-2003.
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 09-JAN-2003.
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13-MAR-2003.
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45.3%; Pred. No. 1.5e-35;

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 ADA87587 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003087345-A1.
 AUA91881 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003082694-A1.
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Pred. No. 1.5e-35;
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 Score 564.5; DB 6;
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Human secreted/transmembrane protein PRO1132.
US2003054359-A1.
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US2003082763-A1.
 Human PRO polypeptide #228.
US2003087349-A1.
 ADB30636 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003068794-A1.
 ADA97144 standard, protein, 293 AA.
Human PRO polypeptide #228.
US2003082705-A1.
 ADA17837 standard; protein; 293 AA
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ID ADB30636 standard; prr.

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 08-MAY-2003.
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 Novel human secreted and transmembrane protein PRO1132. US2003944945-A1.
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Novel human secreted and transmembrane protein PRO1132
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Human secreted/transmembrane protein PRO1132.
US2003059832-A1.
 ADB24815 standard; protein; 293 AA. Human PRO polypeptide SEQ ID NO 456 US2003077713-A1.
 Human PRO polypeptide #228.
US2003077722-A1.
ADB14944 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003087351-A1.
 ADBI3328 standard, protein, 293 AA.
Human PRO polypeptide #228.
US2003082710-A1.
 ADA74582 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003068798-AI.
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 17-APR-2003.
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DB 6; Length 293;

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Human secreted/transmembrane protein PRO1132.
US2003060407-A1.
27-MAR-2003.
 ADA61116 standard; protein; 293 AA.
 ADB24263 standard; protein; 293 AA.
Human PRO polypeptide SEQ ID NO 456
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24-APR-2003.
 Human PRO polypeptide #228.
24-app.
 ADA81164 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003082702-A1.
 ADB31188 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003096386-A1.
 ADB26501 standard, protein; 293 AA.
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Human PRO polypeptide #228.
US2003082690-A1.
 ADA96040 standard; protein; 293 AA.
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01-MAY-2003.
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 22-MAY-2003.
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US2003073216-A1.
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Human PRO polypeptide #228.
US2003073214-A1.
 Human PRO polypeptide #228.
17-APP-2003
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01-Mav-^^^
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Human PRO polypeptide #228.
US2003082761-A1.
 ADA75854 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003082703-A1.
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US2003017982-A1.
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Human secreted/transmembrane protein PRO1132.
V22003055782-A1.
27-MAR-2003.
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US2003059909-A1.
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US2003022239-A1.
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Novel human secreted and transmembrane protein PRO1132.
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US2003054516-A1.
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Novel human secreted and transmembrane protein PRO1132.
US2003082765-A1.
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US2003068797-A1.
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Novel human secreted and transmembrane protein PRO1132.
US2003087347-A1.
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 Augebb68 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US203082689-Al.
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 Human PRO polypeptide #96.
US2003054403-A1.
 ADA67077 standard; protein; 293 AA.
Human PRO polypeptide #228.
US20030687933A1.
IO-APR-2003.
(GETH) GENENTECH INC.
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24-2003/7711-A1.
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US2003082764-A1.
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US2003082687-A1.
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Human PRO polypeptide #228.
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01-MAY-2003.
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US2003082697-A1.
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Human secreted/transmembrane protein PRO1132.
US2003068647-A1.
 ADC11487 standard; protein; 293 AA.
Human secreted/transmembrane protein PRO1132.
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US2003087363-A1.
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Novel human secreted and transmembrane protein Seg ID456.
US2003087366-A1.
ADC50497 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003092106-A1.
 ADC72044 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003092107-A1.
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USZ03092105-A1.
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US2003087354-A1.
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US2003194774-Al.
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Pred. No. 1.5e-35;
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 ADC80089 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003087358-A1.
 ADD06928 standard, protein, 293 AA.
Novel human serreted and transmembrane protein PRO1132.
US2002193300-A1.
 ADD41271 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003203438-A1.
 AUU53702 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003203437-A1.
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Pred. No. 1.5e-35;
 Score 564.5; DB 7;
Pred. No. 1.5e-35;
 Human PRO polypeptide #228.
US2003194792-Al.
16-OCT-2003.
 ADD09558 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003194775-A1.
 ADD52410 standard, protein, 293 AA.
Human PRO polypeptide #228.
US2003194769-A1.
 ADD55282 standard; protein; 293 AA.
Human PRO polypeptide #96.
US2003077593-A1.
 protein; 293 AA.
 ADD56240 standard; protein; 293 AA.
Human PRO polypeptide #96.
 PD 08-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 45.3%;

RESULT 959
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 41.18;
 41.1%;
 41.18;
 41.1%;
 41.1%;
 Match 41.1%;
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Human PRO polypeptide #96.
US2003059783-A1.
 30-OCT-2003.
(GETH) GENENTECH INC.
 16-OCT-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 30-OCT-2003. (GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 Local Similarity
 Best Local Similarity
RESULT 965
 Query Match
Best Local Similarity
 Local Similarity
 Local Similarity
 Local Similarity
 27-MAR-2003
 24-APR-2003.
 19-DEC-200
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RESULT 958
ID ADC800
DE Novel
PN US2003
PD 08-MAY
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 ADD54273 standard; protein; 293°AA.
Novel human secreted and transmembrane protein PRO1132
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 Score 564.5; DB 7
Pred. No. 1.5e-35;
 ADD51858 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003194779-A1.
 ADD02657 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003203431-A1.
 ADD02091 standard, protein; 293 AA.
Human PRO polypeptide #228.
US2003203430-A1.
 ADD54678 standard; protein; 293 AA.
Human PRO polypeptide #96.
US2002132253-Al.
 ADD92590 standard; protein; 293 AA.
 ADD91486 standard, protein, 293 AA.
Human PRO polypeptide #228.
US2003199055-A1.
 ADE04100 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003199057-A1.
 Ouery Match 41.1%;
Best Local Similarity 45.3%;
RESULT 971
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Best Local Similarity 45.3%;
RESULT 972
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 41.18;
 45.38;
 45.38;
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7; Length 293;

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Novel human secreted and transmembrane protein PRO1132.
US2003087305-A1.
 ADE32949 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
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Pred. No. 1.5e-35;
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US2003203429-A1.
 Human PRO polypeptide #228.
US2003199059-Al.
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Human PRO polypeptide #228.
US2003194768-A1.
 ADE19562 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003199025-A1.
 ADE19010 standard, protein, 293 AA.
Human PRO polypeptide #228.
US2003199026-A1.
 ADE43206 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003199033-A1.
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US2003199064-A1.
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Best Local Similarity 45.3%;
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 23-OCT-2003.
(GETH) GENENTECH INC.
 30-OCT-2003.
(GETH) GENENTECH INC.
 16-OCT-2003. (GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 23-OCT-2003.
(GETH) GENENTECH INC.
 23-OCT-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 (GETH) GENENTECH INC
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
RESULT 995
 Best Local Similarity
SULT 990
Best Local Similarity RESULT 986
 Best_Local Similarity RESULT 987
 Query Match
Best Local Similarity
RESULT 988
 Query Match
Best Local Similarity
 Best Local Similarity RESULT 994
 US2003194766-A1.
 08-MAY-2003.
 23-OCT-2003
 23-OCT-2003
 16-OCT-2003
 Query Match
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 RESULT 992
 RESULT 989
 06-NOV-2003.
(GETH) GENENTECH INC.
41.1%; Score 564.5; DB 7; Length 293;
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Novel human secreted and transmembrane protein PRO1132.
US2003194767-A1.
 ADE32397 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003194765-A1.
 ADE34053 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003194791-A1.
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Pred. No. 1.5e-35;
 ADD92038 standard; protein; 293 AA. Human PRO polypeptide #228. US2003199053-A1. 23-OCT-2003. (GETH.) GENENTECH INC.
 Human PRO polypeptide #228.
US2003207417-A1.
 ADE22329 standard, protein, 293 AA.
Human PRO polypeptide #228.
US2003199056-A1.
 __.v.v standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003199023-A1.
 ADD79553 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003203428-Al.
 ADE42089 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003194772-A1.
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RESULT 981
ID ADE1/906 standard; protein; 293
DE Human PRO polypeptide #228.
PN US2001999023-A1.
PD 23-CGT-2003.
 41.18;
 41.1%;
 41.1%;
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 41.1%;
 Local Similarity 45.3%;
 30-OCT-2003.
(GETH) GENENTECH INC.
 16-OCT-2003.
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(GETH) GENENTECH INC.
 23-OCT-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 Query Match
Best Local Similarity
REGULT 983
ID ADE33501 standard, p.
DE Novel human secreted
PN US200319477-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH IN
 Local Similarity
 Best Local Similarity RESULT 978
 Best Local Similarity RESULT 984
 Local Similarity
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 Local Similarity
 Query Match
Best Local Si
RESULT 979
 Query Match
 Query Match
 Query Match
 Query Match
 Best Loca
RESULT 982
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DB 7; Length 293;

DB 7; Length 293;

Length 293;

Length 293;

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Human PRO polypeptide #228.
US2003207370-A1.
06-NOV-2003.
 06-NOV-2003
 06-NOV-2003
 06-NOV-2003
 06-NOV-2003
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Pred. No. 1.5e-35;
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 Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
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 ADG21606 standard, protein, 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207355-A1.
 ADG23247 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207384-A1.
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45.3%; Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
 ADF67236 standard; protein; 293 AA.
Human PRO1132 amino acid sequence SEQ ID NO:309
US2002198148-A1.
26-DEC-2002.
(GETH) GENENTECH INC.
ADE42641 standard; protein; 293 AA.
Human PRO polypeptide #228.
UW2003199032-A1.
23-OCT-2003.
(GETH.) GENENTECH INC.
 ADD89685 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003199028-A1.
 ADE40969 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003199031-A1.
23-0CT-2003.
 ADE04768 standard, protein, 293 AA.
Human PRO polypeptide #228.
US2003199034-A1.
 ADE92897 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003194777-A1.
 J 1004
ADF97582 standard; protein; 293 AA.
 protein; 293 AA
 US20052,
06-NOV-2003.
(GETH) GENENTECH INC.
Match '1rtity 41.18;
 USZUCZ-2003.
23-007-2003.
(GETH) GENENTECH INC.
Match '-1arity 45.3%;
 Usacoccione

06-NOV-2003.

(GETH) GENENTECH INC.

A11.1%;

A10.1%;

A11.1%;
 41.18;
 41.1%;
 41.1%;
 Query Match
Best Local Similarity 45.3%;
RESULT 1000
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Best Local Similarity 45.3%;
 ADD80657 standard; protein;
Human PRO polypeptide #228
US2003207418-A1.
 06-NOV-2003.
(GETH) GENENTECH INC.
 16-OCT-2003.
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 23-OCT-2003.
(GETH) GENENTECH INC.
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 Best Local Similarity RESULT 1004
 Best Local Similarity
RESULT 1002
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Best Local Similarity
RESULT 997
 Best Local Similarity RESULT 999
 Best Local Similarity
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 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
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Best Local Similarity 45.3%; Score 564.5; DB 7; Length 293; RESULT 1005

RESULT 1005

DE Human PRO polypeptide #228.
PN US2003207373-A1.
PD 06-NOV-2003.
A (GETH) GENENTECH INC.
 DB 7; Length 293;
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Novel human secreted and transmembrane protein PRO1132.
US2003207388-A1.
 ADH55386 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207381-A1.
 ADI64157 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207385-A1.
 RESULT 1008

1D ADMS5938 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132
PN US2003207379-A1.
 ADIG5106 standard, protein, 293 AA, Novel human secreted and transmembrane protein PRO1132 US2003207386-A1.
 ADI65605 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003207387-A1.
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Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 7; 45.3%; Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 7 45.3%; Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 7 45.3%; Pred. No. 1.5e-35;
 y Match 41.1%; Score 564.5; DB 7
Local Similarity 45.3%; Pred. No. 1.5e-35;
 Human PRO polypeptide #228.
05-NAV.
 Best Local Similarity 45.3%; Fred. RESULT 1009
ID AD135490 standard; protein; 293 AA. DE Human PRO polypeptide #96.
PN US2003050457-Al.
 41.1%;
 45.3%;
 (GETH) GENENTECH INC.
 (GETH) GENENTECH INC
 (GETH) GENENTECH INC
 GENENTECH INC.
 (GETH) GENENTECH INC.
 (GETH) GENENTECH INC
 Best Local Similarity
RESULT 1006
 Query Match
Best Local Similarity
RESULT 1007
 Best Local Similarity RESULT 1011
 Local Similarity
 Query Match
Best Local Similarity
 Best Local Similarity RESULT 1010
 13-MAR-2003.
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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 Score 564.5; DB 8, Pred. No. 1.5e-35;
 Score 564.5; DB 8 Pred. No. 1.5e-35;
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 Lunan PRO polypeptide #228.
US2003211571-A1.
 Lucas scandard; protein; 293 AA. Human PRO polypeptide #228. US2003092108-AI.
 ADD88005 standard; protein; 293 AA. Human PRO polypeptide #228. US2003092113-A1. IS-MAY-2003. (GETH) GENENTECH INC.
 ADE23985 standard, protein; 293 AA.
Human PRO polypeptide #228.
US2003092110-A1.
 ADD76641 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003100087-A1.
 JA DE24628 standard; protein; 293 AA. Human PRO polypeptide #228.
US2003092111-A1.
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 293 AA
 293 AA
 ADE89319 standard; protein; 2: thumber PRO polypeptide #228. US2003199062-Al. 23-OCT-2003. (GETH.) GENENTECH INC.
 41.1%;
 41.1%;
 41.1%;
 41.1%;
 41.18;
 PD 15-MAY-2003.

PA (GETH) GENENTECH INC.

QUELY MATCh 41.1%;

Best Local Similarity 45.3%;

RESULT 1029
 Human PRO polypeptide #228. US2003203440-Al.
 Query Match 41.1%;
Best Local Similarity 45.3%;
RESULT 1028
 ADD87453 standard, protein;
Human PRO polypeptide #228.
US2003203439-A1.
 15-MAY-2003.
(GETH) GENENTECH INC.
 30-OCT-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 15-MAY-2003.
(GETH) GENENTECH INC.
 29-MAY-2003.
(GETH) GENENTECH INC.
 30-OCT-2003.
(GETH) GENENTECH INC
 Query Match
Best Local Similarity
RESULT 1030
 Query Match
Best Local Similarity
RESULT 1025
ID ADD86409 standard; p
 Best Local Similarity RESULT 1026
 Best Local Similarity
 Query Match
Best Local Similarity
RESULT 1023
 Query Match
Best Local Similarity
 Best Local Similarity
RESULT 1031
 13-NOV-2003
 Ouery Match
 Query Match
 Query Match
 Query Match
 ADN39198 standard; protein; 293 AA.
Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:516
WO2003042661-A2.
 vuery match
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1016
 vuery Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1021
 Score 564.5; DB 7; Length 293; Pred. No. 1.5e-35;
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 Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
 PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1020
 Length 293;
 DB 7; Length 293;
 Length 293
 Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 1015.

DE Novel human secreted and transmembrane protein PRO1132. PD 06-NOV-2003.

RESULT 1015.

RESULT ADMINISTRATION 1.293 AA.

DE Novel human secreted and transmembrane protein PRO1132.

PD 06-NOV-2003.

Query Match
 ADM82636 standard; protein; 293 AA.

Novel human secreted and transmembrane protein PRO1132.
US2003087355-A1.
08-MAY-2003.
(GETH) GENENTECH INC.
 ADN14931 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003087357-A1.
 AUCHIL93 Standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
 Novel human secreted and transmembrane protein PRO1132-US2003049682-A1.
 AUNIOU35 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PROI132.
US200307353-A1.
 ADNI6664 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003087385-A1.
 ADNI5483 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003087356-A1.
 PD 08-MAY-2003.

PA (GETH) GENENTECH INC.

Query Match 41.1%; Score 564.5; DB 7;

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RESULT 1019
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06-NOV-2003.
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 15-MAY-2003.
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 Best Local Similarity
RESULT 1017
 08-MAY-2003
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Human PRO polypeptide #228.
US2003199063-A1.
 ADG03536 standard; protein; 293 AA
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Best Local Similarity 45.3%;
RESULT 1043
 41.1%;
 Query Match 41.1%;
Best Local Similarity 45.3%;
RESULT 1050
 23-OCT-2003.
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 (GETH) GENENTECH INC.
 11-DEC-2003.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC
 (GETH) GENENTECH INC
 (GETH) GENENTECH INC
 Best Local Similarity
RESULT 1049
 Best Local Similarity RESULT 1042
 Best Local Similarity
RESULT 1045
 Best Local Similarity RESULT 1047
 Best Local Similarity RESULT 1046
 06-NOV-2003
 06-NOV-2003
 06-NOV-2003
 Query Match
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 Query Match
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 Query Match
 BESE
 Score 564.5; DB 8; Length 293; Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293; Pred. No. 1.5e-35;
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Novel human secreted and transmembrane protein PRO1132.
US2003199051-A1.
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Human PRO polypeptide #228.
US2003199061-A1.
 ADE95339 standard; protein; 293 AA. Human PRO polypeptide #228. US2003199052-A1. C33-OCT-2003 (GETH) GENENTECH INC.
 ADE18458 standard; protein; 293 AA.
Human PRO polypeptide #228.
US200319474-A1.
16-OCT-2003.
(GETH) GENENTECH INC.
 ADE88767 standard, protein, 293 AA.
Human PRO polypeptide #228.
US2003199054-A1.
 ADF35435 standard; protein; 293 AA.
Human PRO1132 polypeptide.
US2003194760-A1.
 Human PRO polypeptide #228.
US2003199060-Al.
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 protein; 293 AA
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23-007-2003.
(GETH) GENENTECH INC.
41.1%;
 Best Local Similarity 45.3%;
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Best Local Similarity 45.3%;
RESULT 1041
 Query Match
Best Local Similarity 45.3%;
RESULT 1033
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 Watch 41.1%;
Local Similarity 45.3%;
 Match 41.1%;
Local Similarity 45.3%;
 Query Match 41.1%;
Best Local Similarity 45.3%;
RESULT 1040
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Local Similarity 45.3%;
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Human PRO polypeptide #228.
US2003199027-A1.
 Human PRO polypeptide #228.
US2003199029-A1.
 23-OCT-2003.
(GETH) GENENTECH INC.
 23-OCT-2003.
(GETH) GENENTECH INC.
 23-OCT-2003.
(GETH) GENENTECH INC.
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 Best Local Similarity RESULT 1034
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 ADF35030 standard;
 16-OCT-2003.
 23-OCT-2003
 23-OCT-2003
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 Query Match
 Query Match
 Query Match
 Query Match
 RESULT
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41.1%; Score 564.5; DB 8; Length 293; 45.3%; Pred. No. 1.5e-35;
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 Length 293;
 Length 293;
 Length 293;
 DB 8; Length 293;
 Length 293;
 ADE91793 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003199058-A1.
 ADG22158 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207360-A1.
 ADGA4351 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132 US2003207426-A1.
 Score 564.5; DB 8;
Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 8; 45.3%; Pred. No. 1.5e-35;
 vuery Match 41.1%; Score 564.5; DB 8; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT_1048
 Score 564.5; DB 8;
Pred. No. 1.5e-35;
 Score 564.5; DB 8;
Pred. No. 1.5e-35;
 Score 564.5; DB 8 Pred. No. 1.5e-35;
 Human PRO polypeptide #228.
US2003207352-A1.
 ADGII685 standard; protein; 293 AA.
Human PRO1132 polypeptide.
US2003228655-A1.
 ADG20228 standard, protein; 293 AA.
Human PRO polypeptide #228.
US2003207376-A1.
 ADF98134 standard; protein; 293 AA. Human PRO polypeptide #228.
US2003207422-A1.
 ADF98705 standard, protein, 293 AA.
Human PRO polypeptide #228.
US2003208055-A1.
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US2003207374-A1.
. 06-NOV-2003.
(GETH) GENENTECH INC.
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 Best Local Similarity
RESULT 1064
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 Best Local Similarity
 Query Match
 DB 8; Length 293;
 Score 564.5; DB 8; Length 293; Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 8; Length 293; 45.3%; Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293; Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 Length 293;
 Score 564.5; DB 8; Length 293; Pred. No. 1.5e-35;
 ADG08462 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003207424-A1.
 Score 564.5; DB 8;
Pred. No. 1.5e-35;
 Score 564.5; DB 8
Pred. No. 1.5e-35;
 West Local Similarity 45.3%; Pred. 1052

RESULT 1052

ID Angle842 standard; protein; 293 AA. BN US2003207359-Al.
 Human PRO polypeptide #228.
US2003207371-A1.
 ADF92257 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003207353-A1.
 ADG05301 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003207375-A1.
 ADG19568 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003207425-A1.
 protein; 293 AA.
 293 AA
 ADG06215 standard; protein; 293 AA
Human PRO polypeptide #228.
 41.1%;
 06-NOV-2003.
(GETH) GENENTECH INC.
1ry Match 41.1%;
 41.1%;
 41.1%;
 Best Local Similarity 45.3%;
RESULT 1054
 41.1%;
 Best Local Similarity 45.3%;
RESULT 1056
 ADG15632 standard; protein;
Human PRO polypeptide #228.
US2003219885-A1.
 Query Match 41.1%;
Best Local Similarity 45.3%;
 Best Local Similarity 45.3%;
 Human PRO polypeptide #228.
US2003207357-A1.
 Human PRO polypeptide #228
US2003207351-A1.
 06-NOV-2003.
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ID ADG05301 stand*

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 Query Match
Best Local Similarity
RESULT 1051
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 Local Similarity
 ADG13405 standard;
 RESULT 1058
ID ADF97030 standard;
 06-NOV-2003
 Query Match
 Query Match
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Query Match 41.1%; Score 564.5; DB 8; Length 293; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 1062
 Query Match 41.1%; Score 564.5; DB 8; Length 293; Best Local Similarity 45.3%; Pred. No. 1.5e-35;
41.1%; Score 564.5; DB 8; Length 293; 45.3%; Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 8; Length 293; 45.3%; Pred. No. 1.5e-35;
 Length 293;
 Length 293;
 Length 293;
 Length 293;
 Query Match
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1063
ID ADGO7286 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207350-A1.
 Novel human secreted and transmembrane protein PRO1132. US2003299-A1.
 ADG24989 standard, protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207427-A1.
 ADG07838 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207356-A1.
06-NOV-2003.
 ADG55333 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003194778-A1.
 Novel human secreted and transmembrane protein PRO1132. US2003207428-A1.
 ADG60997 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003207390-A1.
 41.1%; Score 564.5; DB 8; 45.3%; Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 8; 45.3%; Pred. No. 1.5e-35;
 Query Match 41.1%; Score 564.5; DB 8; Best Local Similarity 45.3%; Pred. No. 1.5e-35;
 ADG04088 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003207423-A1.
 293 AA
 Query Match
Best Local Similarity 45.3%;
RESULT 1061
 Human PRO polypeptide #228.
US2003207358-A1.
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Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 8; Length 293; 45.3%; Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 8; Length 293; 45.3%; Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293; Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 8; Length 293; 45.3%; Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 8; Length 293; 45.3%; Pred. No. 1.5e-35;
 ADG56437 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207366-A1.
 Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1085
DB ADH12703 standard; protein; 293 AA.
DB Novel human secreted and transmembrane protein PRO1132.
PN US2003207378-A1.
 ADGS4229 standard, protein, 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207416-A1.
 ADH12079 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003207419-A1.
 RESULT 1081
ID ADG52501 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132
PN US2003207414-A1.
 DB 8;
 Score 564.5; DB 8;
Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 8; 45.3%; Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 8 45.3%; Pred. No. 1.5e-35;
 ADH21048 standard; protein; 293 AA.
Human secreted/transmembrane protein PRO1132.
US2003224358-A1.
 ADH19555 standard; protein; 293 AA.
Human secreted/transmembrane protein PRO1132.
1US2003228656-A1.
1L-DEC-2003.
 Human PRO polypeptide #228.
US2003194793-A1.
 ADH30712 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003077723-A1.
 41.1%;
 41.1%;
 Best Local Similarity 45.3%;
RESULT 1084
 41.1%;
Luery Match
Best Local Similarity 4
RESULT 1078
ID ADH19555 standar
ID Human secret
PN US20037
 16-OCT-2003.
(GETH) GENENTECH INC.
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 06-NOV-2003.
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RESULT 1079
 Best Local Similarity
RESULT 1086
 Best Local Similarity
 06-NOV-2003.
 06-NOV-2003
 04-DEC-2003
 24-APR-2003
 06-NOV-2003
 06-NOV-2003
 Query Match
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 Score 564.5; DB 8; Length 293; Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293; Pred. No. 1.5e-35;
 Length 293;
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 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 Length 293;
 / Match 41.1%; Score 564.5; DB 8; Length 293; Local Similarity 45.3%; Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293; Pred. No. 1.5e-35;
 ADG71011 standard, protein, 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207420-A1.
 ADGE8093 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207363-A1.
 ADG57541 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003207362-A1.
 ADG56989 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207364-Al.
 ADGESSER STANDARD; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207365-A1.
 ADG53677 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
 ADG71563 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207421-A1.
 Score 564.5; DB 8;
Pred. No. 1.5e-35;
 Score 564.5; DB 8;
Pred. No. 1.5e-35;
 Score 564.5; DB 8;
Pred. No. 1.5e-35;
 ADG81750 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003207805-A1.
06-NOV-2003.
 41.1%;
 41.18;
 Best Local Similarity 45.3%;
RESULT 1070
 41.1%;
 Query Match
Best Local Similarity 45.3%;
 Query Match 41.1%;
Best Local Similarity 45.3%;
 41.1%;
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Best Local Similarity 45.3%;
 06-NOV-2003.
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 Local Similarity
 Query Match
Best Local Similarity
RESULT 1073
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 US2003207415-A1.
 06-NOV-2003
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Length 293;

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ADI14791 standard; protein; 293 AA. Novel human secreted and transmembrane protein PRO1132. US2003207383-A1.
 Query Match
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 Query Match
 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293; Pred. No. 1.5e-35;
 DB 8; Length 293;
 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 Length 293;
 Length 293;
 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 ADG61549 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
 Novel human secreted and transmembrane protein PRO1132.06-NOV-2003.
 ADG09988 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2004009548-A1.
 ADII5459 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207382-A1.
 ADG54781 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003207367-A1.
 ADG00336 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2004009547-A1.
 Score 564.5; DB 8;
Pred. No. 1.5e-35;
 / Match 41.1%; Score 564.5; DB 8; Local Similarity 45.3%; Pred. No. 1.5e-35;
 Query Match 41.1%; Score 564.5; DB 8, Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 1089
 ADH20088 standard; protein; 293 AA.
Human secreted/transmembrane protein PRO1132.
US2003219856-A1.
 Human PRO polypeptide #228.
US2003207361-A1.
 ADH28636 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003022331-A1.
 US2003zu,...
06-NOV-2003.
(GETH) GENENTECH INC.
41.1%; S'
 41.18;
 41.1%;
 Match 41.1%;
Local Similarity 45.3%;
 Query Match 41.1%;
Best Local Similarity 45.3%;
RESULT 1094
 Watch 41.1%;
Local Similarity 45.3%;
 Query Match 41.1%;
Best Local Similarity 45.3%;
 27-NOV-2003.
(GETH) GENENTECH INC.
 15-JAN-2004.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 06-NOV-2003.
(GETH) GENENTECH INC.
 15-JAN-2004.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 Query Match
Best Local Similarity
RESULT 1096
 Best Local Similarity RESULT 1088
 Query Match
Best Local Similarity
 US2003207429-A1.
 30-JAN-2003
 Query Match
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 RESULT 1091
ID ADG5982
DE Novel h
PN US20032
PD 06-NOV-
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41.1%; Score 564.5; DB 8; Length 293; 45.3%; Pred. No. 1.5e-35;
 Length 293;
 DB 8; Length 293;
 Length 293;
 Length 293;
 DB 8; Length 293;
 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 Length 293;
 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
 ADJ63667 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2004039164-A1.
26-FBB-2004.
 ADI18386 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132. US2003207349-A1.
 41.1%; Score 564.5; DB 8; 45.3%; Pred. No. 1.5e-35;
 Score 564.5; DB 8;
Pred. No. 1.5e-35;
 Score 564.5; DB 8;
Pred. No. 1.5e-35;
 DB 8;
 Score 564.5; DB 8
Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 8 45.3%; Pred. No. 1.5e-35;
 Score 564.5; DB 8 Pred. No. 1.5e-35;
 Duery Match
Best Local Similarity 45.3%; Pred. No
RESULT 1100
ID ADJG5684 standard; protein; 293 AA.
DE Human PRO Polypeptide #228.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
 Human PRO polypeptide #228.
US2004058424-Al.
 ADM28406 standard; protein; 293 AA.
Human PRO polypeptide #228.
US204077064-A1.
(GETH) GENENTECH INC.
 ADJ77562 standard; protein; 293 AA
 293 AA
 Best Local Similarity 45.3%;
RESULT 1101
ID ADM2720 Standard; protein. 7
DE Human Pro.
 41.1%;
 41.1%;
 (MOUN) MOUNT SINAI HOSPITAL. (YOUS/) YOUSEF G.
 Human PRO polypeptide #228. US2004048333-Al.
 41.1%;
 Query Match
Best Local Similarity 45.3%;
RESULT 1104
 protein;
 ADK52481 standard; protein;
Human kallikrein 5 protein.
WO2004021008-A2.
 Human PRO polypeptide #228
US2004038336-A1.
06-NOV-2003.
(GETH) GENENTECH INC.
 11-MAR-2004.
(GETH) GENENTECH INC.
 25-MAR-2004.
(GETH) GENENTECH INC.
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 (GETH) GENENTECH INC
 Query Match
Best Local Similarity
RESULT 1097
 Query Match
Best Local Similarity
RESULT 1105
 Best Local Similarity
RESULT 1098
 Best Local Similarity
RESULT 1099
 Query Match
Best Local Similarity
RESULT 1103
 Best Local Similarity
 06-NOV-2003
 26-FEB-200
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Ovarian cancer-associated protein #46
 WO2002102235-A2.
 22-MAY-2003
 14-SEP-2000
 10-SEP-2004
 Query Match
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 Query Match
 protein.
 ADR72621 standard, protein; 293 AA.
Human renal cell carcinoma-related kallikrein 5 (hK5) protein.
WO2004077060-A2.
 ADR72873 standard; protein; 293 AA.

Human ovarian cancer-related tumour marker kallikrein 5 (hK5)
W02004075713-A2.

10-SEP-2004.

WOUN) MOUNT SINAI HOSPITAL.

ETY MATCh

St. Local Similarity 45.3%; Pred. No. 1.5e-35;
 Score 564.5; DB 8; Length 293; Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 2; Length 322; 45.3%; Pred. No. 1.6e-35;
 Length 293;
 PD 10-SEP-2004.

PA (MOUN) MOUNT SINAI HOSPITAL.

Query Match 41.1%; Score 564.5; DB 8; Length 293;

Best Local Similarity 45.3%; Pred. No. 1.5e-35;

RESULT 1108
 AAB21327 standard; protein; 276 AA.

Human NES1.

WO200053776-A2.

14-SEP-2000.

Query Match

Query Match

Best Local Similarity 45.9%; Pred. No. 1.5e-35;
 41.0%; Score 564; DB 5; Length 276; 45.9%; Pred. No. 1.5e-35;
 Length 276;
 Length 276;
 Novel human secreted and transmembrane protein PRO1132.06-NOV-2003.
 Score 564.5; DB 8;
Pred. No. 1.5e-35;
 AAU82729 standard; protein; 276 AA.
Amino acid sequence of novel human protease #28.
WO200200860-AZ.
 12-DEC-1996.
(NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC. ery Match 41.0%; Score 564; DB 2;
 41.0%; Score 564; DB 5; 45.9%; Pred. No. 1.5e-35;
Human PRO polypeptide #228.
24.2003077659-A1.
 AAW07620 standard, protein, 276 AA. Human NES1 polypeptide. W09639175-A1.
 RESULT 1112

ID ABG96356 standard; protein; 276 AA.

DE Human ovarian cancer marker OV32.

PN W0200271928-A2.

PD 19-SEP-2002.
 AAY14072 standard; protein; 322 AA.
Human BS247 specific epitope.
WO9922027-A1.
 ADB80527 standard; protein; 276 AA
 (MILL-) MILLENNIUM PHARM INC.
 Query Match
Best Local Similarity 45.3%;
RESULT 1107
 Query Match
Best Local Similarity 45.3%;
 24-APR-2003.
(GETH) GENENTECH INC.
 (GETH) GENENTECH INC.
 Query Match
Best Local Similarity
 Best Local Similarity
RESULT 1110
 Best Local Similarity
RESULT 1113
 Query Match
Best Local Similarity
 (ABBO) ABBOTT LAB
 03-JAN-2002.
(SUGE-) SUGEN INC.
 06-MAY-1999
 Query Match
 Query Match
 Query Match
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ADR72886 standard, protein, 276 AA.
Human ovarian cancer-related tumour marker kallikrein 10 (hK10) protein.
WO2004075713-A2.
 ADN39880 standard; protein; 276 AA.
Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C250.
WO2003042661-A2.
 ADR72628 standard; protein; 276 AA.
Human renal cell carcinoma-related kallikrein 10 (hK10) protein.
WO2004077060-A2.
10-SEP-2004.
 40.9%; Score 561.5; DB 3; Length 256; 49.1%; Pred. No. 2.2e-35;
 Length 237;
 Length 276;
 Length 276;
 Length 276;
 Length 276;
 Length 276;
 Length 276;
 Length 276;
 AD089070 standard; protein; 276 AA.
Human urological disorder related protein 2045 SEQ:22.
WO2004065576-A2.
27-DEC-2002.
(BOSB-) BOS BIOTECHNOLOGY INC.
(ESSB-) BOS BIOTECHNOLOGY INC.
(ery Match 41.0%; Score 564; DB 7;
ery Match 45.9%; Pred. No. 1.5e-35;
 WOZOUS 2003.
28-AUC-2003.
(MILL-) MILLENNIUM PHARM INC.
(MILL-) MILLENNIUM 71.0%; Score 564; DB 7; erry Match 41.0%; Pred. No. 1.5e-35;
 41.0%; Score 564; DB 8; 45.9%; Pred. No. 1.5e-35;
 41.0%; Score 564; DB 8;
45.9%; Pred. No. 1.5e-35;
 40.9%; Score 562; DB 3; 48.1%; Pred: No. 1.9e-35;
 (EOSB-) EOS BIOTECHNOLOGY INC.
ry Match
t Local Similarity 45.9%; Pred. No. 1.5e-35;
 41.0%; Score 564; DB 8; 45.9%; Pred. No. 1.5e-35;
 41.0%; Score 564; DB 8; 45.9%; Pred. No. 1.5e-35;
 RESULT 1115
ID ADEA4073 standard; protein; 276 AA.
DE Human Kallikrein 10 (gene ID 2045) protein.
PN W02003070883-A2.
 ADNO4446 standard; protein; 276 AA. Antipsoriatic protein sequence #416. WO2004028479-A2.
 AAB21305 standard; protein; 237 AA Human KLK-L6 protein #1. WO200053776-A2.
 AAB21299 standard; protein; 256 AA
Human KLK-L4 protein #1.
WO200053776-A2.
 AAB21309 standard; protein; 287 AA
Human KLK-L2.
 05-AUG-2004.
(MILL-) MILLENNIUM PHARM INC.
 14-SEP-2000.
(MOUN) MOUNT SINAI HOSPITAL.
 (MOUN) MOUNT SINAI HOSPITAL.
 (MOUN) MOUNT SINAI HOSPITAL.
 (MOUN) MOUNT SINAI HOSPITAL.
 08-APR-2004.
(GETH) GENENTECH INC.
 Query Match
Best Local Similarity
 Best Local Similarity RESULT 1116
 Best Local Similarity RESULT 1123
 Query Match
Best Local Similarity
RESULT 1118
 Query Match
Best Local Similarity
RESULT 1117
 Best Local Similarity
RESULT 1122
 Best Local Similarity
RESULT 1119
 Best Local Similarity
RESULT 1120
 Query Match
Best Local Similarity
RESULT 1121
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Query Match
 ADN39212 standard; protein; 244 AA.
Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:530.
 vuery Match 40.9%; Score 561.5; DB 3; Length 287; Best Local Similarity 46.1%; Pred. No. 2.5e-35; RESULT 1124
 PA (HOFF) ROCHE DIAGNOSTICS GWBH.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

Query Match

40.8%; Score 561; DB 5; Length 228;

Best Local Similarity 46.7%; Pred. No. 2.1e-35;

ID AAB21310 standard; protein; 239 AA.

DE Human zyme.

PN WO200053776-A2.

PD 14-SEP-2000.

PA (MOUN) MOUNT SINAI HOSPITAL.
 Query Match 40.8%; Score 561; DB 2; Length 244; Best Local Similarity 46.7%; Pred. No. 2.3e-35; RESULT 1127
 40.8%; Score 561; DB 3; Length 239; 46.7%; Pred. No. 2.3e-35;
 Length 244;
 Length 244;
 Query Match
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
 Length 244;
 Length 244;
 40.8%; Score 561; DB 2; 46.7%; Pred. No. 2.3e-35;
 19-MAR-1998.
(DAND) DANA FARBER CANCER INST INC.
10 84; Score 561; DB 2;
st Local Similarity 46.7%; Pred. No. 2.3e-35;
 Match 40.8%; Score 561; DB 7;
Local Similarity 46.7%; Pred. No. 2.3e-35;
 40.8%; Score 561; DB 3; 46.7%; Pred. No. 2.3e-35;
 Synthetic shortened trypsinogen SEQ ID NO 23. W0200261064-A2.
 ADB80567 standard; protein; 244 AA.
Ovarian cancer-associated protein #66.
W72002102235-A2.
(FOSB-) EOS BIOTECHNOLOGY INC.
 AAW51006 standard; protein; 244 AA.
Protease M, a novel serine protease.
WO9811238-A2.
 AAR44532 standard; protein; 244 AA.
Zyme APP-cleaving protease.
EP576152-A1.
 AAW22985 standard; protein; 244 AA.
Human serine protease 59 (SP59).
JP09149790-A.
 AAB21323 standard; protein; 244 AA.
 RESULT 1130

DE AAR37572 standard, protein, 244 AA.
DE Human 2047 protein.
PN W02003037258-A2.
WO200053776-A2.
14-SEP-2000.
(MOUN) MOUNT SINAI HOSPITAL.
 14-SEP-2000.
(MOUN) MOUNT SINAI HOSPITAL.
 (MILL-) MILLENNIUM PHARM INC.
 O 29-DEC-1993.

(ELIL) LILLY & CO ELI.

Query Match
 Best Local Similarity RESULT 1126
 (SUNR) SUNTORY LTD.
 Local Similarity
 Local Similarity
 Human zyme.
WO200053776-A2.
 08-AUG-2002
 10-JUN-1997
 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
```

```
ADR72676 standard; protein; 244 AA.
Human ovazian cancer-related tumour marker kallikrein 6 (hK6) protein.
WO2004075713-A2.
10-SER-2004.
 ADRIZE24 standard; protein; 244 AA.
Human renal cell carcinoma-related kallikrein 6 (hK6) protein.
WO2004077060-A2.
 RESULT 1140
ID AAR67888 standard; protein; 253 AA.
DE Human stratum corneum chymotrophic recombinant enzyme (SCCE)
PN W09500651-A1.
 Length 244;
 Length 244;
 Length 244;
 Length 244;
 Length 244;
 Length 244;
 Length 296;
 Length 253;
 Jairo
1928076 standard; protein; 244 AA.
Human urological disorder related protein 2047 SEQ:28
WO2004065576-A2.
WO2003042661-A2.
22.MAY-2003.
(EOSB-) EOS BIOTECHNOLOGY INC.
40.8%; Score 561; DB 7;
40.8%; Score 561; DB 7;
46.7%; Pred. No. 2.3e-35;
 Score 561; DB 8;
Pred. No. 2.3e-35;
 40.8%; Score 561; DB 8;
46.7%; Pred. No. 2.3e-35;
 PD 20-MAY-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 40.8%; Score 561; DB 8;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1135
 (MILL.) MILLENNIUM PHARM INC.

Query Match
40.8%; Score 561; DB 8;

Best Local Similarity 46.7%; Pred. No. 2.3e-35;
 40.8%; Score 561; DB 8; 46.7%; Pred. No. 2.3e-35;
 (MILL-) MILLENNIUM PHARM INC.
ry Match
t Local Similarity 46.9%; Pred. No. 2.7e-35;
 (MOUN) MOUNT SINAI HOSPITAL.
ry Match
t Local Similarity 46.1%; Pred. No. 5.7e-35;
 40.4%; Score 555; DB 2; 44.6%; Pred. No. 6.9e-35;
 AAW05383 standard; protein; 253 AA.
Human amyloid precursor protein protease.
W09631122-A1.
 ADN22289 standard; protein; 244 AA.
Human kallikrein 6 associated protein.
US2004097452-A1.
 Antipsoriatic protein; 244 AA. NO2004028479-A2. 08-APR-2004
 ABG96357 standard; protein; 244 AA.
Human ovarian cancer marker OV33.
WO200271928-A2.
 AAB21297 standard; protein; 296 AA.
Human KLK-L3 protein #1.
WO200053776-A2.
 10-SEP-2004.
(MOUN) MOUNT SINAI HOSPITAL.
 (MOUN) MOUNT SINAI HOSPITAL.
 Query Match 40.8%;
Best Local Similarity 46.7%;
RESULT 1134
 GENENTECH INC.
 Best Local Similarity RESULT 1133
 Best Local Similarity RESULT 1136
 Best_Local Similarity RESULT 1139
 SYMBICOM AB.
 Best Local Similarity
 Best Local Similarity RESULT 1137
 Best Local Similarity RESULT 1138
 Best Local Similarity
 08-APR-2004
(GETH) GENI
 05-JAN-1995
(SYMB-) SYM
 05-AUG-2004
 14-SEP-2000
 19-SEP-2002
 Query Match
 Query Match
 Query Match
```

```
ADN04182 standard; protein; 253 AA. Antipsoriatic protein sequence #286. WO2004028479-A2.
 ADA05734 standard; protein; 252 AA.
Human NOV18b protein SEQ ID NO:94.
WO2003029424-A2.
 Query Match
Best Local Similarity 46.6%; Pred.
SSULT 1155
ADN62898 standard; protein; 252 AA.
 ADR72880 standard; protein; 253 AA
 EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
 (GETH) GENENTECH INC.
 SHIMKETS R A. ROTHENBERG M ELEACH M D.
 (GETH) GENENTECH INC.
 (CURA-) CURAGEN CORP.
 ZERHUSEN B D.
ANDERSON D W.
 PATTURAJAN M.
 Best Local Similarity RESULT 1154
 MILLER C E. RASTELLI L. STONE D J. PENA C E A. SHENOY S G.
 MILLET I.
PEYMAN J A.
KEKUDA R.
 CATTERTON E.
 DIPIPPO V A
 SPYTEK K A.
 SMITHSON G.
 AGEE M L.
BERGHS C.
 GORMAN L.
 JS2004038223-A1.
 ZHONG M.
 Human NOV18b
 08-APR-2004
 10-SEP-2004,
 -FEB-2004
 26-FEB-2004
 10-APR-2003
 Query Match
 (BERG/)
(DIPI/)
 PEYM/)
 EDIN/)
 SHIM/)
ROTH/)
 ZHON/)
 STON/)
 SHEN/)
 ZERH/
 MILL/
RAST/
 MALY/
 ANDE/
 JIWW/
 PENA/
 GORM/
 ABRS8471 standard; protein; 253 AA.
Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
WO2003029468-A1.
10-APR-2003.
 ADJ68833 standard; protein; 253 AA.
Human heat mitochondrial protein as a therapeutic target SeqID639.
WO2003087768-A2.
 Query Match
Best Local Similarity 44.6%; Score 555; DB 7; Length 253;
RESULT 1150
ID ADN39180 standard; protein; 253 AA.
 Length 253;
 Length 253;
 Length 253;
 Length 253;
 Length 253
 Length 253
 Length 253
 ABU07471 standard, protein, 253 AA.
Protein differentially regulated in prostate cancer #74.
WO200281638-A2.
 ABU07440 standard; protein; 253 AA.
Protein differentially regulated in prostate cancer #43.
WO200281638-A2.
 ABB84421 standard; peptide; 253 AA.
Human SCCE protein N-terminal fragment SEQ ID 48.
WO200262135-A2.
 AAU82740 standard; protein; 253 AA.
Amino acid sequence of novel human protease #39.
WO200200860-A2.
 17-CCT-2002.
(ORIG-) ORIGENE TECHNOLOGIES INC.
(ery Match 40.4%; Score 555; DB 6;
 Score 555; DB 5;
Pred. No. 6.9e-35;
 40.4%; Score 555; DB 6; 44.6%; Pred. No. 6.9e-35;
 Score 555; DB 5;
Pred. No. 6.9e-35;
 40.4%; Score 555; DB 6; 44.6%; Pred. No. 6.9e-35;
 Score 555; DB 5;
Pred. No. 6.9e-35;
 27-DBC-2002.
(BOSB-) EOS BIOTECHNOLOGY INC.
FY WATCH 40.4%; Score 555; DB 7;
it Local Similarity 44.6%; Pred. No. 6.9e-35;
 ADB80484 standard; protein; 253 AA.
Ovarian cancer-associated protein #24.
WO2002102235-A2.
 ABB84406 standard; protein; 253 AA.
Human SCCE protein.
WO200262135-A2.
 (ORIG-) ORIGENE TECHNOLOGIES INC.
 40.4%;
 40.4%;
 40.48;
 (MITO-) MITOKOR.
(BUCK-) BUCK INST AGE RES.
) 10-OCT-1996.
(ELIL) LILLY & CO ELI.
Query Match 40
 (CORI-) CORIXA CORP.
 Local Similarity
 Query Match
Best Local Similarity
RESULT 1143
 Query Match
Best Local Similarity
RESULT 1144
 Query Match
Best Local Similarity
 15-AUG-2002.
(EGEL/) EGELRUD T.
(HANS/) HANSSON L.
 Best Local Similarity
 15-AUG-2002.
(EGEL/) EGELRUD T.
(HANS/) HANSSON L.
 03-JAN-2002.
(SUGE-) SUGEN INC.
 17-OCT-2002
 Query Match
 Query Match
 Ouery Match
```

```
Human ovarian cancer-related tumour marker kallikrein 7 (hK7) protein.
WO2004075713-A2.
Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:498.
WO2003042661-A2.
 Query Match
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
RESULT 1151:
ADLO5515 standard; protein; 253 AA.
DE Human tumour-associated antigenic target (TAT) polypeptide #14.
PN W02004016225-A2.
 40.3%; Score 553.5; DB 6; Length 252; 46.6%; Pred. No. 9e-35;
 Length 253;
 Length 253;
 Length 253;
 vuery Match
40.4%; Score 555; DB 8;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
SULT 1152
 (EOSB-) EOS BIOTECHNOLOGY INC.
ry Match 40.4%; Score 555; DB 7;
L Local Similarity 44.6%; Pred. No. 6.9e-35;
 Query Match 40.4%; Score 555; DB 8; Best Local Similarity 44.6%; Pred. No. 6.9e-35; RESULT 1153
 (MOUN) MOUNT SINAI HOSPITAL.

ry Match 40.4%; Score 555; DB 8;

t Local Similarity 44.6%; Pred. No. 6.9e-35;
```

```
Recombinant trypsin. WO200017332-A1. 30-MAR-2000. (ELIL) LILLY & CO ELI.
 19-SEP-2000
 02-AUG-2001
 02-AUG-200
 Query Match
 Query Match
Best Local Similarity 46.6%; Pred. No. 9e-35;
RESULT 1156

ID AAY08025 standard; protein; 253 AA.

DE Mouse protease-related protein (PVP).

PD 24-DEC-1998.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 Ouery Match 40.3%; Score 553.5; DB 2; Length 253;
Best Local Similarity 43.5%; Pred. No. 9e-35;
RESULT 1157
 Ouery Match
40.2%; Score 552; DB 2; Length 230;
Best Local Similarity 47.5%; Pred. No. 1.1e-34;
RESULT 1160
ID AAY91926 standard; protein; 231 AA.
 Ouery Match
Best Local Similarity 44.8%; Pred. No. 9.8e-35;
 Match
Local Similarity 46.3%; Pred. No. 1.1e-34;
 24-DEC-1998.
(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 ADN62896 standard; protein; 250 AA.
 RESULT 1158
ID AAY77494 standard; protein; 229 AA
 AAR53638 standard; protein; 230 AA
 STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
LEACH M D.
 GUO X.
PATTURAJAN M.
SPYTEK K A.
EDINGER S R.
ELLERMAN K.
 18-MAY-1994.
(ELIL) LILLY & CO ELI.
 AGEE M L.
BERGHS C.
DIPIPPO V A.
EISEN A.
GANGOLLI E A.
RIEGER D K.
 03-FEB-2000.
(PROD-) PRODIGENE INC.
 GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
(EISE/) EISEN A.
(GANG/) GANGOLLI E A.
(RIEG/) RIEGER D K.
(SPAD/) SPADERNA S K.
 SPADERNA S K.
 ZHONG M.
CATTERTON E.
 MILLET I.
PEYMAN J A.
KEKUDA R.
 (SMIT/) SMITHSON G.
 MILLER C E.
RASTELLI L.
 Bovine trypsinogen.
WO200005384-A1.
 Bovine trypsinogen.
EP597681-Al.
 US2004038223-A1.
 Human NOV18a.
 Query Match
 (BERG/)
(DIPI/)
 PENA/)
 RIEG/)
 (SPAD/)
 SHEN/)
 LEAC/)
 AGEE/)
 MALY/)
 (ELLE/)
 ANDE/
 STON/
 SHIM/
 EISE/
 SPYT/
 ZHON/
```

```
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 547.5; DB 7; Length 247;
Best Local Similarity 46.1%; Pred. No. 2.68-34;
RESULT 1169
 (HUMA-) HUMAN GENOME SCI INC.
Query Match
39.8%; Score 547.5; DB 4; Length 247;
Best Local Similarity 46.1%; Pred. No. 2.6e-34;
 40.1%; Score 550.5; DB 5; Length 249; 46.7%; Pred. No. 1.5e-34;
 DB 3; Length 247;
 Length 247;
 39.8%; Score 547.5; DB 4; Length 247; 46.1%; Pred. No. 2.6e-34;
vuery Match 40.2%; Score 552; DB 3; Length 231; Best Local Similarity 46.3%; Pred. No. 1.1e-34; RESULT 1161
 Length 231;
 Length 250;
 AAU86677 standard; protein; 247 AA.
Novel human connective tissue related polypeptide #243.
WO200155343-A1.
 ABB6420 standard; peptide; 249 AA.
Porcine SCCE protein N-terminal fragment SEQ ID 47.
WO200262135-A2.
 (HUMA-) HUMAN GENOME SCI INC.

19.8%; Score 547.5; DB 4;

t Local Similarity 46.1%; Pred. No. 2.6e-34;
 PD 22-MAR-2001.

PA (ELIL) LILLY & CO ELI.

Query Match 40.2%; Score 552; DB 4;

Best Local Similarity 46.3%; Pred. No. 1.1e-34;
 Query Match
Best Local Similarity 44.8%; Pred. No. 1.2e-34;
RESULT 1163
 40.0%; Score 549.5; DB 3 44.0%; Pred. No. 1.8e-34;
 RESULT 1167
ID AAU17043 standard; protein; 247 AA.
DE Human novel secreted protein, SEQ ID 284.
PN W0200155441-A2.
 AAB35701 standard; protein; 247 AA.
Human trypsin hL amino acid sequence.
JP2000253887-A.
 ADB60011 standard; protein; 247 AA.
Connective tissue antigen (CTA) #243.
US2003054375-A1.
 AAU23752 standard; protein; 247 AA. Novel human enzyme polypeptide #838.WO200155301-A2.
 ADA05732 standard; protein; 250 AA.
Human NOV18a protein SEQ ID NO:92.
WO2003029424-A2.
 AAB80953 standard; protein; 231 AA
 AAW81767 standard; peptide; 223 AA
 (HUMA-) HUMAN GENOME SCI INC.
 Bovine met-phe-trypsinogen WO200119970-A2.
 10-APR-2003.
(CURA-) CURAGEN CORP.
 (TTPH-) TT PHARMA KK.
 Best Local Similarity RESULT 1168
 Query Match
Best Local Similarity
RESULT 1165
 Best Local Similarity
RESULT 1164
 Query Match
Best Local Similarity
RESULT 1166
 nd 15-AUG-2002.
A (EGEL/) EGELRUD T.
A (HANS/) HANSSON L.
Query Match
```

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10-APR-2003
 Query Match
 (SHEN/)
(SHIM/)
(ROTH/)
 (MILL/)
(RAST/)
(STON/)
(PENA/)
 (LEAC/)
 ZERH/)
 JIWM/
 ABG31841 standard; protein; 223 AA.
Example protein #3 used in three-dimensional structure analysis method.
WO200257954-A1.
25-UJU-2002.
 PD 18-MAY-1994.

PA (ELL) LILLY & CO ELI.

Query Match

Antch

Best Local Similarity 46.1%; Pred. No. 2.5e-34;

RESULT 1175

ID AAY91925 standard; protein; 233 AA.

DE WOO0017332-A1.
Bovine TRYP peptide fragment.
JP10287696-A.
27-OCT-1998.
IYAKU BUNSHI SEKKEI KENKYUSHO KK.
39.8%; Score 547; DB 2; Length 223; st Local Similarity 46.1%; Pred. No. 2.5e-34;
 PD 02-DEC-1999.
PA (MEDI-) INST MEDICINAL MOLECULAR DESIGN INC.
QUETY MATCH 39.8%; Score 547; DB 3; Length 223;
Best Local Similarity 46.1%; Pred. No. 2.5e-34;
 Query Match 39.8%; Score 547; DB 3; Length 233; Best Local Similarity 46.1%; Pred. No. 2.6e-34; RESULT 1176
 39.8%; Score 547; DB 7; Length 223; 46.1%; Pred. No. 2.5e-34;
 Length 223;
 Query Match 39.7%; Score 546; DB 8; Length 244;
Best Local Similarity 45.8%; Pred. No. 3.3e-34;
 Score 546; DB 8; Length 244;
Pred. No. 3.3e-34;
 39.8%; Score 547; DB 5; Length 223; 46.1%; Pred. No. 2.5e-34;
 39.8%; Score 547; DB 7; 46.1%; Pred. No. 2.5e-34;
 ADC73287 standard; protein; 223 AA.
Bovine 2PTC E protein - SEQ ID 13.
WAC200360765-Al.
 ADD35545 standard; protein; 223 AA. Cationic bovine trypsinogen TRY1. WO2003040093-A2.
 ADĪ39734 standard; protein; 244 AA.
Human protease M (proM) protein.
US6642013-B1.
 AAY69973 standard; protein; 223 AA.
TRYP protein.
W09962004-A1.
 AAR53637 standard; protein; 224 AA
 (UYAR-) UNIV ARKANSAS MEDICAL SCI.
 ADI37158 standard; protein; 244 AA
 (MITU) MITSUBISHI CHEM CORP. (UMEY/) UMEXAMA H.
 USZUCZ-2003.
23-OCT-2003.
(UYAR-) UNIV ARKANSAS.
Match ''rrity 45.8$;
 Human protease m (Protm). US2003199010-A1.
 (AJIN) AJINOMOTO CO INC. (UMEY/) UMEYAMA H.
 30-MAR-2000.
(ELIL) LILLY & CO ELI.
 Best Local Similarity RESULT 1173
 Query Match
Best Local Similarity
RESULT 1172
 Query Match
Best Local Similarity
RESULT 1174
 Ouery Match
Best Local Similarity
RESULT 1178
 Best Local Similarity
 (FARB) BAYER AG.
 Bovine trypsin.
EP597681-A1.
 15-MAY-2003
 Query Match
```

```
AAB99502 standard, protein; 225 AA.
Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.
WO200129056-A1.
 39.7%; Score 545; DB 3; Length 246; 44.2%; Pred. No. 4e-34;
 Length 247;
 Length 247;
 Length 247;
 Length 225
AAY78974 standard; protein; 247 AA.
Canine cationic trypsinogen amino acid sequence.
WO20009739-A1.
24-FED-2000.
(FUJY) FUJI YAKUHIN KOGYO KK.
39.7%; Score 546; DB 3;
pt Local Similarity 45.6%; Pred. No. 3.3e-34;
 PD 26-APR-2001.

PA (UYAR-) UNIV ARKANSAS.

Query Match

Best Local Similarity 46.5%; Pred. No. 3.6e-34;

RESULT 1182
 Query Match 39.7%; Score 546; DB 6; Best Local Similarity 45.5%; Pred. No. 3.3e-34; RESULT 1180
ID ADN02906 standard; protein; 247 AA.
 Score 546; DB 8;
Pred. No. 3.3e-34;
 AAY78975 standard; protein; 246 AA.
Canine anionic trypsinogen amino acid sequence.
WO200009739-A1.
 ADAO5742 standard; protein; 247 AA.
Human NOV18f protein SEQ ID NO:102.
WO2003029424-A2.
 24-FEB-2000.
(FUJY) FUJI YAKUHIN KOGYO KK.
 Best Local Similarity 45.5%;
RESULT 1181
 (BERG/) BERGHS C.
(DIPI/) DIPIPPO V A.
(BISE/) EISEN A.
(GARG/) GANGOLLI E A.
(RIEG/) RIEGER D K.
(SPAD/) SPADERNA S K.
 SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
 STORE D. J. STORE D. J. STORE D. J. SHENOY S. G. SHIMKETS R. A. ROTHENBERG M. E.
 (CURA-) CURAGEN CORP.
 GUO X.
PATTURAJAN M.
 ZERHUSEN B D. ANDERSON D W.
 MILLET I.
PEYMAN J A.
KEKUDA R.
 Best Local Similarity RESULT 1179
 CATTERTON E.
 Query Match
Best Local Similarity
RESULT 1183
 LEACH M D.
AGEE M L.
BERGHS C.
 SMITHSON G.
 MILLER C E.
 GORMAN L.
 Human NOV18f.
US2004038223-A1.
 ZHONG M.
```

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Amino acid sequence of trypsin. US2002072863-A1.
 39.2%;
 37.6%;
 18-JUL-2002.
(CURA-) CURAGEN CORP.
 (CURA-) CURAGEN CORP.
 21-MAR-2002.
(FUIT) FUJITSU LTD.
 Query Match
Best Local Similarity
RESULT 1198
 13-JUN-2002.
(FUIT) FUJITSU LTD.
 Query Match
Best Local Similarity
RESULT 1194
 Query Match
Best Local Similarity
RESULT 1190
 Best Local Similarity
 Best Local Similarity RESULT 1192
 Best Local Similarity
 15-AUG-2002.
(EGEL/) EGELRUD T.
(HANS/) HANSSON L.
 15-AUG-2002.
(EGEL/) EGELRUD T.
(HANS/) HANSSON L.
 14-NOV-2002
 Query Match
 Query Match
 Query Match
 Query Match
 RESULT 1193
 ADI16686 standard; protein; 259 AA.
Human NOVX protein to treat human pathological conditions SeqID222.
WO200268649-A2.
 vuery Match
39.3%; Score 539.5; DB 8; Length 259;
Best Local Similarity 44.4%; Pred. No. 1.1e-33;
RESULT 1189
 Match 39.3%; Score 539.5; DB 5; Length 259. Local Similarity 44.4%; Pred. No. 1.1e-33;
 DB 3; Length 257;
 39.5%; Score 543; DB 2; Length 246; 44.5%; Pred. No. 5.7e-34;
 39.4%; Score 541; DB 7; Length 279; 46.8%; Pred. No. 9.2e-34;
 Length 220;
 Score 541; DB 7;
Pred. No. 7.2e-34;
 AAW64260 standard; protein; 246 AA.
Human amyloid beta-protein precursor inhibitor.
WO9824886-A1.
ID AAB21326 standard; protein; 257 AA.

DE Human HSCEE.

PN WG200053776-A2.

PD 14-SEP-2000.

PA (MOUN) MOUNT SINAI HOSPITAL.

Query Match 39.6%; Score 544; DB 3; Best Local Similarity 44.1%; Pred. No. 5e-34;
 ADC73299 standard; protein; 220 AA.
Stereostructure-related 2PTC_E protein.
WO2003060765-A1.
24-UUL-2003.
 ADC73301 standard; protein; 279 AA.
Stereostructure-related 2PTC protein.
WO2003060765-A1.
 ADN42340 standard; protein; 259 AA
 11-JUN-1998.
(BGHM) BRIGHAM & WOMENS HOSPITAL.
 ABB78122 standard; peptide; 223 AA
 39.4%;
 Human novel proteinNOV 62.
US2004033493-A1.
 (AJIN) AJINOMOTO CO INC. (UMEY/) UMEYAMA H.
 (AJIN) AJINOMOTO CO INC. (UMEY/) UMEYAMA H.
 GANGOLLI E A.
PADIGARU M.
ANDERSON D W.
 SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
SHIMKETS R A.
 (CURA-) CURAGEN CORP.
 TCHERNEV V T.
 COLMAN S D.
WOLENC A R.
PENA C E A.
GROSSE W M.
ALSOBROOK J ELEPLEY D M.
RIEGER D K.
 RASTELLI L.
MILLER C E.
GERLACH V.
 BURGESS C E.
 TAUPIER R J. GUSEV V Y.
 Best Local Similarity
 Best Local Similarity
RESULT 1185
 Local Similarity
 24-JUL-2003.
 06-SEP-2002
 Query Match
 Query Match
 Query Match
 Query Match
 (RIEG/)
(BURG/)
 TCHE/)
 SPYT/)
 PATT/)
 RAST/)
 ZERH/
 TAUP/
GUSE/
 COLM/
 PENA/
 PADI/
ANDE/
 FURT/
 GERL/
```

```
Length 243;
 Length 249;
 Length 261;
 Length 247;
 Length 223;
 Length 232;
Length 223;
 Length 240;
 Length 232;
 ABB04644 standard; protein; 240 AA.

Engraulis japonicus trypsinogen (aTry I) SEQ ID NO:1.
J02001269173-A.
02-0CT-2001.
(NISB) JAPAN TOBACCO INC.
38.2%; Score 525; DB 5; Lengt et Local Similarity 45.7%; Pred. No. 1.3e-32;
 Best Local Similarity 45.6%; Pred. No. 1.2e-33; RESULT 1191
ID ABB84419 standard; peptide; 243 AA.
DE Bovine SCCE protein N-terminal fragment SEQ ID 46.
 ABB84423 standard; peptide; 249 AA.
Murine SCCE protein N-terminal fragment SEQ ID 50.
WO200262135-A2.
 38.0%; Score 521.5; DB 5; 43.0%; Pred. No. 2.6e-32;
 Query Match 37.8%; Score 519.5; DB 6;
Best Local Similarity 40.0%; Pred. No. 3.9e-32;
RESULT 1196
 DB 5;
 Score 538; DB 5;
Pred. No. 1.2e-33;
 38.7%; Score 531.5; DB 5 43.8%; Pred. No. 4.3e-33;
 Score 516; DB 5;
Pred. No. 6.9e-32;
 39.2%; Score 538; DB 5; 45.6%; Pred. No. 1.2e-33;
 38.1%; Score 524; DB 2; 43.6%; Pred. No. 1.6e-32;
 Ouery Match 37.8%; Score 519; DB 7; Best Local Similarity 44.5%; Pred. No. 3.8e-32; RESULT 1197
 ABG70276 standard; protein; 247 AA.
Human Serine Protease TLSP-like protein.
WO200255702-A2.
 11-DEC-2002
(REMI-) REMIN HOSPITAL SHENZHEN CITY
 ABBB3322 standard; protein; 223 AA.
Partial trypsin sequence.
US2002035434-A1.
 Human NOV13a protein; 261 AA. Human NOV13a protein SEQ ID NO:70. 14-NOV.
 AAW64261 standard, protein, 232 AA.
Kallikrein substrate binding site.
WO9824886-A1.
 ADLI5205 standard, protein; 232 AA.
Pancreatic kallikrein #1.
CN1384199-A.
 11-JUN-1998.
(BGHM) BRIGHAM & WOMENS HOSPITAL.
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04-OCT-2001
 Query Match
 Match
 -FEB-2
 (HOUG/)
 (SKEI/)
(HEPL/)
 JIAN/)
KALO/)
FANG/)
 HURA/)
 HARL/)
 JIAN/)
 KALO/)
 (LISX/)
 FANG/
 SKEI/
 Query
 Query Match 36.5%; Score 501; DB 8; Length 247; Best Local Similarity 43.3%; Pred. No. 9.8e-31; RESULT 1203
 H4-SEP-2000.
(MoUN) MOUNT SINAI HOSPITAL.
ery Match 36.2%; Score 498; DB 3; Length 254;
ery Match 43.1%; Pred. No. 1.7e-30;
 ABR41530 standard; protein; 261 AA.

Human DITHP protein modification/maintenance protein.
W0200297031-A2.
05-DEC-2002.
INCYTE GENOMICS INC.
36.5%; Score 501; DB 6; Length 261;
st Local Similarity 43.3%; Pred. No. 1e-30;
 OB-AEK-ZOUJ.
(GETH) GENENTECH INC.
sry Match 36.5%; Score 501; DB 8; Length 247;
rocal Similarity 43.3%; Pred. No. 9.8e-31;
 Score 514; DB 2; Length 268;
Pred. No. 1.1e-31;
 36.5%; Score 501; DB 5; Length 247; 43.3%; Pred. No. 9.8e-31;
 Length 247;
 Length 223;
 Length 241;
 'ABB04645 standard; protein; 241 AA.
Engraulis japonicus trypsinogen (aTry II) SEQ ID NO:2
JP2001269173-A.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

QUETY MATCH
BEST LOCAL Similarity 43.3%; Pred. No. 9.8e-31;
RESULT 1204
 Query Match 36.4%; Score 500; DB 3; Best Local Similarity 43.5%; Pred. No. 1.1e-30; RESULT 1206
 Score 504; DB 5;
Pred. No. 5.6e-31;
 ADQ30589 standard; protein; 247 AA.
Pancreas cancer marker - trypsin II precursor.
WO2004055519-A2.
 06-MAY-2004.
(FIVE-) FIVE PRIME THERAPEUTICS INC.
 ADN04140 standard; protein; 247 AA. Antipsoriatic protein sequence #265.WO2004028479-A2.
 ADN99594 standard; protein; 247 AA.
Novel human protein sequence #410.
WO2004038003-A2.
 AAU87693 standard; protein; 247 AA.
Human pancreatic tumour protein #5.
WO200212331-A2.
 protein; 223 AA.
 Human neurosin amino acid sequence.
WOZ00031284-Al.
OZ-JUN-Z000.
(FUSO) FUSO PHARM IND LTD.
 AAB21294 standard; protein; 254 AA.
Human KLK-Ll protein #2.
WO200053776-A2.
 AAW94493 standard; protein; 268 AA
AAW94493 Branna
Human kallikrein.
WOS942849-Al.
01-057-1998.
A (INCY-) INCYTE PHARM INC.
A "Match "--ity 46.4%; Pr
 JPZOULES...
02-001.
(NISB) JAPAN TOBACCO INC.
erv Match
 14-FEB-2002.
(CORI-) CORIXA CORP.
 Query Match
Best Local Similarity
RESULT 1201
 Best Local Similarity RESULT 1202
 Query Match
Best Local Similarity
RESULT 1199
 Query Match
Best Local Similarity
RESULT 1200
 Query Match
Best Local Similarity
RESULT 1207
 AAB03862 standard;
 08-APR-2004
 Query Match
 Query
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Length 254;
 Length 254;
 Length 254;
 Length 254;
 ABB95279 standard; protein; 254 AA.
Human P703P putative full length protein SEQ ID NO 525.
US2002022248-A1.
AAM01174 standard, protein; 254 AA.
Human prostate-specific amino acid sequence P703P.
WO200151633-A2.
 36.2%; Score 498; DB 4; 43.1%; Pred. No. 1.7e-30;
 36.2%; Score 498; DB 4; 43.1%; Pred. No. 1.7e-30;
 36.2%; Score 498; DB 4; 43.1%; Pred. No. 1.7e-30;
 36.2%; Score 498; DB 4; 43.1%; Pred. No. 1.7e-30;
 AAG99059 standard; protein; 254 AA.
Human prostate-specific amino acid of P703B.
WO200134802-A2.
 ABU71710 standard; protein; 254 AA.
Prostate cancer specific antigen P703P #7.
US2002192763-A1.
 AAU69819 standard; protein; 254 AA.
Human prostate cDNA encoded protein #27
WO200173032-A2.
 HOUGHTON R L.
Y DE BASSOLS C V.
 SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
 LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
 XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S I
 19-JUL-2001.
(CORI-) CORIXA CORP.
 Query Match
Best Local Similarity
RESULT 1209
 XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S I
 Query Match
Best Local Similarity
RESULT 1208
 (CORI-) CORIXA CORP.
 (CORI-) CORIXA CORP.
 MCNEILL P D.
 DAY C H.
VEDVICK T S.
 Best Local Similarity
 FANGER G R.
RETTER M W.
STOLK J A.
 DAY C H. VEDVICK T S.
 Local Similarity
 FANGER G R. RETTER M W.
 STOLK J A.
 KALOS M D.
 CARTER D.
 CARTER D.
 HURAL J.
 FOY T M.
 LI S X.
WANG A.
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PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DABA/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M. 36.2%;
Query Match 36.2%;
 (MILL) MILLET I.
(SCIO/) SCIORE P.
(ELLE/) ELLERMAN K.
(MACD/) MACDOUGALL J R.
(SMIT/) SMITHSON G.
 LI L.
CASMAN S J.
BOLDOG F L.
GORMAN L.
GANGOLLI E A.
FERNANDES E R.
 (ALSO/) ALSOBROOK J P. (TCHE/) TCHERNEV V T. (LIUX/) LIU X. (SPYT/) SPYTEK K A.
 SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
LEPLEY D M.
BURGESS C E.
SHIMKETS R A.
GROSSE W M.
SZEKERES E S.
 CURAGEN CORP.
 RIEGER D K.
EDINGER S R.
GUNTHER E.
 (CURA-) CURAGEN CORP.
 Best Local Similarity RESULT 1220
 Ouery Match
Best Local Similarity
RESULT 1222
 Best Local Similarity RESULT 1219
 06-SEP-2007
 Query Match
 (FERN/)
(RIEG/)
(EDIN/)
(GUNT/)
 (LEPL/)
(BURG/)
(SHIM/)
(GROS/)
(SZEK/)
(LILL/)
(LILL/)
(CASM/)
(GORM/)
(GANG/)
 ZERH/)
 AAB74830 standard; protein; 1079 AA.
Prostate tumour antigen amino acid sequence for a fusion protein.
WO200125272-A2.
 36.2%; Score 498; DB 4; Length 1079; 43.1%; Pred. No. 7.6e-30;
 36.2%; Score 498; DB 7; Length 254; 43.1%; Pred. No. 1.7e-30;
 Query Match 36.2%; Score 498; DB 5; Length 254; Best Local Similarity 43.1%; Pred. No. 1.7e-30; RESULT 1212
 O3-OCT-2002.
(UYQU-) UNIV QUEENSLAND TECHNOLOGY.
ery Match 36.2%; Score 498; DB 6; Length 254;
ery Match 43.1%; Pred. No. 1.7e-30;
 Length 254;
 36.2%; Score 498; DB 6; Length 254; 43.1%; Pred. No. 1.7e-30;
 36.2%; Score 498; DB 7; Length 254; 43.1%; Pred. No. 1.7e-30;
 ABRS4391 standard; protein; 254 AA.
Prostate tumour specific protein sequence SEQ ID 525.
WO200289747-A2.
 Query Match 36.2%; Score 498; DB 6; Best Local Similarity 43.1%; Pred. No. 1.7e-30; RESULT 1214
 ABU71860 standard; protein; 1079 AA.
Prostate specific antigen fusion protein #2.
 AbG26391 standard; protein; 254 AA.
Human prostate-specific polypeptide #60.
21-AuG-2003.
(CORI-) CORIXA CORP.
 ADB13975 standard; protein; 254 AA.
Human prostate specific protein P703P.
US2003185830-A1.
 03-OCT-2002, (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 ABP54357 standard; protein; 254 AA.
Human KLK4 protein SEQ ID NO:6.
WO200277243-A1.
 ABP54360 standard; protein; 254 AA.
Human KLK4 protein SEQ ID NO:13.
WO200277243-A1.
 XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S L.
 WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
 MOLC

(CORI-) CORIXA

(CORI-) CORIXA

QUETY MATCH

BEST Local Similarity #

3SULT 1218

D ABUT1860 standard; F

B PROSTATE specific #

2N (22002192763-A1.)

PA (XUJ/) XU J.

PA (XUJ/) XU J.

PA (MITC/) MITCHP

PA (MITC/) MITCHP

PA (MITC/) MITCHP

PA (MITC/) MITCHP

PA (RALO/) KAI

PA (RALO/) RAI

PA (RALO/) PA (RALO/) PA (RALO/) PA (RALO/) PA (RALO/) PA (RALO/) PA (RALO/) PA (RANO/) PA (RANO
 (HEND/) HENDERSON R A.
 14-NOV-2002.
(CORI-) CORIXA CORP.
 02-OCT-2003.
(CORI-) CORIXA CORP.
 Query Match
Best Local Similarity
RESULT 1217
ID AAB14830 standard, pr
DE Prostate tumour antig
PN WG20012527-A2.
PD 12-ARR-2001.
PA (CORI-) CORIXA CORP.
 Query Match
Best Local Similarity
RESULT 1213
 Query Match
Best Local Similarity
RESULT 1215
 Query Match
Best Local Similarity
```

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36.2%; Score 497.5; DB 5; Length 230; 47.4%; Pred. No. 1.7e-30;
 Ouery Match 36.2%; Score 497.5; DB 5; Length 230; Best Local Similarity 47.4%; Pred. No. 1.7e-30; RESULT 1221
 Score 497.5; DB 7; Length 230;
Pred. No. 1.7e-30;
 36.2%; Score 497.5; DB 8; Length 280; 42.7%; Pred. No. 2.1e-30;
 36.2%; Score 497.5; DB 8; Length 461;
Length 1079;
 ADII1276 standard; protein; 230 AA.
Polypeptide homologous to a human NOVX domain SeqID 812.
WO200268649-A2.
 ADI17268 standard; protein; 230 AA.
Polypeptide homologous to a human NOVX domain SegID 804
WO200268649-A2.
06-SEP-2002.
 99
36.2%; Score 498; DB 4; 43.1%; Pred. No. 7.6e-30;
 ADJ83075 standard; protein; 230 AA.
Trypsin-like serine protease protein - SEQ ID
US2003170630-AI.
 D ADIZING standard; peptide; 461 AA.

B Amino acid sequence of trypsinogen-0aa-sp55.

N WO2004019878-A2.

D 11-MAR-2004.

A (COMP-) COMPOUND THERAPEUTICS INC.

A AFEY/) AFEYAN N B. 36.2%; Score 497.5. P.
 Amino acid sequence of trypsinogen WO2004019878-A2.
 ADL27345 standard; peptide; 280 AA
 (COMP-) COMPOUND THERAPEUTICS INC. (AFEY) AFEYAN N B.
 36.2%;
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Query Match 36.0%; Score 494.5; DB 6; Length 247; Best Local Similarity 41.9%; Pred. No. 3.1e-30; RESULT 1240
 36.1%; Score 496.5; DB 4; Length 248; 43.4%; Pred. No. 2.2e-30;
 (SMIX) SMITHKLINE BEECHAM BIOLOGICALS.

ry Match 36.1%; Score 496.5; DB 5; Length 248; t Local Similarity 43.4%; Pred. No. 2.2e-30;
 (SMIK.) SMITHKLINE BEECHAM BIOLOGICALS.

Query Match
36.1%; Score 496.5; DB 5; Length 248;
Best Local Similarity 43.4%; Pred. No. 2.2e-30;
 36.0%; Score 494.5; DB 8; Length 246; 41.9%; Pred. No. 3.1e-30;
 36.0%; Score 494.5; DB 3; Length 247; 41.9%; Pred. No. 3.1e-30;
 36.0%; Score 495; DB 5; Length 262; 40.4%; Pred. No. 3e-30;
 AAU74931 standard; protein; 248 AA.
Maino acid sequence of prostase protein fragment #2.
WOZ00220867-A1.
03-JAN-2002.
 (HOFF) HOFFMANN LA ROCHE & CO AG F. (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN. FY MATCH SINGENIATION 41.9%; Pred. No. 3.1e-30; t Local Similarity 41.9%; Pred. No. 3.1e-30;
 36.0%; Score 494.5; DB 6; 41.9%; Pred. No. 3.1e-30;
 Pancreas cancer marker - trypsin I precursor. W02004055519-A2.
 AAU74770 standard; protein; 248 AA.
Protein sequence of prostase homologue #2.
WO20020708-A2.
03-JAN-2002.
(SMIK) SMITHKLINE BEECHAM BIOLOGICALS. (CORI-) CORIXA CORP.
 ABG76997 standard; protein; 262 AA. Human kallikrein protein variant #1. WO200261131-A2.
 Best Local Similarity 40.4%; Pred. RESULT 1236
ID ADRESOUS standard; protein; 246 AA. DE Human trypsinogen partial protein. PN WO2004078777-A2.
 AAB21321 standard; protein; 247 AA
 ABRE4239 standard; protein; 247 AA. Human NOV35a protein SEQ ID NO:146.WO2003023001-A2.
 ABRE4241 standard; protein; 247 AA.
Human NOV35c protein SEQ ID NO:150.
WO2003023001-A2.
 AAM01173 standard; protein; 254 AA
 ADQ30588 standard; protein; 247 AA
 (BRIM) BRISTOL-MYERS SQUIBB CO. (TSUC/) ISUCHHASHI Z. (HUIL/) HUI L.
 (MOUN) MOUNT SINAI HOSPITAL.
 (BIOR-) BIOREXIS PHARM CORP.
 (CURA-) CURAGEN CORP.
 Ouery Match
Best Local Similarity
RESULT 1234
 Query Match
Best Local Similarity
RESULT 1241
 PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity
RESULT 1233
 Query Match
Best Local Similarity
RESULT 1239
 Query Match
Best Local Similarity
 Best Local Similarity RESULT 1237
 Human trypsinogen.
WO200053776-A2.
 14-SEP-2000
 16-SEP-2004
 20-MAR-2003
 20-MAR-200
 Query Match
 Query Match
 Query Match
 RESULT 1238
 Lesty Match 36.2%; Score 497; DB 3; Length 249; Best Local Similarity 43.1%; Pred. No. 2e-30; RESULT 1227
ID AAB21320 standard; protein; 254 AA.
DE Human prostase.
PN WC20053776-A2.
PD 14-SEP-2000
 Score 497.5; DB 8; Length 485; Pred. No. 3.6e-30;
 Score 497.5; DB 8; Length 464;
Pred. No. 3.5e-30;
 Length 248;
 vuery Match 36.2%; Score 497; DB 4; Length 254; Beet Local Similarity 43.1%; Pred. No. 2.1e-30; RESULT 1229
 Length 254;
 Length 254;
 Length 254,
 AMU/4932 standard; protein; 254 AA.
Amino acid sequence of prostase protein fragment #3.
W0200200867-A1.
 AAW60592 standard, protein, 248 AA.
Human prostate-specific kallikrein (HPSK) protein
W09820117-A1.
 Score 496.5; DB 2;
Pred. No. 2.2e-30;
 36.2%; Score 497; DB 5; 43.1%; Pred. No. 2.1e-30;
 42.7%; Pred. No. 3.5e-30;
 Match 36.2%; Score 497; DB 3;
Local Similarity 43.1%; Pred. No. 2.1e-30;
 36.2%; Score 497; DB 5; 43.1%; Pred. No. 2.1e-30;
 ADL27348 standard; peptide; 485 AA.
Amino acid sequence of trypsinogen-20aa-sp55.
WO2004019878-A2.
I-MAR-2004.
 ADL27347 standard; peptide; 464 AA.
Amino acid sequence of trypsinogen-3aa-sp55.
W22004019878-A2.
(COMP-) COMPOUND THERAPEUTICS INC.
(AFEY/) AFEYAN N B.
 Protein standard; protein; 254 AA.
Protein sequence of prostase homologue #3.
W0200200708-A2.
 (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 (CORI-) CORIXA CORP.
 (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 Human prostase antigen #3.
18-JAN-2001
 AAY72524 standard; protein; 248 AA.
Human prostase antigen #2.
WO200104143-A2.
 (COMP-) COMPOUND THERAPEUTICS INC. (AFEY/) AFEYAN N B.
 MOSSc.--
14-MAY-1998.
(INCY-) INCYTE PHARM INC.
36.1%;
 36.2%;
 36.28;
Best Local Similarity RESULT 1224
 Best Local Similarity RESULT 1231
 Local Similarity
 Local Similarity
 Local Similarity
 18-JAN-2001
 18-JAN-2001
 03-JAN-2002
 03-JAN-2002
 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
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Length 247;

Length 247;

Length 254;

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21-AUG-2003.
(CORI-) CORIXA CORP.
 14-NOV-2002.
(CORI-) CORIXA CORP.
 Best Local Similarity
RESULT 1249
 Query Match
Best Local Similarity
RESULT 1250
 (CORI-) CORIXA CORP.
 Best_Local_Similarity
RESULT 1251
 Query Match
'Best Local Similarity
 Best Local Similarity RESULT 1246
 Query Match
Best Local Similarity
RESULT 1247
 Best Local Similarity
SULT 1252
 WO200053776-A2.
 Human KLK2
 Query Match
 Query Match
 RESULT 1253
 Query Match 36.0%; Score 494; DB 4; Length 254; Best Local Similarity 42.7%; Pred. No. 3.5e-30; RESULT 1243
 36.0%; Score 494; DB 4; Length 254; 42.7%; Pred. No. 3.5e-30;
 36.0%; Score 494; DB 4; Length 254; 42.7%; Pred. No. 3.5e-30;
 Length 254;
Human prostate-specific amino acid mature form of P703P. WO200151633-A2.
 AAG99958 standard; protein; 254 AA.
Human prostate-specific mature protein of P703P.
WO200134802-A2.
 Score 494; DB 4;
Pred. No. 3.5e-30;
 ABB95278 standard; protein; 254 AA.
Human P703P mature protein SEQ ID NO 523
US2002022248-A1.
 AAUG9818 standard; protein; 254 AA.
Human prostate cDNA encoded protein #26.
WO200173032-A2.
 ABU71709 standard; protein; 254 AA.
Prostate cancer associated protein #12.
US2002192763-A1.
 Query Match 36.0%;
Best Local Similarity 42.7%;
RESULT 1242
 HURAL J.
MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
 JIANG Y.
KALOS M D.
FANGER G R.
FENGER G R.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
SKEIKY Y A W.
HEPLER W T.
 DILLON D C.
MITCHAM J L.
HARLOCKER S L.
 DILLON D C.
MITCHAM J L.
HARLOCKER S L.
 LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
 HENDERSON R A.
 19-JUL-2001.
(CORI-) CORIXA CORP.
 04-OCT-2001.
(CORI-) CORIXA CORP.
 17-MAY-2001.
(CORI-) CORIXA CORP.
 JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
VEDVICK T S.
CARTER D.
 Best Local Similarity RESULT 1244
 Local Similarity
 Query Match
 (DBAS/)
(FOYT/)
 (HEPL/)
 (JIAN/)
(KALO/)
(FANG/)
 (MCNE/)
(HOUG/)
 (HARL/)
(JIAN/)
 KALO/)
 HEND/)
 HARL/
 SKEI/)
 FANG/
 (SKEI/
 VEDV
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ADQ39654 standard; protein; 262 AA.
Human myocardial infarction-associated gene derived protein, SEQ ID 1317.
WO2004058052-A2.
 Length 254;
 Length 254;
 Length 254;
 Length 262;
 Length 262;
 Length 262;
 Length 262;
 Prostate tumour specific protein sequence SEQ ID W0200289747-A2.
36.0%; Score 494; DB 5; 42.7%; Pred. No. 3.5e-30;
 (MOUN) MOUNT SINAI HOSPITAL.

ry Match
16.0%; Score 494; DB 3;

t Local Similarity 40.4%; Pred. No. 3.6e-30;
 36.0%; Score 494; DB 7; 42.7%; Pred. No. 3.5e-30;
 36.0%; Score 494; DB 7; 42.7%; Pred. No. 3.5e-30;
 36.0%; Score 494; DB 7; 40.4%; Pred. No. 3.6e-30;
 36.0%; Score 494; DB 8; 40.4%; Pred. No. 3.6e-30;
 36.0%; Score 494; DB 6; 42.7%; Pred. No. 3.5e-30;
 36.0%; Score 494; DB 5; 40.4%; Pred. No. 3.6e-30;
 ADB13973 standard; protein; 254 AA.
Human mature prostate specific protein P703P.
U2003185890-A1.
 Query Match
Best Local Similarity 42.7%; Pred. No. 3
RESULT 1248
DD ADG26389 standard; protein; 254 AA.
DE Human prostate-specific polypeptide #59.
PN US2003157089-A1.
 11-DEC-2002.
(REMI-) REMIN HOSPITAL SHENZHEN CITY Query Match
 ABR54390 standard; protein; 254 AA.
 ADL15197 standard; protein; 262 AA.
Human pancreatic kallikrein.
CN1384199-A.
 ADL64969 standard, protein, 262 AA.
Human kallikrein protein (KLK1).
US2004033582-A1.
 AAB21319 standard; protein; 262 AA
 ABG76996 standard; protein; 262 AA
 08-AUG-2002.
(BRIM) BRISTOL-MYERS SQUIBB CO.
(TSCC/) TSUCTIHASHI Z.
(HUIL/) HUI L.
 Human kallikrein protein.
WO200261131-A2.
 (EDMO) EDMONDS M.
(HUIL/) HUI L.
(PERR/) PERRONE M.
(POWE) POWELL J R.
(RAMA/) RAMANATHAN C S.
(SARAN/) SANNSON B.
(TSUC/) TSUCHIHASHI Z.
(ZERB/) ZERBA K.
 (APPL-) APPLERA CORP
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```
35.9%; Score 493.5; DB 3; Length 241; 42.6%; Pred. No. 3.6e-30;
 DB 6; Length 240;
 ABP74711 standard; protein; 262 AA.
Human glandular kallikrein 1 precursor protein SEQ ID NO:600
WO200281646-A2.
 Query Match 35.9%; Score 493; DB 8; Length 247; Best Local Similarity 42.1%; Pred. No. 4.1e-30;
36.0%; Score 494; DB 8; Length 262; 40.4%; Pred. No. 3.6e-30;
 Length 258;
 35.9%; Score 493; DB 7; Length 262;
 Length 262;
 Length 253;
 Score 493; DB 6; Length 262;
Pred. No. 4.3e-30;
 Length 262
 Human autoimmune disease-related protein - SEQ ID 105. WO200408303-A2.
 AAW71005 standard; protein; 262 AA.
Human prostate-associated kallikrein designated HPAK.
WO9832865-A1.
 35.9%; Score 493.5; DB 6 42.6%; Pred. No. 3.6e-30;
 , DB 3;
4.2e-30;
 Ouery Match 35.9%; Score 493; DB 2;
Best Local Similarity 40.4%; Pred. No. 4.3e-30;
 36.0%; Score 494; DB 8; 40.4%; Pred. No. 3.6e-30;
 Query Match 35.9%; Score 493; DB 3; Best Local Similarity 42.8%; Pred. No. 4.2e-30; RESULT 1259
 14-SEP-2000.

(MOUN) MOUNT SINAI HOSPITAL.

ery Match 35.3%; Score 493;
 ABR54277 standard; protein; 240 AA.
Human trypsinogen protein SEQ ID NO:341.
WOZ003023001-AZ.
20-MAR-2003.
 (REMI-) REMIN HOSPITAL SHENZHEN CITY
 ADN04297 standard; protein; 247 AA. Antipsoriatic protein sequence #343. WO2004028479-A2.
 AAB21316 standard; protein; 241 AA.
 RESULT 1256
ID AAB1308 standard; protein; 253 AA.
DE Human EMSP.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
 AAB21324 standard; protein; 258 AA.
Human EMSP.
WO200053776-A2.
 ADL15204 standard; protein; 262 AA
 (CTLI-) CTL IMMUNOTHERAPIES CORP.
 14-SEP-2000. (MOUN) MOUNT SINAI HOSPITAL.
 40.48;
 30-JUL-1998.
(INCY-) INCYTE PHARM INC.
 08-APR-2004.
(GETH) GENENTECH INC.
 (APPL-) APPLERA CORP.
 (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity
 Best Local Similarity RESULT 1255
 Query Match
Best Local Similarity
RESULT 1254
 Local Similarity
 Best Local Similarity
RESULT 1262
 Query Match
Best Local Similarity
 Human trypsinogen. WO200053776-A2.
 Query Match
 Ouery Match
 Query Match
 Query Match
 RESULT 1256
```

```
AAB5293 standard; protein; 267 AA.
AAB5293 standard; protein; 267 AA.
Human pancreatic cancer antigen protein sequence SEQ ID NO:745.
WO200055320-A1.
21-SEP-2000.
(HUMA-) HUMAN GENOME SCI INC.
 Length 263;
 Length 225;
 Length 262;
 Length 230;
 Length 256;
 Length 262;
 Length 267;
 Length 262;
 ADM72846 standard; protein; 263 AA.
Human glandular kallikrein 1 protein SEQ ID NO:105.
MO2004022799.A2.
18-MAR-2004.
(MANN-) MANNKIND CORP.
 Query Match
Best Local Similarity 40.4%; Pred. No. 4.3e-30;
RESULT 1264
 AAB98503 standard; protein; 225 AA.
Human trypsin serine protease catalytic domain.
WO200129056-A1.
26-ARR-2001.
(UYAR-) UNIV ARKANSAS.
 35.8%; Score 492; DB 4; 43.7%; Pred. No. 4.4e-30;
 35.8%; Score 492; DB 2; 43.7%; Pred. No. 4.5e-30;
 35.8%; Score 492; DB 3; 41.1%; Pred. No. 5e-30;
 35.8%; Score 492; DB 1; 40.4%; Pred. No. 5.2e-30;
 35.8%; Score 492; DB 3; 40.4%; Pred. No. 5.3e-30;
 35.7%; Score 491; DB 5; 40.4%; Pred. No. 6.2e-30;
Best Local Similarity 40.4%; Pred. No. 4.3e-30; RESULT 1263
 35.8%; Score 492; DB 5; 40.4%; Pred. No. 5.2e-30;
 protein; 262 AA.
by clone lambda HK65a.
 Human kallikrein 1 polymorphic sequence
 Human TRYI trypsinogen variant protein
 ABG76998 standard; protein; 262 AA. Human kallikrein protein variant #2 WO200261131-A2.
 ADA05744 standard, protein, 224 AA.
Human NOV189 protein SEQ ID NO:104.
WO2003029424-A2.
 AAW93488 standard; protein; 230 AA
 AAB21315 standard; protein; 256 AA
 ABG77002 standard; protein; 262 AA
 (BRIM) BRISTOL-MYERS SQUIBB CO. (TSUC/) TSUCHIHASHI Z. (HUIL/) HUI L.
 (BRIM) BRISTOL-MYERS SQUIBB CO. (TSUC/) TSUCHIHASHI Z. (HUIL/) HUI L.
 (HOFF) ROCHE DIAGNOSTICS GMBH.
 14-SEP-2000.
(MOUN) MOUNT SINAI HOSPITAL.
 wery Match
Best Local Similarity 4
RESULT 1271
ID ADA65744 81*
PN Humar
 Best Local Similarity RESULT 1266
 Best Local Similarity
RESULT 1265
 Query Match
Best Local Similarity
RESULT 1268
 Query Match
Best Local Similarity
 Best Local Similarity RESULT 1270
 Best Local Similarity
RESULT 1267
 AAP95121 standard;
Kallikrein encoded
 Human KLK1.
WO200053776-A2.
 WO200261131-A2.
 04-JAN-1989.
(AMGE-) AMGEN.
 WO9910503-A1.
 08-AUG-2002
 04-MAR-1999
 Ouery Match
 Query Match
 Query Match
 Query Match
```

Length 247;

(PEYM/) (KEKU/)

ELLE/

ANDE/

JIWM/ ZHON/

RAST

PENA/

SHEN/

```
Score 487.5; DB 5; Length 449; Pred. No. 2e-29;
 Score 487.5; DB 4; Length 449; Pred. No. 2e-29;
 Score 487.5; DB 4; Length 449; Pred. No. 2e-29;
 35.5%; Score 487.5; DB 4; Length 449; 44.1%; Pred. No. 2e-29;
 Query Match
Best Local Similarity 44.1%; Pred. No. 2e-29;
RESULT 1279
ID ABU71763 standard; protein; 449 AA.
DE Prostate cancer specific antigen fusion protein #1.
PN US2002192763-A1.
 AAUG9872 standard; protein; 449 AA.
Human prostate serum antigen/P703P fusion protein.
WO200173032-A2.
(CORI-) CORIXA CORP.
 FIVE-) FIVE PRIME THERAPEUTICS INC.
35.5%; Score 48%; DB 8; Local Similarity 42.3%; Pred. No. 9.9e-30;
 ABB95332 standard; protein; 449 AA.
Human P703P/PSA fusion protein SEQ ID NO 617.
US2002022248-A1.
 AAM01227 standard, protein, 449 AA.
P703P and PSA fusion amino acid sequence.
WO200151633-A2.
 35.5%;
 35.5%;
 35.5%;
 HOUGHTON R L.
Y DE BASSOLS C V.
 XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S L.
 DILLON D C.
MITCHAM J L.
HARLOCKER S L.
 LI S X.
WANG A.
SKEIKY Y A W.
 HEPLER W T.
HENDERSON R A.
 LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
 (HEND/) HENDERSON R A.
 19-JUL-2001.
(CORI-) CORIXA CORP.
 STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
 STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
 ACNEILL P D.
 "Ouery Match
Best Local Similarity
RESULT 1277
 Best Local Similarity RESULT 1278
 KALOS M D.
FANGER G R.
RETTER M W.
 Query Match
Best Local Similarity
 Local Similarity
 FANGER G I
 DBAS/) Y DE BAS:
FOYT/) FOY T M.
 HURAL J
 JIANG Y
 JIANG
 06-MAY-2004
 -FEB-2002
 Query Match
 Query Match
 JIAN/)
 HEPL/)
 HARL/)
JIAN/)
KALO/)
FANG/)
 MCNE/
 FANG/)
 (RETT/)
(STOL/)
 Best
RESULT
 35.6%; Score 489.5; DB 4; Length 234; 43.0%; Pred. No. 7.2e-30;
 35.6%; Score 488.5; DB 2; Length 231; 43.9%; Pred. No. 8.4e-30;
 vuery Match
35.7%; Score 490; DB 8; Length 224;
Best Local Similarity 45.3%; Pred. No. 6.3e-30;
RESULT 1273
 Query Match 35.7%; Score 490; DB 6; Length 224; Best Local Similarity 45.3%; Pred. No. 6.3e-30; RESULT 1272
 Ouery Match 35.5%; Score 488; DB 8; Length 247; Best Local Similarity 42.3%; Pred. No. 9.9e-30;
 Human prostate serine protease protein.
EP936270-A2.
 ADNO4726 standard; protein; 247 AA. Antipsoriatic protein sequence #544. WO2004028479-A2.
 AAE00397 standard; protein; 234 AA.
E Human serine protease, PROST 07.
N W0200125446-A1.
D 12-APR-2001.
A (SCHD) SCHERING AG.
Query Match
 ADN99593 standard; protein; 247 AA. Novel human protein sequence #409. WO2004038003-A2.
 AAY25510 standard; protein; 231 AA.
 ADN62908 standard; protein; 224 AA
 MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
 GUO X.
PATTURAJAN M.
SPYTEK K A.
EDINGER S R.
ELLERMAN K.
 (LEACY) EASTH MENT OF THE CAGE AGEE M L. (BERGY) BERGHS C. (DIPLY) DIPIPPO V A. (EISE) EISEN A. (GANG) CANGOLLI E A. (RIEGY) SPADERNA S K. (SPAD)
 (GETH) GENENTECH INC.
10-APR-2003.
(CURA-) CURAGEN CORP.
 GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
 Best Local Similarity RESULT 1274
 PEYMAN J A.
KEKUDA R.
 CATTERTON E.
 Best Local Similarity
 SMITHSON G.
 18-AUG-1999.
(BADI) BASF AG.
 Human NOV18g.
US2004038223-A1.
 ZHONG M.
 08-APR-2004
 Query Match
```

```
ADL15207 standard; protein; 261 AA.
Pancreatic kallikrein #3.
 35.5%;
 35.5%;
 HURAL J.
MCNETLL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
 (MCNE/) MCNEILL P D.
(HOUG/) HOUGHTON R L.
(DBAS/) Y DE BASSOLS C V.
(FOYT/) FOY T M.
 LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
 HENDERSON R A.
 Query Match
Best Local Similarity
RESULT 1291
ID ADL:15207 standard; pr
DE Pancreatic kallikreir
 14-NOV-2002.
(CORI-) CORIXA CORP.
 STOLK J A.
DAY C H.
VEDVICK T S.
 CORIXA CORP.
 (CORI-) CORIXA CORP.
 MITCHAM J L.
HARLOCKER S
 Query Match
Best Local Similarity
RESULT 1287
 Best Local Similarity RESULT 1288
 Local Similarity
 Best Local Similarity RESULT 1290
 Query Match
Best Local Similarity
RESULT 1286
 DILLON D C.
 FANGER G R.
RETTER M W.
 07-SEP-1999.
(AMGE-) AMGEN INC.
 KALOS M D.
 CARTER D.
 21-AUG-2003
 Query Match
 Query Match
 Query Match
 (HURA/)
 DBAS/)
FOYT/)
 (HEPL/)
 RESULT
Score 487.5; DB 4; Length 585;
Pred. No. 2.6e-29;
 Length 449;
 Score 487.5; DB 7; Length 449;
Pred. No. 2e-29;
 35.5%; Score 487.5; DB 7; Length 449; 44.1%; Pred. No. 2e-29;
 ADB14067 standard; protein; 449 AA. .
Human prostate specific protein P703P/PSA fusion protein.
US2003185830-A1.
 ABR54444 standard; protein; 449 AA.
Prostate tumour specific protein sequence SEQ ID 617.
 ABUT1889 standard; protein; 585 AA.
Prostate cancer specific antigen fusion protein #3.
US2002192763-A1.
 Score 487.5; DB 6;
Pred. No. 2e-29;
 ABU71888 standard; protein; 585 AA.
Prostate cancer associated protein #72.
US2002192763-A1.
 Query Match 35.5%;
Best Local Similarity 44.1%;
RESULT 1282
 35.5%;
 Query Match
Best Local Similarity 44.1%;
 HURAL J.
MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
 LISX.
WANGA.
SKEIKYYAW.
HEPLERWT.
HENDERSONRA.
 DILLON D C.
MITCHAM J L.
HARLOCKER S L.
 LI S X.
WANG A.
SKEIKY Y A W.
 WO200289747-A2.
14-NOV-2002.
(CORI-) CORIXA CORP.
 02-OCT-2003.
(CORI-) CORIXA CORP.
 DILLON D C.
MITCHAM J L.
HARLOCKER S I
 JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
 21-AUG-2003.
(CORI-) CORIXA CORP.
 STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
 Best Local Similarity
RESULT 1284
 Local Similarity
 ABR54444 standard;
 FANGER G R.
 Query Match
 Query Match
 (LISX/)
(WANG/)
(SKEI/)
 DBAS/)
 (HARL/
 JIAN/
 FANG/
 JIAN/
```

```
Score 487.5; DB 4; Length 585; Pred. No. 2.6e-29;
 35.5%; Score 487.5; DB 6; Length 585; 44.1%; Pred. No. 2.6e-29;
 35.5%; Score 487.5; DB 7; Length 585; 44.1%; Pred. No. 2.6e-29;
 DB 4; Length 801;
 35.5%; Score 487.5; DB 7; Length 585; 44.1%; Pred. No. 2.6e-29;
 Length 224;
 ABU71890 standard; protein; 801 AA.
Prostate cancer specific antigen fusion protein #4
US2002192763-A1.
 Score 487.5; DB 4
Pred. No. 3.6e-29;
 35.4%; Score 487; DB 2; 43.4%; Pred. No. 1.1e-29;
 AAV31160 standard; protein; 224 AA.
Human trypsin serine protease protein domain.
USS948892-A.
 Prostate tumour-related protein, 585 AA.
WO200289747-A2.
 ADG26993 standard; protein; 585 AA.
Human prostate-specific polypeptide #249.
US2003157089-A1.
 ADB14470 standard; protein; 585 AA.
FOPP/PAPE fusion protein, FOPP3.
US2003185830-A1.
```

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03-JAN-2002.
(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
ery Match 34.8%; Score 477.5; DB 5; Length 226;
 Best Local Similarity RESULT 1301
 (INCY-) INCYTE CORP
 WO200200708-A2.
 ". Query Match
"- Best Local Si
RESULT 1306
 Ouery Match
 Ouery Match
 Query Match
 Query Match
 (HARL/)
(JIAN/)
(KALO/)
 (HEPL/)
 (MCNE/)
(HOUG/)
 (LISX/)
 DBAS/)
 FANG/)
 (VEDV/)
 SKEI/)
 HURA/)
PN CN1384199-A.
PD 11-DEC-2002.
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
Query March 35.3%; Score 484.5; DB 7; Length 261;
Best Local Similarity 40.2%; Pred. No. 1.9e-29;
RESULT 1292
 Score 477.5; DB 4; Length 226;
Pred. No. 5.8e-29;
 Score 483.5; DB 2; Length 240;
Pred. No. 2.1e-29;
 35.1%; Score 482.5; DB 3; Length 237; 42.2%; Pred. No. 2.5e-29;
 4; Length 216;
 vuery Match 35.2%; Score 483; DB 7; Length 260; Best Local Similarity 39.8%; Pred. No. 2.5e-29; RESULT 1296
 35.0%; Score 481; DB 1; Length 262; 40.0%; Pred. No. 3.6e-29;
 Query Match 35.2%; Score 484; DB 8; Length 333; Best Local Similarity 43.5%; Pred. No. 2.7e-29;
 Length 261
 ABM83250 standard; protein; 333 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:3499.
MO2004023373-A2.
25-MAR-2004.
(INCY-) INCYTE CORP.
 ABM83249 standard; protein; 261 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:3498
WO2004023973-A2.
 AAP70568 standard; protein; 262 AA.
Human kallikrein-like substance has hypotensive activity
 Score 484; DB 8;
Pred. No. 2.1e-29;
 (SMIK) SMITHKLINE BEECHAM PLC.

ry Match

t Local Similarity 44.3%; Pred. No. 5.5e-29;
 RESULT 1300
ID AAU74902 standard; protein; 226 AA.
DE Protein sequence of prostase homologue #4.
 AAY72526 standard, protein; 226 AA.
Human prostase antigen P703PDE5 sequence.
WO200104143-A2.
 18-JAN-2001.
(SMIK) SNITHKLINE BEECHAM BIOLOGICALS.
(CORI-) CORIXA CORP.
 (REMI-) REMIN HOSPITAL SHENZHEN CITY.
 AAW57740 standard; protein; 240 AA.
 AAU01290 standard; protein; 216 AA.
Human serine protease HETAA37p.
WO200123587-A2.
 protein; 260 AA
 AAB21293 standard; protein; 237 AA
 (MOUN) MOUNT SINAI HOSPITAL.
 Query Match 35.2%;
Best Local Similarity 43.5%;
 35.2%;
 Watch 34.8%;
Local Similarity 43.8%;
 ADL15206 standard; protei
Pancreatic kallikrein #2.
 Trypsinogen-like protein. JP10099080-A.
 Human KLK-L1 protein #1.
WO200053776-A2.
14-SEP-2000.
 21-APR-1998.
(SHIS) SHISEIDO CO LTD.
 25-MAR-2004.
(INCY-) INCYTE CORP.
 09-JUN-1987.
(NAKA/) NAKANISHI S.
 Query Match
Best Local Similarity
 Best Local Similarity
RESULT 1295
 Best Local Similarity RESULT 1297
 JP62126980-A.
 CN1384199-A.
 05-APR-2001
 Query Match
 Query Match
 Query Match
 Query Match
```

```
AAU74929 standard; protein; 312 AA.
Amino acid sequence of wild-type NS1-P703P-His fusion protein
WO200200867-A1.
33-JAN-2002.
 Length 226;
 34.8%; Score 477.5; DB 4; Length 312; 43.8%; Pred. No. 8.1e-29;
 34.8%; Score 477.5; DB 5; Length 312; 43.8%; Pred. No. 8.1e-29;
 Length 312;
 34.8%; Score 477.5; DB 4; Length 344; 43.8%; Pred. No. 8.9e-29;
 AAU74768 standard; protein; 312 AA.
Amino acid sequence of wild-type NS1-p703-His fusion protein.
WO200200708-AZ.
03-JAN-2002.
 ABM82601 standard; protein; 239 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2850.
 #4
 34.8%; Score 477.5; DB 5; 43.8%; Pred. No. 8.1e-29;
 ABU71886 standard, protein, 344 AA.
Human prostate specific antigen (PSA) epitope #26.
US2002192763-A1.
Amino acid sequence of prostase protein fragment WO200200867-Al.
 2
 PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Querry Match 34.8%; Score 477.5; DB 5
Best Local Similarity 43.8%; Pred. No. 5.8e-29;
RESULT 1302
 (SMIK) SMITHKLINE BEECHAM BIOLOGICALS. (CORI-) CORIXA CORP.
 (SMIK) SMITHKLINE BEECHAM BIOLOGICALS
 (SMIK) SMITHKLINE BEECHAM BIOLOGICALS
 AAY72522 standard; protein; 312 AA.
NSI-P703P-His fusion protein.
WO200104143-A2.
 MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
 LISX.
WANGA.
SKEIKYYAW.
HEPLERWT.
HENDERSONRA.
 MITCHAM J L.
HARLOCKER S L.
 STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
 Best Local Similarity
RESULT 1304
 FANGER G R.
RETTER M W.
 Best Local Similarity RESULT 1303
 Local Similarity
1305
 XU J.
DILLON D C.
 Local Similarity
 KALOS M D.
 WO2004023973-A2.
25-MAR-2004.
 HURAL J.
 JIANG Y
```

```
43.8%; Pred. No. 1.4e-28;
 ADG26193 standard, protein, 220 AA.
Human prostate-specific polypeptide #9
 34.48;
 (MCNE/) MCNEILL P D.
(HOUG/) HOUGHTON R L.
(DBAS/) Y DE BASSOLS C V.
(FOYT/) FOY T M.
 (VEDV/) VEDVICK T S.
(CART/) CARTER D.
(LISX/) LI S X.
(WANG), WANG A.
(KEEL/) HEPLER W T.
(HEPL/) HEPLER W T.
 LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
 HENDERSON R A.
 DILLON D C.
MITCHAM J L.
HARLOCKER S I
 02-OCT-2003.
(CORI-) CORIXA CORP.
 Query Match
Best Local Similarity
 Best Local Similarity
 14-NOV-2002.
(CORI-) CORIXA CORP.
 MITCHAM J L.
HARLOCKER S
 Best_Local Similarity RESULT 1319
 Best Local Similarity RESULT 1316
 FANGER G R.
RETTER M W.
 STOLK J A.
DAY C H.
 Local Similarity
 FANGER G R.
RETTER M W.
 CARTER D.
 HURAL J.
 /EDVICK
 WO200289747-A2.
 Query Match
 Query Match
 Match
 JIAN/)
KALO/)
 risx/
 Ouery
 Prostate tumour antigen predicted amino acid sequence for P703PDES. WO200125272-A2.
 AAY82008 standard; protein; 220 AA.
Human immunogenic prostate tumour protein sequence SEQ ID NO:327.
WO200004149-A2.
 Score 475.5; DB 8; Length 239;
Pred. No. 8.8e-29;
 Score 472.5; DB 4; Length 220; Pred. No. 1.4e-28;
 34.4%; Score 472.5; DB 4; Length 220; 43.8%; Pred. No. 1.4e-28;
 34.4%; Score 472.5; DB 4; Length 220;
 34.6%; Score 475.5; DB 8; Length 239; 40.1%; Pred. No. 8.8e-29;
 34.6%; Score 475.5; DB 8; Length 239; 40.1%; Pred. No. 8.8e-29;
 Score 472.5; DB 4; Length 220; Pred. No. 1.4e-28;
 Score 472.5; DB 3; Length 220; Pred. No. 1.4e-28;
 Query Match 34.4%; Score 472.5; DB 4; Length 220. Best Local Similarity 43.8%; Pred. No. 1.4e-28;
 Length 280;
 ABM82603 standard; protein; 239 AA,
Human diagnostic and therapeutic pprotein SEQ ID NO:2852
WO2004023973-A2.
 ABM82602 standard; protein; 239 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2851
 лымил123 standard; protein; 220 AA.
Human prostate-specific amino acid sequence P703PDE6.
W0200151633-A2.
 AAG99008 standard; protein; 220 AA.
Human prostate-specific amino acid sequence P703PDE5.
WO200134802-A2.
 (FIVE-) FIVE PRIME THERAPEUTICS INC.
34.4%; Score 473; DB 8;
t Local Similarity 37.7%; Pred. No. 1.6e-28;
 AAG62147 standard; protein; 220 AA.
Human P703P inventive antigen SEQ ID NO: 330.
W0200125273-A2.
 AAU69768 standard; protein; 220 AA.
Human prostate cDNA encoded protein #8.
WO200173032-A2.
 ADN99649 standard; protein; 280 AA.
Novel human protein sequence #465.
WO2004038003-A2.
 AAB74806 standard; protein; 220 AA
 34.6%;
 34.4%;
 34.4%;
 Match 34.4%;
Local Similarity 43.8%;
Ly Match
Best Local Similarity 4
RESULT 1307
ID ABM82602 stand>
DE Human diagr
PN W020040*
PP 25-**
 12-APR-2001.
(CORI-) CORIXA CORP.
 27-JAN-2000.
(CORI-) CORIXA CORP.
 19-JUL-2001.
(CORI-) CORIXA CORP.
 04-OCT-2001.
(CORI-) CORIXA CORP.
 12-APR-2001.
(CORI-) CORIXA CORP.
 25-MAR-2004.
(INCY-) INCYTE CORP.
 (INCY-) INCYTE CORP. Query Match
 (CORI-) CORIXA CORP.
 Local Similarity
 Best Local Similarity RESULT 1308
 Query Match
Best Local Similarity
 Local Similarity
 Local Similarity
 06-MAY-2004
 17-MAY-200
 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
```

```
34.4%; Score 472.5; DB 4; Length 220; 43.8%; Pred. No. 1.4e-28;
 34.4%; Score 472.5; DB 7; Length 220; 43.8%; Pred. No. 1.4e-28;
 Length 220;
 Score 472.5; DB 6; Length 220;
Pred. No. 1.4e-28;
 ABRS4340 standard; protein; 220 AA.
Prostate tumour specific protein sequence SEQ ID 327
 34.4%; Score 472.5; DB 5; 43.8%; Pred. No. 1.4e-28;
Prostate cancer specific antigen P703P #4.
928021929763-A1.
 ADB13777 standard; protein; 220 AA.
Human prostate specific protein P703PDES.
US2003185830-A1.
 ABB95228 standard; protein; 220 AA.
Human P703PDES protein SEQ ID NO 327.
US2002022248-A1.
```

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PD 02-DEC-1999.

PA (ENTR-) ENTREMED INC.

Query March 34.2%; Score 470.5; DB 3; Length 261;

Best Local Similarity 40.4%; Pred. No. 2.3e-28;
 Human PSA protein; 261 AA. WOZOO28166-A2.
 RESULT 1330
ID AAB21317 standard; protein; 261 AA.
 (MCNE/) MCNEILL P D.
(HOUG/) HOUGHTON R L.
(DBAS/) Y DE BASSOLS C V.
(FOYT/) FOY T M.
 MITCHAM J L.
HARLOCKER S L.
 LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
 HENDERSON R A.
 STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
 12-APR-2001.
(CORI-) CORIXA CORP.
 12-APR-2001.
(CORI-) CORIXA CORP.
 Query Match
Best Local Similarity
RESULT 1333
 12-APR-2001.
(CORI-) CORIXA CORP.
 Best Local Similarity RESULT 1331
 Query Match
Best Local Similarity
RESULT 1332
 Query Match
Best Local Similarity
RESULT 1334
 FANGER G R.
RETTER M W.
 XU J.
DILLON D C.
 Best Local Similarity
 KALOS M D.
 Human PSA.
WO200053776-A2.
14-SEP-2000.
 JIANG Y.
 Query Match
 Query Match
 (HURA/)
(MCNE/)
(HOUG/)
 (JIAN/)
(KALO/)
 RESULT 1335
TD ABP7420
DE Human PP
PN WO20028
PD 17-OCT-
PA (CTLI-)
 (HEPL/)
 (LISX/)
 FANG/)
 CART/)
 SKEI/
 14-NOV-2002.

1 (CURA-) CURAGEN CORP.

Query Match

Best Local Similarity 40.7%; Pred. No. 1.7e-28;
 Query Match 34.2%; Score 470.5; DB 4; Length 257; Best Local Similarity 40.4%; Pred. No. 2.3e-28; RESULT 1327
 PD 04-NOV-2003.
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.
Query Match 34.4%; Score 472.5; DB 8; Length 262;
Best Local Similarity 38.9%; Pred. No. 1.6e-28;
 O2-DEC-1999.

(UVPE-) UNIV PENNSYLVANIA.

Query Match

Best Local Similarity 40.4%; Pred. No. 2.3e-28;
 34.4%; Score 472.5; DB 7; Length 220; 43.8%; Pred. No. 1.4e-28;
 Length 261;
 Length 262;
 34.2%; Score 470.5; DB 3; Length 255; 40.4%; Pred. No. 2.3e-28;
 34.3%; Score 471; DB 1; Length 245; 40.2%; Pred. No. 2e-28;
 DE Human glandular kallikrein (hHk2) protein.
DE Human glandular kallikrein (hHk2) protein.
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UYAR-) UNIV ARKANSAS.
Query Match
Best Local Similarity 38.9%; Pred. No. 1.6e-28;
 WORC-) WORCESTER FOUND BIOMEDICAL RES.

(WORC-) WORCESTER FOUND BIOMEDICAL RES.

34.2%; Score 470.5; DB 2;

ery Match

34.2%; Pred. No. 2.3e-28;
 AXY77842 standard; protein; 261 AA.
Human prostate-specific antigen (PSA) sequence.
WO9960984-A2.
 AAU06276 standard; protein; 257 AA.
Prostate specific Antigen (PSA) polypeptide.
WO200145728-A2.
 ADI39732 standard; protein; 262 AA.
Human glandular kallikrein (Hk2) protein.
US6642013-Bl.
 AAP92314 standard; protein; 245 AA. Human recombiant kallikrein gene. BP297913-A. 04-JAN-1989. (AMGE-) AMGEN.
 MBR96163 standard; protein; 274 AA.
Human NOV12a protein SEQ ID NO:68.
WO200290568-A2.
 Human prostate-specific antigen.
W09961068-A1.
 AAWI3649 standard; protein; 261 AA.
Human prostatic specific antigen.
WO9711172-A1.
 AAB21313 standard; protein; 255 AA.
 Human PSA.
WO200053776-A2.
14-SEP-2000.
(MOUN) MOUNT SINAI HOSPITAL.
Job-Al.

AI - CORIXA CORP.

AT Match
Best Local Similarity 4:
RESULT 1321
ID ADI39732 standa
DE Human gland.
PN US66420'
PD 04-'
 28-JUN-2001.
(EPIM-) EPIMMUNE INC.
 Best Local Similarity
 Query Match
Best Local Similarity
RESULT 1325
 Best Local Similarity RESULT 1326
 RESULT 1328
ID AAYS6048 standard;
 Query Match
 Query Match
```

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OCTLI-2002.
(CTLI-) CTL IMMUNOTHERAPIES CORP.
ery Match 34.2%; Score 470.5; DB 6; Length 261;
ery Match 40.4%; Pred. No. 2.38-28;
 DB 3; Length 261;
 34.2%; Score 470.5; DB 4; Length 261; 40.4%; Pred. No. 2.3e-28;
 Length 261;
 34.2%; Score 470.5; DB 4; Length 261; 40.4%; Pred. No. 2.3e-28;
 Length 261;
 AAG62144 standard; protein; 261 AA.
Human prostate specific membrane antigen SEQ ID NO: 327.
WO200125273-A2.
 AAB74821 standard; protein; 261 AA.
Prostate tumour antigen amino acid sequence for PSA.
WO200125272-A2.
 DB 4;
 אסטינום (PSMA).
Human prostatic specific membrane antigen (PSMA).
10220021923-A1.
(MOUN) MOUNT SINAI HOSPITAL.

ry Match
24.2%; Score 470.5; DB 3
t Local Similarity 40.4%; Pred. No. 2.3e-28;
 Human prostate specific antigen SEQ ID NO: 329.
W0200125273-A2.
 34.2%; Score 470.5; DB 4 40.4%; Pred. No. 2.3e-28;
 34.2%; Score 470.5; DB 4
40.4%; Pred. No. 2.3e-28;
 Best Local Similarity
```

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AAB67545 standard; protein; 284 AA.
Maino acid sequence of protease MH2 catalytic domain in PFEK2-6XHIS-TAG.
MC200116289-A2.
08-WAR-2001.
(ORTH) ORTHO-MCNEIL PHARM INC.
134.1%; Score 469; DB 4; Length 284;
PR MACCH SELO.
 Query Match 34.0%; Score 467; DB 1;
Best Local Similarity 40.9%; Pred. No. 4.1e-28;
RESULT 1353
 Score 467; DB 2;
Pred. No. 4.1e-28;
 PD 03-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 34.0%; Score 467.5; DB 5
Best Local Similarity 43.4%; Pred. No. 4.8e-28;
RESULT 1352
 PD 12-JUN-2003.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

Query Match 34.1%; Score 468.5; DB 7.

Best Local Similarity 40.4%; Pred. No. 3.3e-28;

RESULT 1347
 34.0%; Score 467.5; DB 4
43.4%; Pred. No. 4.8e-28;
 AAP81243 standard; protein; 247 AA.
Human spleen trypsin III (trysinogen III)
JP63160582-A.
 18-JAN-2001.
(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
(CORI-) CORIXA CORP.
 AAY72521 standard; protein; 312 AA. NS1-P703P mutated-His fusion protein. WO200104143-A2.
 ADJ59024 standard; protein; 261 AA.
Human PSA precursor protein sequence.
WO2003047506-A2.
 AAR82703 standard; protein; 247 AA.
Human pancreatic trypsin III.
 34.0%;
 25-JUL-1995.
(SANY) SANKYO CO LTD.
 (SANY) SANKYO CO LID
 Best Local Similarity RESULT 1351
 Best Local Similarity
 Best Local Similarity
 Best Local Similarity RESULT 1346
 Best Local Similarity RESULT 1348
 Best Local Similarity
 04-JUL-1988
 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
 RESULT 1349
 RESULT 1336,

ID ADB827777 standard; protein; 261 AA.

DE Human protein sequence useful for the treatment of cancer (SeqID 1558).

PN WO2003050236-A2.

PD 19-JUM-2003.

PD 19-JUM-2003.

PA (CHIR) CHIRON CORP.

PA (HYSE-) HYSEQ INC. 14 7%: Score 470.5; DB 7; Length 261;
 Query Match 34.2%; Score 470.5; DB 7; Length 261; Best Local Similarity 40.4%; Pred. No. 2.3e-28; RESULT 1339
 Query Match 34.2%; Score 470.5; DB 8; Length 261; Best Local Similarity 40.4%; Pred. No. 2.3e-28; RESULT 1341
 Score 470.5; DB 4; Length 692;
Pred. No. 6.3e-28;
 Score 470.5; DB 8; Length 261;
Pred. No. 2.3e-28;
 Length 261;
 34.2%; Score 470.5; DB 8; Length 261; 40.4%; Pred. No. 2.3e-28;
 Score 470.5; DB 8; Length 261;
Pred. No. 2.3e-28;
 / Match 34.2%; Score 470.5; DB 3; Length 375; Local Similarity 40.4%; Pred. No. 3.4e-28;
 Score 470.5; DB 7; Length 261;
Pred. No. 2.3e-28;
 AAB08449 standard; protein; 375 AA.
A human prostate specific antigen variant polypeptide.
WO200049158-A2.
 Score 470.5; DB 7;
Pred. No. 2.3e-28;
 AAG62154 standard; protein; 692 AA.
Human WT1/PSA fusion protein SEQ ID NO: 357.
WO200125273-A2.
 ADJS902 standard; protein; 261 AA.
Human PSA precursor protein sequence.
Maco103047566-A2.
12-UNN-2003.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
 ADI37157 standard; protein; 261 AA.
Human prostate specific antigen (hPSA).
US2003199010-A1.
 ADM72819 standard; protein; 261 AA.
Human PSA protein SEQ ID NO:78.
WO2004022709-A2.
(MARR-2004)
 ADC09580 standard; protein; 261 AA. PSA protein #SEQ ID 78. WO2003008537-A2.
 (UYAR-) UNIV ARKANSAS MEDICAL SCI.
 30-JAN-2003.
(CTLI-) CTL IMMUNOTHERAPIES CORP.
ery Match
ery Match 34.2%; Score
 34.2%;
 34.2%;
 34.2%;
 Match 34.2%;
Local Similarity 40.4%;
 15-APR-2004.
(GETH) GENENTECH INC.
 23-OCT-2003.
(UYAR-) UNIV ARKANSAS.
 24-AUG-2000.
(COMP-) COMPUGEN LTD.
 12-APR-2001.
(CORI-) CORIXA CORP.
 Query Match
Best Local Similarity
RESULT 1337
 Query Match
Best Local Similarity
RESULT 1338
 Best Local Similarity RESULT 1340
 Local Similarity
 Query Match
Best Local Similarity
 04-NOV-2003
 Query Match
 Ouery Match
 Query Match
 Query Match
```

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(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

ry Match 34.0%; Score 467.5; DB 5; Length 231; t Local Similarity 43.4%; Pred. No. 3.5e-28;
DB 7; Length 261;
 DB 4; Length 312;
 34.0%; Score 467.5; DB 5; Length 231; 43.4%; Pred. No. 3.5e-28;
 Length 312
 DB 5; Length 312
 AAU74928 standard, protein, 312 AA.
Amino acid sequence of NS1-P703P mutated-His fusion protein.
WO200200867-A1.
 Length 247;
 Length 247;
 RESULT 1350

ID AAU74767 standard; protein; 312 AA.

DE Amino acid sequence of NS1-p703 mutated-His fusion protein.

PN WO200200708-A2.

PD 03-JAN-2002.
 AAU74934 standard; protein; 231 AA.
Amino acid sequence of P703P mutated-His fusion protein.
WO200200867-A1.
03-JAN-2002.
 AAUT4903 standard; protein; 231 AA.
Amino acid sequence of p703 mutated-His fusion protein.
W0200200708-A2.
03-JAN-2002.
(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
ry Match
t Local Similarity 43.4%; Pred. No. 4.8e-28;
```

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(HERM/) HERMANN K.
(PILA/) PILARSKY C.
 Human KLK2.
WO200053776-A2.
14-SEP-2000.
 FR2848569-A1.
 23-MAY-2002
 Query Match
 ADASOS49 standard; protein; 237 AA.
Rhesus macaque prostate specific antigen (PSA/KLK3), SBQ ID NO:4.
WO2003031559-A2.
17-APR-2003.
(CENZ) CENTOCOR INC.
 12-JUN-2003.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
Ery Match 33.8%; Score 464.5; DB 7; Length 261;
Et Local Similarity 40.4%; Pred. No. 6.8e-28;
 ADMI2395 standard; protein; 261 AA.

E Human prostate-specific antigen protein.

N US2003235594-A1.

D 25-DEC-2003.

A (ANTI-) ANTIGEN EXPRESS INC.

Query Match

Dest Local Similarity 40.0%; Pred. No. 8.1e-28;
 33.7%; Score 462.5; DB 8; Length 248; 40.2%; Pred. No. 9.2e-28;
 Length 261;
 33.8%; Score 464.5; DB 5; Length 226; 42.7%; Pred. No. 5.8e-28;
 33.7%; Score 462.5; DB 8; Length 248; 40.2%; Pred. No. 9.2e-28;
 Ouery Match 33.8%; Score 464; DB 6; Length 237; Best Local Similarity 42.6%; Pred. No. 6.7e-28;
 ADJS9028 standard; protein; 261 AA.
Human PSA analogue (L155/Y154) precursor protein sequence.
WO2003047506-A2.
 ADR66277 standard; protein; 248 AA.
Human prostatic carcinoma derived protein SEQ ID 131 #2.
WO2004076614-A2.
RESULT 1354

ID ADJ59026 standard; protein; 261 AA.

DB Human PSA analogue (Y154) precursor protein sequence.

PN W0203047506-A2.

PD 12-JUN-2003.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

Query Match 34.0%; Score 466.5; DB 7; Ler
 ADR66934 standard; protein; 251 AA.
Human prostatic carcinoma derived DNA SEQ ID 232 #4.
WO2004076614-A2.
 ADR66838 standard; protein; 248 AA.
Human prostatic carcinoma derived DNA SEQ ID 131 #4.
WO2004076614-A2.
 ABB8422 standard; peptide; 226 AA.
Rat SCCE protein N-terminal fragment SEQ ID 48.
W0200263135-A2.
I5-AUG-2002.
(RGEL), EGELRUD T.
(HANS/), HANSSON L.
 (HINZ/) HINZMANN B.
(DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
(HERM/) HERVANN K.
(PILA/) PILARSKY C.
 10-SEP-2004.
(HINZ/) HINZKANN B.
(DAHL/) DAHL B.
(ROSE/) ROSENTHAL A.
(HERM/) HERMANN K.
(PILA/) PILARSKY C.
 A data,

J047506-A2,

USSH) US DEPT HE.

LABET LOCAL SIMILATITY

RESULT 1355

ID ABB4422 standar

DE RAT SCCE proform W02002621

PD 15-AU
 Query Match
Best Local Similarity
RESULT 1356
ID ADJS9028 standard, p)
DE Human PSA analogue (7
PN W02003047506-A2.
PD 12-JUN-2003.
PA (USSH) US DEPT HEALY
 (HINZ/) HINZMANN B.
(DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
 Query Match
Best Local Similarity
 Local Similarity
 10-SEP-2004.
 Query Match
 Query Match
```

```
vuery Match 33.5%; Score 460.5; DB 2; Length 261;
Best Local Similarity 40.2%; Pred. No. 1.4e-27;
RESULT 1366
 33.4%; Score 459.5; DB 5; Length 245; 41.4%; Pred. No. 1.5e-27;
33.7%; Score 462.5; DB 8; Length 251; 40.2%; Pred. No. 9.3e-28;
 33.7%; Score 462.5; DB 8; Length 251; 40.2%; Pred. No. 9.3e-28;
 2; Length 261;
 ADP27545 standard, protein; 297 AA.
Human kallikrein-3 (KLK-3) BHT103 protien a variant SeqID 19.
FR2848569-A1.
 ADP27546 standard; protein; 281 AA.
Human kallikrein-3 (KLK-3) EHT103 protien b variant SeqID 20
 Length 297;
 Length 238;
 Length 281;
 DE Human prostatic carcinoma derived protein SEQ ID 232 #1.
PN WAZO040776614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (BAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (HINZ/) PILARSKY C.
OUETY MATCH
 BEPS....
07-UL-1999.
(HOFF) ROCHE DIAGNOSTICS GMBH.
33-4%; Score 459; DB 2;
ery Match
city Match
1.6e-27;
 (EXON-) EXONHIT THERAPEUTICS SA.

ry Match
13.6%; Score 462; DB 8;

t Local Similarity 41.0%; Pred. No. 1.1e-27;
 PD 18-JUN-2004.
PA (EXON-) EXONHIT THERAPEUTICS SA.
Query Match
Best Local Similarity 41.0%; Pred. No. 1.2e-27;
RESULT 1365
 Query Match 33.5%; Score 460.5; DB 2
Best Local Similarity 40.2%; Pred. No. 1.4e-27;
RESULT 13cal
 AAU98921 standard; protein; 245 AA.
Human prostate specific antigen (PSA) variant.
WO200240059-A2.
 AAWI0600 standard; protein; 261 AA.
Human prepro-Trp226-glandular kallikrein-2.
W09701630-Al.
 (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.
(LOUK/) LOUKINOV D I.
(ZOUB/) ZOUBAK S.
 AAY08894 standard; protein; 238 AA. Chimeric serine protease FXT protein. EP927764-A2.
 AAR84668 standard; protein; 261 AA.
Prepro-hK2 kallikrein.
WOO530758-Al.
16-NOV-1995.
 AAB21314 standard; protein; 255 AA
 16-JAN-1997.
(ORIN) ORION YHTYMAE OY.
 (MAYO-) MAYO FOUNDATION. (HYBR-) HYBRITECH INC.
 Ouery Match
Best Local Similarity
RESULT 1364
 Best Local Similarity RESULT 1368
 Best Local Similarity RESULT 1369
 Ouery Match
Best Local Similarity
RESULT 1362
 Best Local Similarity RESULT 1363
```

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Ouery Match 33.4%; Score 458.5; DB 3; Length 261; Best Local Similarity 40.8%; Pred. No. 2e-27; RESULT 1376
(MOUN) MOUNT SINAI HOSPITAL.
33.4%; Score 458.5; DB 3; Length 255; st Local Similarity 40.8%; Pred. No. 1.9e-27;
 Score 458.5; DB 2; Length 261;
Pred. No. 2e-27;
 Match 33.4%; Score 458.5; DB 2; Length 261; Local Similarity 40.8%; Pred. No. 2e-27;
 Score 458.5; DB 2; Length 261;
Pred. No. 2e-27;
 Query Match 33.4%; Score 458.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
 33.4%; Score 458.5; DB 2; Length 261; 40.8%; Pred. No. 2e-27;
 Ouery Match 33.4%; Score 458.5; DB 4; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
 33.4%; Score 458.5; DB 7; Length 261;
 AAW45397 standard; protein; 261 AA.
Prostate-specific glandular kallikrein precursor prepro-hK2.
WO9802748-A1.
 AAW83203 standard; protein; 261 AA.
Prostate-specific glandular kallikrein protein pphK2
 AAW06971 standard; protein; 261 AA.
Prostate-specific glandular kallikrein prepro-hK2
 AAW96189 standard; protein; 261 AA.
Prepro human Kallikrein 2 (preprohK2).
WO9859073-Al.
 Wild-type human Kallikrein; 261 AA. WOSE1365-A2.
 AAU06279 standard, protein, 261 AA.
Human Kallikrein2 polypeptide.
WO200145728-A2.
 ADB75390 standard; protein; 261 AA. Prostate cancer marker protein. WO2003009814-A2. GEFB-2003. (MILL-) MILLENNIUM PHARM INC.
 AAB21318 standard, protein, 261 AA
 22-OCT-1998.
(BAYU) BAYLOR COLLEGE MEDICINE.
(MAYO-) MAYO FOUNDATION.
 14-SEP-2000.
(MOUN) MOUNT SINAI HOSPITAL.
 Query Match 33.4%;
Best Local Similarity 40.8%;
 Query Match
Best Local Similarity 40.8%;
 30-DEC-1998.
(MAYO-) MAYO FOUNDATION.
(YOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
 22-JAN-1998.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
 (MAYO-) MAYO FOUNDATION. (HYBR-) HYBRITECH INC.
 07-NOV-1996
(HYBR-) HYBRITECH INC.
(MAYO-) MAYO FOUNDATION.
 28-JUN-2001.
(EPIM-) EPIMMUNE INC.
 Best Local Similarity RESULT 1370
 Query Match
Best Local Similarity
RESULT 1375
 Human KLK2.
WO200053776-A2.
 WO9846795-A1
 22-MAY-1998.
 Query Match
 Query Match
 Query Match
```

```
AAB19819 standard; protein; 237 AA.
Prostate specific antigen specific to benign prostatic hyperplasia.
09-NOV 2000.
 "ABB19818 standard; protein; 237 AA.
Prostate specific antigen elevated in benign prostatic hyperplasia.
WO200066718-A1.
 vuery Match 33.3%; Score 457.5; DB 2; Length 237;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1380
 Length 237;
 Score 457.5; DB 6; Length 237; Pred. No. 2.1e-27;
 Length 237;
 Best Local Similarity 41.6%; Pred. No. 2.1e-27; RESULT 1384
 Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1383
 Length 237;
 Length 237
 ADASOS46 standard; protein; 237 AA.
Human prostate specific antigen (PSA/KLK3), SEQ ID NO:1
WO2003031369-A2.
 AAB11041 standard, peptide, 237 AA.
Human prostate-specific antigen N-terminal fragment #2
EP1043394-A2.
 Query Match
33.3%; Score 457.5; DB 2;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
RESULT 1379
ID AAW56086 standard; protein; 237 AA.
DE Human prostate specific antigen protein.
PN W09810292-A1.
 33.3%; Score 457.5; DB 6; 41.6%; Pred. No. 2.1e-27;
 33.3%; Score 457.5; DB 3; 41.6%; Pred. No. 2.1e-27;
 33.3%; Score 457.5; DB 2; 41.6%; Pred. No. 2.1e-27;
Best Local Similarity 40.8%; Pred. No. 2e-27; RESULT 1378
 ADA09840 standard; protein; 237 AA.
Human mature prostate specific antigen (PSA).
US2003059864-A1.
 AAM96187 standard; protein; 237 AA.
Human prostate specific antigen (PSA).
WO9859073-A1.
30-DEC-1998.
(MAXO-) MAYO FOUNDATION.
(YOUN/) YONG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
 (SERA-) SERATEC GES BIOTECHNOLOGIE MBH.
 AAW83213 standard; protein; 237 AA.
Prostate-specific antigen protein hK3
WO9846795-A1.
 22-OCT-1998.
(BAYU) BAYLOR COLLEGE MEDICINE.
(MAYO-) MAYO FOUNDATION.
 (HYBR.) HYBRITECH INC.
(BAYU) BAYLOR COLLEGE MEDICINE.
ry Match
 (HYBR-) HYBRITECH INC. (BAYU) BAYLOR COLLEGE MEDICINE.
 Query Match 33.3%;
Best Local Similarity 41.6%;
RESULT 1386
 (MIKO/) MIKOLAJCZYK S D. (RITT/) RITTENHOUSE H G.
 12-MAR-1998.
(CENZ) CENTOCOR INC.
 (CENZ) CENTOCOR INC.
 Ouery Match
Best Local Similarity
RESULT 1382
 Best Local Similarity
RESULT 1381
 Local Similarity
 17-APR-2003
 Query Match
 Query Match
```

```
J3.1%; Score 454.5; DB 2; Length 244;

Loui 1398

D AD038617 standard; protein; 261 AA.

DE Prostate Specific Antigen (PSA).

PN US2004058881-A1.

PD 25-MAR-2004.

PA (ANTL-) ANTIGEN EXPRESS INC.

Query Match

Best Local Similarity 39.6%; Pred. No. 4e-27;

RESULT 1399

ID ADJ59027 standard; protein; 237 AA.

DE Human PSA analogue (Y154) mature

PN WC2003047506-A2.

PN WC2003047506-A2.
 PD 03-JAN-2002.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

QUETY MATCh 33.1%; Score 454.5; DB 5; Length 232;

Best Local Similarity 43.8%; Pred. No. 3.5e-27;

RESULT 1396
 Length 232;
 Query Match 32.9%; Score 452.5; DB 2; Length 244; Best Local Similarity 41.8%; Pred. No. 5.3e-27; RESULT 1402
 32.9%; Score 452.5; DB 2; Length 244;
 Length 232;
 Length 237;
 Length 244;
 AAW45396 standard; protein; 244 AA.
Prostate-specific glandular kallikrein precursor pro-hK2
WO9802748-A1.
 AAW83204 standard; protein; 244 AA.
Prostate-specific glandular kallikrein protein phK2.
W09846795-A1.
 33.1%; Score 454.5; DB 4; 43.8%; Pred. No. 3.5e-27;
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 33.1%; Score 454.5; DB 5;
Best Local Similarity 43.8%; Pred. No. 3.5e-27;
RESULT 1397
 33.0%; Score 453.5; DB 7; 41.6%; Pred. No. 4.3e-27;
 Ouery Match 32.9%; Score 452.5; DB 2;
Best Local Similarity 41.8%; Pred. No. 5.3e-27;
RESULT 1401
 AAU74930 standard; protein; 232 AA.
Amino acid sequence of prostase protein fragment
WO200200867-A1.
 AAU74769 standard, protein; 232 AA.
Protein sequence of prostase homologue #1.
WO200200708-A2.
 A (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
A (CORL-) CORIXA CORP.
33.1%; Score 454.
Best Local Similarity 43.8%; Pred. No.
 AAR84669 standard; protein; 244 AA.
Pro-hK2 kallikrein.
W09530758-Al.
 AAW96188 standard; protein; 244 AA.
Pro human Kallikrein 2 (prohK2).
WO9859073-Al.
 (BAYU) BAYLOR COLLEGE MEDICINE. (MAYO-) MAYO FOUNDATION. SCO.
 (MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
 (MAYO-) MAYO FOUNDATION.
(YOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
 Best Local Similarity RESULT 1400
 03-JAN-2002
 Query Match
 Query Match
33.3%; Score 457.5; DB 8; Length 237; 41.6%; Pred. No. 2.1e-27;
 PD 12-JUN-2003.
PA (USAH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 33.2%; Score 455.5; DB 7; Length 237;
Best Local Similarity 41.6%; Pred. No. 3e-27;
 Query Match 33.2%; Score 455.5; DB 2; Length 237; Best Local Similarity 41.6%; Pred. No. 3e-27;
 query Match
33.2%; Score 455.5; DB 2; Length 261;
BBSt Local Similarity 40.8%; Pred. No. 3.3e-27;
RESULT 1392
 Query Match 33.2%; Score 455.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 3.3e-27;
 (MILL-) MILLENNIUM PHARM INC.
ry Match 33.1%; Score 454.5; DB 2; Length 232;
t Local Similarity 43.8%; Pred. No. 3.5e-27;
 07-MAY-1987.
(BIOT-) BIOTECHN RES PARTN.
(CALB-) CALIF BIOTECHNOL INC.
Query Match
Best Local Similarity 39.7%; Pred. No. 2.9e-27;
 AAW45400 standard; protein; 261 AA.
Prostate-specific glandular kallikrein hK2v217.
WO9802748-A1.
 AAWS5129 standard; protein; 232 AA.
Homo sapiens Tub Interactor (hTI-1) protein.
WO9812302-A1.
 AAW45398 standard; protein; 237 AA.
Prostate-specific antigen protein hK3 (PSA).
WO9802748-A1.
 AAP70677 standard; protein; 245 AA.
Human kallikrein gene product.
WO8702709-A.
 ADJ59025 standard; protein; 237 AA.
Human PSA mature protein sequence.
WO2003047506-A2.
 AAW06972 standard; protein; 261 AA.
Kallikrein prepro-hK2v217 variant.
WO9634964-A2.
 AAY72523 standard; protein; 232 AA.
Human prostase antigen #1.
WO200104143-A2.
18-JAN-2001.
 22-JAN-1998.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
 (MAYO-) MAYO FOUNDATION. (HYBR-) HYBRITECH INC.
 07-NOV-1996.
(HYBR-) HYBRITECH INC.
(MAYO-) MAYO FOUNDATION.
 Query Match
Best Local Similarity
RESULT 1388
 22-JAN-1998
 26-MAR-1998
```

Length 237;

Length 217;

```
ADJ83076 standard; protein; 217 AA.
Trypsin protein which is related to human NOVX protein - SEQ ID 67.
 Score 448.5; DB 2; Length 237; Pred. No. 1e-26;
 32.6%; Score 447.5; DB 7; Length 217; 44.4%; Pred. No. 1.1e-26;
 32.6%; Score 447.5; DB 2; Length 237; 42.0%; Pred. No. 1.3e-26;
 Query Match
32.6%; Score 447.5; DB 5; Length 217,
Best Local Similarity 44.4%; Pred. No. 1.1e-26;
 ADI17269 standard; protein; 217 AA.
Polypeptide homologous to a human NOVX domain SeqID 805.
WO200268649-A2.
 Polypeptide homologous to a human NOVX domain SeqID 813
WO200268649-A2.
 32.8%; Score 450.5; DB 6; 42.0%; Pred. No. 7.4e-27;
 Query Match 32.6%; Score 447.5; DB 5; Best Local Similarity 44.4%; Pred. No. 1.1e-26; RESULT 1414
 AAR84667 standard; protein; 237 AA. Mature kallikrein hK2. W09530758-A1. 16-NOV-1995. (MAYO-) MAYO FOUNDATION. (HYBR-) HYBRITECH INC.
 ADI17277 standard; protein; 217 AA
 AAW83212 standard; protein; 237 AA hK2 variant A217V. W09846795-A1.
 (BAYU) BAYLOR COLLEGE MEDICINE. (MAYO-) MAYO FOUNDATION.
 32.6%;
42.0%;
 GANGOLLI E A.
FERNANDES E R.
RIEGER D K.
 ALSOBROOK J P.
 LIU X.
SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
LEPLEY D M.
BURGESS C E.
 GROSSE W M.
SZEKERES E S.
VERNET C A M.
 CURAGEN CORP.
 (CURA-) CURAGEN CORP.
 TCHERNEV V T.
 CENTOCOR INC.
 SHIMKETS R A.
 (EDIN/) EDINGER S R. (GUNT/) GUNTHER B. (MILL/) MILLET I. (SCIO/) SCIORE P. (ELIEA/) ELLERWAN K. (MACD/) MACDOUGALL J (SMIT/) SMITHSON G.
 Best Local Similarity RESULT 1413
 CASMAN S J.
BOLDOG F L.
GORMAN L.
 Best Local Similarity RESULT 1412
 Local Similarity
 Query Match
Best Local Similarity
RESULT 1417
 WO2003031569-A2.
 06-SEP-2002
 Query Match
 LILL/)
CASM/)
BOLD/)
 RIEG/)
 Query Match 32.9%; Score 452.5; DB 2; Length 250; Best Local Similarity 40.5%; Pred. No. 5.4e-27; RESULT 1404 App27538 standard; protein; 281 AA. DE Human kallikrein-2 (KLK-2) EHT102 protein b variant SeqID 12. PD RESURGES69-A1. PD RENAPEUTICS SA. PA. (EXON-) EXONHIT THERAPEUTICS SA.
 vuery Match 32.9%; Score 451.5; DB 7; Length 236; Best Local Similarity 41.6%; Pred. No. 6.1e-27; RESULT 1407
 Match 32.8%; Score 450.5; DB 2; Length 237; Local Similarity 40.7%; Pred. No. 7.4e-27;
 (EXON-) EXONHIT THERAPEUTICS SA.

Query Match
32.9%; Score 452.5; DB 8; Length 297;
Best Local Similarity 41.8%; Pred. No. 6.5e-27;
 Query Match 32.8%; Score 450.5; DB 2; Length 237; Best Local Similarity 42.0%; Pred. No. 7.4e-27;
 32.8%; Score 450.5; DB 2; Length 237; 42.0%; Pred. No. 7.4e-27;
 18-JUN-2004.
(EXCN-) EXONHIT THERAPEUTICS SA.
ery Match 32.9%; Score 452.5; DB 8; Length 281;
 Match 32.8%; Score 450.5; DB 2; Length 237; Local Similarity 42.0%; Pred. No. 7.4e-27;
 ADP27537 standard; protein; 297 AA.
Human kallikrein-2 (KLK-2) EHT102 protein a variant SegID 11
 ADJ59029 standard; protein; 236 AA.
Human PSA analogue (L155/Y154) mature protein sequence.
WO2003047506-A2.
 RESULT 1408

ID AAW83202 standard; protein; 237 AA.

DE Prostate-specific glandular kallikrein protein hK2.

PN W09846795-A1.
 AAW45395 standard, protein, 237 AA.
Mature prostate-specific glandular kallikrein hK2.
WO9802748-A1.
Best Local Similarity 41.8%; Pred. No. 5.3e-27; RESULT 1403
 12-JUN-2003.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
 AAW03130 standard; protein; 250 AA.
Prostate-specific antigen.
W09621042-242.
Il-JUL-1996.
(UYBO-) UNIV BOSTON.
 AAW96186 standard; protein; 237 AA.
Mature human Kallikrein 2 (hK2).
WO9859073-Al.
 AAR77098 standard; protein; 237 AA.
 ADASOS61 standard, protein, 237 AA.
Kallikrein KLK2, SEQ ID NO:16.
 22-OCT-1998.
(BAYU) BAYLOR COLLEGE MEDICINE.
(MAYO-) MAYO FOUNDATION.
 26-OCT-1995. (UYCO) UNIV COLUMBIA NEW YORK.
 Prostate-specific antigen. WO9528498-A1.
 22-JAN-1998.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
 (MAYO-) MAYO FOUNDATION. (YOUN/) YOUNG C Y F. (TIND/) TINDALL D J. (KLEE/) KLEE G G.
 Local Similarity
 Best Local Similarity RESULT 1405
 FR2848569-A1.
 30-DEC-1998
 Query Match
 Query Match
 Ouery Match
```

Query Match

Query Match

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30-NOV-2000.
(SAAT/) SAATCIOGLU F.
 DE Protein encoded by pa
PN W09837093-A2.
PD 27-AUG-1998.
PA (CORI-) CORIXA CORP.
 27-AUG-1998.
(CORI-) CORIXA CORP.
 Best Local Similarity RESULT 1433
 (CORI-) CORIXA CORP.
 Best Local Similarity RESULT 1430
 (CORI-) CORIXA CORP.
 Query Match
. Best Local Similarity
RESULT 1426
 (CORI-) CORIXA CORP.
 11-JUL-2002.
(XUJJ/) XU J.
(DILL/) DILLON D C.
 Best Local Similarity
RESULT 1429
 Best Local Similarity RESULT 1431
 Query Match
Best Local Similarity
 Best Local Similarity
 27-JAN-2000
 04-OCT-2001
 Query Match
 Query Match
 Query Match
 Query Match
 Query Match
 AAMS2944 standard; protein; 260 AA.
Agkistrodon halys brevicaudus thrombin-likle protease, salmobin.
 Score 447.5; DB 2; Length 237; Pred. No. 1.3e-26;
 Score 441.5; DB 2; Length 238; Pred. No. 3.6e-26;
 Score 447.5; DB 2; Length 237;
Pred. No. 1.3e-26;
 Score 444.5; DB 2; Length 237;
Pred. No. 2.1e-26;
 Score 436.5; DB 4; Length 233; Pred. No. 8.7e-26;
 Score 445; DB 2; Length 240;
Pred. No. 2e-26;
 Length 279;
 Match 32.2%; Score 443; DB 8; Length 227; Local Similarity 39.6%; Pred. No. 2.7e-26;
 ABMB2643 standard; protein; 227 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2892.
WO2004023973-A2.
 AAR94526 standard; protein; 279 AA.
Korean Viper Salmosa thrombin-like protease, Halybin.
EP707067-A2.
 , DB 2;
6.7e-26;
 (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
ry Match
12.0%; Score 439;
t Local Similarity 37.7%; Pred. No. 6
 AAG79000 standard; protein; 233 AA.
Mamushi fibrinolytic enzyme, brevinase.
KR2001045716-A.
(DE-UN-2001.
(LEEJ) LEE J W.
(PARK/) PARK W.
AAW49087 standard; protein; 237 AA.
Mutant human Kallikrein 2 (hK2) A217V.
WO9821365-A2.
 Human prostate specific antigen. W09640754-Al.
 AAW96190 standard; protein; 237 AA.
Variant human Kallikrein 2 (hK2).
 AAR84671 standard; protein; 237 AA.
Mature kallikrein hK3.
WO9530758-A1.
 AAR84670 standard; protein; 238 AA
 32.6%;
 Best Local Similarity 40.9%;
RESULT 1423
 31.8%;
37.9%;
 Match 32.6%;
Local Similarity 42.0%;
 Query Match 32.4%;
Best Local Similarity 41.0%;
RESULT 1420
 Match 32.4%;
Local Similarity 41.1%;
 30-DEC-1998.
(MAXO-) MAXO FOUNDATION.
(YOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
 19-DEC-1996.
(TEXA) UNIV TEXAS SYSTEM
 (MAYO-) MAYO FOUNDATION. (HYBR-) HYBRITECH INC.
 22-MAY-1998.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
 16-NOV-1995. (MAYO-) MAYO FOUNDATION. (HYBR-) HYBRITECH INC.
 Mature kallikrein hK2
 25-MAR-2004.
(INCY-) INCYTE CORP.
 Local Similarity
 Local Similarity
 WO9530758-A1.
```

Query Match

17-APR-199

Query Match

```
AAB74803 standard; protein; 205 AA.
Prostate tumour antigen predicted amino acid sequence for P703P-DE13.
 AAW71872 standard; protein; 205 AA.
Protein encoded by prostate tumour clone P703 splice variant DE13.
WO9837093-A2.
 AAY82005 standard; protein; 205 AA.
Human immunogenic prostate tumour protein sequence SEQ ID NO:176.
WQ200004149-A2.
 ADE78966 standard; protein; 227 AA.
Human protein modification and maintenance molecule (PMMM)-4.
WO2003063688-A2.
 Length 205;
 Length 205;
 31.0%; Score 426.5; DB 2; Length 205; 43.7%; Pred. No. 4.5e-25;
 31.0%; Score 426.5; DB 3; Length 205; 43.7%; Pred. No. 4.5e-25;
 DB 4; Length 205;
 Score 426.5; DB 4; Length 205;
Pred. No. 4.5e-25;
 31.0%; Score 426.5; DB 2; Length 205; 43.7%; Pred. No. 4.5e-25;
 Length 260;
 Length 227;
 ABG94414 standard; protein; 205 AA.
Human prostate tumour protein partial variant sequence #2.
US2002090372-A1.
 ANNULLZU standard; protein; 205 AA..
Human prostate-specific amino acid sequence P703P-DE13.
WO200151633-A2.
 AABS0447 standard; protein; 205 AA.
Human prostate cancer-related intracellular protein #1
WO200071711-A2.
 Query Match 31.4%; Score 431.5; DB 4;
Best Local Similarity 44.2%; Pred. No. 1.8e-25;
RESULT 1427
 31.0%; Score 426.5; DB 3; 43.7%; Pred. No. 4.5e-25;
 AAW69388 standard; protein; 205 AA.
Prostate tumour specific gene clone DE13 protein.
WO9837418-A2.
 PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 39.2%; Pred. No. 2.7e-25;
RESULT 1428
(MOKA-) MOKAM BIOTECHNOLOGY RES INST.
ry Match 31.7%; Score 436; DB 2;
t Local Similarity 36.1%; Pred. No. 1.1e-25;
 31.0%; Score 426.5; DB 4 43.7%; Pred. No. 4.5e-25;
 AAU69766 standard; protein; 205 AA.
Human prostate cDNA encoded protein #6.
WO200173032-A2.
 31.0%;
```

```
Best Local Similarity 43.7%; Pred. No. 4.5e-25; RESULT 1439
 ABG76668 standard; protein; 205 AA. Prostate tumour protein #6.
 Query
 Score 426.5; DB 4; Length 205; Pred. No. 4.5e-25;
 Score 426.5; DB 4; Length 205; Pred. No. 4.5e-25;
 Score 426.5; DB 4; Length 205; Pred. No. 4.5e-25;
 31.0%; Score 426.5; DB 5; Length 205;
 Score 426.5; DB 4; Length 205; Pred. No. 4.5e-25;
 Human prostate-specific amino acid sequence P703P-DE13.
 ABU71656 standard; protein; 205 AA.
Prostate cancer specific antigen P703P #2.
US2002192763-A1.
 ABB95225 standard; protein; 205 AA.
Human P703P-DE13 protein SEQ ID NO 176.
US200202248-A1.
 Human prostate tumour protein, 205 AA. USG262245-B1.
 31.0%;
 31.0%;
 31.0%;
 Match 31.0%;
Local Similarity 43.7%;
 MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
 LISX.
WANGA.
SKEIKY YAW.
HEPLER W T.
HENDERSON R A.
 DILLON D C.
MITCHAM J L.
HARLOCKER S L.
 MITCHAM J L.
HARLOCKER S L.
 2001.
..f.) CORIXA COR.
.ry Match
.ry Match
.est Local Similarity ..
RESULT 1435
ID AA099005 stand?
ID AA099005 stand?
PN WOLOO!?
PN WOLOO!?
 HENDERSON R A.
 KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
 SKEIKY Y A W. HEPLER W T.
 17-JUL-2001.
(CORI-) CORIXA CORP.
 12-APR-2001.
(CORI-) CORIXA CORP.
 STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
 KALOS M D.
FANGER G R.
RETTER M W.
 (XUJJ/) XU J.
(DILL/) DILLON D C.
 Best Local Similarity RESULT 1438
 Local Similarity
 JIANG Y.
 LI S X.
WANG A.
 FOY T M.
 19-DEC-2002
 Query Match
 Query Match
 Query Match
 Query Match
 (LISX/)
(WANG/)
(SKEI/)
(HEPL/)
 (JIAN/)
(KALO/)
(FANG/)
 (JIAN/)
(KALO/)
(FANG/)
 DBAS/)
 (HARL/)
 HARL/)
 HOUG/)
 HURA/
 (SKEI/
```

```
ABBÖ9589 standard; protein; 234 AA.
Delnagkistrodon acutus venom thrombin-like protein (234 residue variant).
CN1181421-A.
13-MAY-1998.
(SANA-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
ASTANDALCH 30.7%; Score 422.5; DB 5; Length 234;
ELOCAL Similarity 36.4%; Pred. No. 1e-24;
 ABU02024 standard; protein; 218 AA.
Human protein modification and maintenance molecule-4 (PMMM-4)
WO2003031939-A2.
 31.0%; Score 426.5; DB 5; Length 205; 43.7%; Pred. No. 4.5e-25;
 31.0%; Score 426.5; DB 6; Length 205; 43.7%; Pred. No. 4.5e-25;
 31.0%; Score 426.5; DB 7; Length 205; 43.7%; Pred. No. 4.5e-25;
 31.0%; Score 426.5; DB 7; Length 205; 43.7%; Pred. No. 4.5e-25;
 Length 281;
 ADEISS82 standard; protein; 218 AA.
G-coupled protein receptor related polypeptide, SEQ ID No 12.
WO200283841-A2.
 30.6%; Score 420; DB 7; Length 218;
 Length 218;
 Length 225;
 ABRS4337 standard; protein; 205 AA.
Prostate tumour specific protein sequence SEQ ID 176.
WO200289747-A2.
 DB 5;
 17-AER-2003.

(INCY-) INCYTE GENOMICS INC.

(INCY-) INCYTE GENOMICS INC.

30.7%; Score 422; DB 6;

ery Match 11.1e-24;
 30.7%; Score 422.5; DB 5
39.3%; Pred. No. 1.3e-24;
 30.6%; Score 421; DB 4; 44.3%; Pred. No. 1.3e-24;
 AAB31579 standard; peptide; 225 AA.
Amino acid sequence of cod trypsin isozymes.
WO200078332-A2.
 ADB13626 standard; protein; 205 AA.
Human prostate specific protein P703P-DB13.
US2003185830-A1.
 Jr 1442
ADGS6042 standard; protein; 205 AA.
Human prostate-specific polypeptide #6.
US2003157089-A1.
 ADK36957 standard; protein; 281 AA.
Novel human polypeptide SegID9039.
WO200216439-A2.
 (BJAR/) BJARNASON J B.
 CURAGEN CORP.
 CORIXA CORP.
 (CORI-) CORIXA CORP.
 (CORI-) CORIXA CORP.
 Query Match
Best Local Similarity
 Best Local Similarity
 Query Match
Best Local Similarity
RESULT 1444
 Query Match
Best Local Similarity
 Best Local Similarity RESULT 1447
 (xu3J/) xu J.
(DILL/) DILLON D C.
 Best Local Similarity
 Best Local Similarity RESULT 1445
 Query Match
Best Local Similarity
 (HYSE-) HYSEQ INC.
US2002081580-A1.
 28-FEB-2002
 24-OCT-2002
 14-NOV-2002
 21-AUG-2003
 02-OCT-2003
 Query Match
 Query Match
 Match
 (CURA-) (
Query Match
 Query Match
 RESULT 1440
 RESULT 1441
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(MILL/) (SPYT/) (ZERH/) (GERL/)

PENA/

SHEN/ ZHON/ SMIT/ CASM/ (RAST/ (ANDE/ ZHON/

(BOLD/ (VOSS/ (VERN/

```
vuery Match

29.8%; Score 409; DB 6; Length 194;

Best Local Similarity 38.7%; Pred. No. 9.5e-24;

RESULT 1456

ID ADG75684 standard; protein; 215 AA.

BE Human protein modification and maintenance molecule polypeptide SeqID8.

PN W02003083084-A2.

PD 09-0CT-2003.
30.0%; Score 412.5; DB 6; Length 198; 36.8%; Pred. No. 5.2e-24;
 DB 8; Length 198;
 Length 215;
 Length 215
 ABM83829 standard; protein; 215 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:3078.
WO2004023973-A2.
 ABM83248 standard; protein; 299 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:3497.
WO2004023973-A2.
 Query Match
Best Local Similarity 36.8%; Pred. No. 5.2e-24;
RESULT 1455
ID ADA50560 standard; protein; 194 AA.
DE Prostate specific antigen (PSA/KLK3), SEQ ID NO:15.
PN W02003031559-A2.
 29.8%; Score 409; DB 7; 37.1%; Pred. No. 1.1e-23;
 29.8%; Score 409; DB 8; 37.1%; Pred. No. 1.1e-23;
 ADN62900 standard; protein; 198 AA.
 ZERHUSEN B D.
ANDERSON D W.
ZHONG M.
 PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
 MALYANKAR U M
 17-APR-2003.
(CENZ) CENTOCOR INC.
 SPYTEK K A.
EDINGER S R.
ELLERMAN K.
 (GANG/) GANGOLLI E A.
(RIEG/) RIEGER D K.
(SPAD/) SPADERNA S K.
 GUO X.
PATTURAJAN M.
 (INCY-) INCYTE CORP.
 (INCY-) INCYTE CORP.
 MILLET I.
PEYMAN J A.
KEKUDA R.
 CATTERTON E.
 DIPIPPO V A.
EISEN A.
 Best Local Similarity RESULT 1457
 Query Match
** Best Local Similarity
RESULT 1458
 25-MAR-2004.
(INCY-) INCYTE CORP
 떠그
 Query Match
Best Local Similarity
RESULT 1454
 SMITHSON G.
 RASTELLI L. STONE D J.
 AGEE M L.
BERGHS C.
 GORMAN L.
 MILLER C
 Human NOV18c.
US2004038223-A1.
 JI W.
 25-MAR-2004
 Ouery Match
 PENA/)
 ANDE/)
 JIWM/
 MILL/
 RAST/
 MALY/
 ZHON/
 SHIM/
 EDIN/
 GORM/
 29-DEC-1997.
(MOGA-) MOGAM BIOTECHNOLOGY RES INST.
ery Match
st Local Similarity 36.6%; Pred. No. 2.5e-24;
 30.3%; Score 416.5; DB 5; Length 226; 42.6%; Pred. No. 2.9e-24;
 DB 6; Length 226;
 PD 12-AUG-1999.

PA (HUMA-) HUMAN GENOME SCI INC.

Querry Match
30.4%; Score 418; DB 2; Length 207;

BEST Local Similarity 46.1%; Pred. No. 2e-24;

RESULT 1450
 Score 420; DB 8; Length 218;
Pred. No. 1.5e-24;
 ADL93921 standard; protein; 218 AA.
Human G-coupled protein receptor-related protein #6.
US2004006205-A1.
 30.3%; Score 416.5; DB 6; 42.6%; Pred. No. 2.9e-24;
 37.8%; Pred. No. 1.5e-24;
 AAY28641 standard; protein; 207 AA.
Human secreted protein from cDNA clone HKAET41.
WO9940183-A1.
 AAE21442 standard; protein; 226 AA.
Human trypsin domain consensus protein #2.
WO200226802-A2.
(MILL-) MILLENNIUM PHARM INC.
 ABG75786 standard; protein; 226 AA.
Trypsin domain consensus sequence, SMART.
US2002165152-A1.
 AAW46773 standard; protein; 233 AA. Amino acid sequence of Salmonase. EP814164-A2.
 ADA05736 standard; protein; 198 AA.
Human NOV18c protein SEQ ID NO:96.
WO2003029424-A2.
 (KAPE/) KAPELLER-LIBERMANN R.
 30.6%;
 ZHONG H.
SMITHSON G.
CASMAN S J.
BOLDOG F L.
VOSS E Z.
VERNET C A.
 (FURT/) FURTAK K.
(PATT/) PATTRAJAN M.
(BURG/) BURGESS C E.
(MALY/) MALYANKAR U M.
(SHIM/) SHINKETS R A.
(TAUP/) TAUPIER R J.
(EDIN/) EDINGER S.
 ANDERSON D W.
ZHONG M.
MEZES P S.
 MILLER C E.
SPYTEK K A.
ZERHUSEN B D.
 (CURA-) CURAGEN CORP.
 Query Match
Best Local Similarity
RESULT 1453
 PENA C E A.
SHENOY S G.
 Best Local Similarity
RESULT 1452
Best Local Similarity
RESULT 1448
 Local Similarity
 GERLACH V.
```

Query Match

Best Loca RESULT 1449

07-NOV-2002

Query Match

Query Match

```
ABB09590 standard; protein; 218 AA.
Definaghistrodon acutus venom thrombin-like protein (218 residue variant).
CN1181421-A.
13-MAY-1998.
(SIRAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
ery Match
st. Local Similarity 36.5%; Pred. No. 2e-23;
 29.4%; Score 403.5; DB 3; Length 230; 37.0%; Pred. No. 3e-23;
 29.2%; Score 401.5; DB 5; Length 249; 40.3%; Pred. No. 4.6e-23;
29.6%; Score 406.5; DB 2; Length 231; 36.2%; Pred. No. 1.8e-23;
 ABM64665 standard; protein; 220 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:4914,
WC2004023973-A2.
25-MAR-2004.
 AABOSUSII standard; protein; 230 AA.
Blosynthetic variant of protein C activator polypeptide
WO200050612-A2.
 UFVALL...
11-MAY-1990.
(FUJI) FUJISAWA PHARM CO LTD.
(ELY MATCh 29.3%; Score 402; DB 2;
(ELY MATCh 32.9%; Pred. No. 4.3e-23;
 29.3%; Score 403; DB 2; 36.7%; Pred. No. 3.3e-23;
 29.5%; Score 405; DB 8; 36.7%; Pred. No. 2.2e-23;
 Score 402; DB 1;
Pred. No. 4.3e-23;
 29.3%; Score 402; DB 2; 32.9%; Pred. No. 4.3e-23;
 (MOKA-) MOKAM BIOTECHNOLOGY RES INST.
ry Match 29.1%; Score 400; DB 2;
 ARIO557 standard; protein; 234 AA.
Fibrinogenolytic protein #4 from snake venom.
DE4023699-A.
 AAE21441 standard; protein; 249 AA.
Human trypsin domain consensus protein #1.
WO200226802-A2.
 AAR05436 standard; protein; 255 AA. Batroxobin gene product. JP02124092-A.
 AAM52946 standard, protein, 231 AA.
Batroxobin, a snake venom protease.
KR98002267-A.
 AAY17869 standard; protein; 255 AA. Araraca batroxobin. WO9929838-A1.
 AAP81333 standard; protein; 255 AA
 17-JUN-1999.
(BRIM) BRISTOL-MYERS SQUIBB CO.
 (MILL-) MILLENNIUM PHARM INC.
 29.3%;
 31-AUG-2000.
(INLI) INSTRUMENTATION LAB.
 01-MAR-1988.
(YAMA/) YAMASHINA I.
 Query Match
Best Local Similarity
RESULT 1470
 Best Local Similarity RESULT 1471
 (INCY-) INCYTE CORP.
 Best Local Similarity RESULT 1469
 Best Local Similarity RESULT 1465
 Best Local Similarity
RESULT 1464
 Best Local Similarity RESULT 1466
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 Best Local Similarity
RESULT 1468
 Best Local Similarity RESULT 1472
 30-JAN-1992.
(BADI) BASF AG.
 JP63049084-A.
 30-MAR-1998
 04-APR-2002
 Batroxobin
 Query Match
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 Query Match
 Score 408.5; DB 8; Length 181; Pred. No. 9.6e-24;
 Score 408.5; DB 6; Length 181; Pred. No. 9.6e-24;
 29.6%; Score 406.5; DB 3; Length 230; 36.2%; Pred. No. 1.8e-23;
 Score 409; DB 8; Length 299;
Pred. No. 1.5e-23;
 Length 222
 ABM82641 standard; protein; 222 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2890
WO2004023973-A2.
 AAW76538 standard; protein; 231 AA.
A. contortrix protein C activator protein fragment.
WO9842850-A1.
 29.6%; Score 407; DB 8; 36.7%; Pred. No. 1.6e-23;
 A recombinant protein C activator polypeptide.
 ADA05738 standard; protein; 181 AA. Human NOV18d protein SEQ ID NO:98. WO2003029424-A2. IO-ARR-2003. (CURA-) CURAGEN CORP.
 AAB08510 standard; protein; 230 AA.
 ADN62902 standard; protein; 181 AA.
 29.8%;
 29.7%;
 (INLI) INSTRUMENTATION LAB.
 Match 29.7%; Local Similarity 37.4%;
 01-OCT-1998.
(RPMS-) RPMS TECHNOLOGY LTD.
 MILL/) MILLER C E.
RAST/) RALTELI L.
STON/) STONE D J.
PEDNA/) BENA C E A.
(SHEN/) SHENOY S G.
(SHIN/) SHENOY S G.
(SHEN/) SHENOY S G.
(LEAC/) LEACH M D.
(AGES/) AGES M L.
(BERG/) BERGHS C.
(DIPI/) DIPIPPO V A.
(EISE/) EISEN A.
(GANG/) GANGOLLI E A.
(GANG/) GANGOLLI E A.
(SREG/) STEGER D K.
 SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
 GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
ZHONG M.
 PATTURAJAN M.
 Best Local Similarity
RESULT 1459
ID ADAOS738 standard; pp
DE Human NOV18d procein
PN WO200302944-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
 MILLET I.
PEYMAN J A.
KEKUDA R.
 (INCY-) INCYTE CORP.
 Query Match
Best Local Similarity
RESULT 1460
 SMITHSON G.
 Local Similarity
 Local Similarity
 US2004038223-A1.
 WO200050612-A2.
 Human NOV18d
 25-MAR-2004
 31-AUG-2000
 Query Match
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(KEKU/)
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 GORM/
 ANDE/
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MALY/

Length 234;

Length 220;

Length 255;

Length 231;

Length 255;

Length 255;

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38.5%; Pred. No. 6.2e-22;

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Best Local Similarity RESULT 1482
 RESULT
 Score 395.5; DB 3; Length 264; Pred. No. 1.4e-22;
 DB 7; Length 253;
 Length 236;
 Length 227;
 Score 389; DB 7; Length 253;
Pred. No. 4.3e-22;
 Score 388; DB 1; Length 269;
Pred. No. 5.5e-22;
 28.2%; Score 387; DB 7; Length 253;
 Length 236
 Score 392; DB 8; Length 233; Pred. No. 2.3e-22;
 nemezesı standard; protein; 233 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:3080.
WC2004023973-A2.
 AAB11711 standard; protein; 264 AA.
Mouse serine protease BSSPS (mBSSPS) SEQ ID NO:4.
WO200031243-A1.
 30-MRA-1998.
(MOKA-) MOKAM BIOTECHNOLOGY RES INST.
ery Match 28.7%; Score 394; DB 2;
 Pred. No. 5.6e-23;
 DB 2;
 28.3%; Score 389; DB 6; 40.4%; Pred. No. 3.9e-22;
 Score 393; DB 2
Pred. No. 2e-22;
 28.5%; Score 391; DB 7 38.0%; Pred. No. 3e-22;
 AAR20556 standard; protein; 236 AA.
Fibrinogenolytic protein #3 from snake venom
 Trypsin domain consensus sequence, PFAM US2002165152-A1.
 ADE58223 standard; protein; 253 AA.
Human Protein P00746, SEQ ID NO 4094.
WO2003016475-A2.
 AAM52945 standard, protein, 236 AA. Flaboxobin, a snake venom protease. KR98002267-A.
 ABG75785 standard; protein; 227 AA.
 AAE39992 standard; protein; 253 AA. Human adipsin protein #1. US2003092620-A1. I5-MAY-2003. (GEST) GENSET SA.
 protein; 253 AA
 protein; 269 AA
 (KAPE/) KAPELLER-LIBERMANN R.
 28.8%;
 28.6%;
 28.5%;
 28.3%;
 28.2%;
34.2%;
 02-JUN-2000.
(FUSO) FUSO PHARM IND LTD.
 (GEHO) GEN HOSPITAL CORP. (FARB) BAYER AG.
 Human adipsin protein #2.
US2003092620-A1.
 Pig pancreas elastase-2. JP62000276-A.
 (SANY) SANKYO CO LTD.
 25-MAR-2004.
(INCY-) INCYTE CORP.
 Local Similarity
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RESULT 1480
ID AAP70758 standard;
Best Local Similarity
 Best Local Similarity
RESULT 1475
 Best Local Similarity
RESULT 1478
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Best Local Similarity
 Best Local Similarity
RESULT 1481
 Best Local Similarity
 AAR20556 standard;
 15-MAY-2003.
(GEST) GENSET SA.
 AAE39993 standard;
 30-JAN-1992.
(BADI) BASF AG.
 27-FEB-2003.
 DE4023699-A
 06-JAN-1987
 Query Match
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ABM81778 standard; protein; 264 AA.
Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580.
WO2004030615-A2.
 Length 264;
 Length 264;
 Length 212;
 Length 264;
 Length 212
 Score 385; DB 8; Length 213; Pred. No. 7.4e-22;
 Length 271;
 Length 213;
 ABMB1830 standard; protein; 212 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:3079.
WO2004023973-A2.
 ADMW62644 standard; protein; 212 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2893.
W0200603973-A2.
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 Αμκευυ37 standard; protein; 213 AA.
Human prostatic carcinoma derived protein SEQ ID 233
W0200016614-A2.
 AUNOSUJS Btandard; protein; 213 AA.
Human prostatic carcinoma derived DNA SEQ ID 233 #4.
WO2004076614-A2.
 Score 386.5; DB 3;
Pred. No. 7e-22;
 28.1%; Score 386.5; DB 6; 36.8%; Pred. No. 7e-22;
 28.1%; Score 385.5; DB 8; 36.3%; Pred. No. 6.7e-22;
 Score 385.5; DB 8;
Pred. No. 8.4e-22;
AAB11710 standard; protein; 264 AA.
Human serine protease BSSP5 (hBSSP5) SEQ ID NO:2.
WO20031241-A1.
02-JUN-2000.
 DB 8;
 (MILL-) MILLENNIUM PHARM INC.

28.1%; Score 386; DB 6;

t Local Similarity 39.1%; Pred. No. 7.9e-22;
 Score 385.5; DB 8
Pred. No. 6.7e-22;
 Score 385; DB 8;
Pred. No. 7.4e-22;
 ABR39439 standard; protein; 264 AA.
Human GENSET polypeptide clone name vCTRL-1.
WO2003014151-A2.
 ABU00382 standard; protein; 271 AA.
Consensus sequence of trypsin-like domain.
WO2003031463-A2.
 WO2004050.
15-APR-2004.
(GETH) GENENTECH INC.
28.1%;
 28.1%;
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40.2%;
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 28.0%;
 (FUSO) FUSO PHARM IND LTD.
 (DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
(HERM/) HERMANN K.
 25-MAR-2004.
(INCY-) INCYTE CORP.
 (INCY-) INCYTE CORP.
 Query Match
Best Local Similarity
 Best Local Similarity RESULT 1487
 DAHL/) DAHL E.
ROSE/) ROSENTHAL A.
 Query Match
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SULT 1486
 Query Match
Best Local Similarity
RESULT 1483
 HINZ/) HINZMANN B.
 Local Similarity
 10-SEP-2004.
(HINZ/) HINZMANN B.
 20-FEB-2003.
(GEST) GENSET SA.
 Best Local Similarity
 Best Local Similarity
 PILA/) PILARSKY C
 (PILA/) PILARSKY C
 25-MAR-2004
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27-FEB-2003.

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ADNIO933 standard; protein; 171 AA.
Human kallikrein 15, marker of endocrine cancer.
Human kallikrein 15, marker of endocrine cancer.
Human kallikrein 15, marker of endocrine cancer.
08-APR-2004.
(MOUN) MOUNT SINAI HOSPITAL.
27.8%; Score 382.5; DB 8; Length 171;
ELocal Similarity 35.8%; Pred. No. 9.2e-22;
 Match 27.8%; Score 382; DB 2; Length 250; Local Similarity 38.4%; Pred. No. 1.5e-21;
 Query Match 27.8%; Score 382; DB 8; Length 212; Best Local Similarity 35.5%; Pred. No. 1.2e-21; RESULT 1496
 27.8%; Score 382; DB 2; Length 250; 37.2%; Pred. No. 1.5e-21;
 Score 384; DB 1; Length 269;
Pred. No. 1.1e-21;
 27.9%; Score 383; DB 2; Length 258; 34.3%; Pred. No. 1.3e-21;
 Length 272;
 ABM82642 standard; protein; 212 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2891
WO2004023973-A2.
 (MOUN) MOUNT SINAI HOSPITAL.

ry Match 27.8%; Score 382.5; DB 5; t Local Similarity 35.8%; Pred. No. 9.2e-22;
 RESULT 1493 Standard; 33.9%; Pred. No. 1.4e-21; RESULT 149393 standard; protein; 171 AA.

DE Novel human kallikrein KLKI5, splice variant #3.

PN W0200214485-A2.
 AAR05772 standard; protein; 250 AA.
Human adipsin gene product from the clone phg31.
WO9006365-A.
 27.9%; Score 383; DB 2; 33.9%; Pred. No. 1.4e-21;
 ADE58221 standard; protein; 263 AA.
Rat Protein AAB31922, SEQ ID NO 4092.
WO2003016475-A2.
 (BETH-) BETH ISRAEL HOSPITAL ASSOC. (BANA-) DANA-FARBER CANCER INST. (META-) METABOLIC BIOSYSTEMS INC. (BETH-) BETH ISRAEL HOSPITAL ASSOC.
 AAR07513 standard; protein; 258 AA.
Ancrod-like polypeptide #2.
EP395375-A.
 protein; 272 AA.
polypeptide.
 AAR05421 standard; protein; 250 AA.
Human adipsin/D encoded by a cDNA.
WO9001540-A.
protein; 269 AA
 27.9%;
 (CALB-) CALIF BIOTECHN INC.
 26-AUG-1986.
(KIRI) KIRIN BREWERY KK.
 25-MAR-2004.
(INCY-) INCYTE CORP.
 Porcine elastase II
JP61192289-A.
 AAR05775 standard;
Snake venom ancrod
WO9006362-A.
AAP61724 standard;
 Local Similarity
 Local Similarity
 31-OCT-1990.
(GLAX) GLAXO INC.
(KNOL) KNOLL AG.
 Local Similarity
 (BADI) BASF AG.
(BACH/) BACH A.
 21-FEB-2002
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Length 171;

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ABU92049 standard; protein; 220 AA. Human protein modification and maintenance molecule-29 (PMMM-29) WO2003031939-A2.
 GENAY-2004.
(FIVE-) FIVE PRIME THERAPEUTICS INC.
(FIVE-) FIVE PRIME THERAPEUTICS INC.
27.6%; Score 379.5; DB 8; Length 187;
ery Match
27.6%; Pred. No. 1.7e-21;
 Length 263;
 Length 220;
 Score 381; DB 7;
Pred. No. 1.9e-21;
 27.6%; Score 379; DB 6; 37.2%; Pred. No. 2.2e-21;
 ADN99596 standard; protein; 187 AA
Novel human protein sequence #412.
WO2004038003-A2.
 27.78;
 17-APR-2003.
(INCY-) INCYTE GENOMICS INC.
 protein;
(GEHO) GEN HOSPITAL CORP. (FARB) BAYER AG.
 Best Local Similarity
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Post-processing:

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Minimum DB Maximum DB

Title: Perfect score:

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Scoring table:

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| 25.8<br>25.8<br>25.8                                                                                                | 25.7<br>25.7                                                                  | 25.7                                                                           | 25.7                                     | 25.7                              | 25.7                                   | 25.7                            | 25.7                              | 25.7                                                 | 7.07                                                          | 7. 2.                                        | 7.07                                           | 0.00                                      | 4.02                                                                                                                                                                                                                                                                           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| 354<br>354<br>354                                                                                                   | 353.5<br>353.5                                                                | 353                                                                            | 323                                      | 353                               | 353                                    | 353                             | 323                               | 253                                                  | 200                                                           | 200                                          | 100                                            | 0.10                                      | 0.0                                                                                                                                                                                                                                                                            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| Sequence<br>Sequence<br>Sequence                                                                                    | Sequence 10<br>Patent No. 9                                                   | Semience 9                                                                     | Sequence 11                              | Patent No.                        | Sequence 5,                            | Patent No.                      | Patent No. 5                      | Patent No.                                           | Datent No.                                                    | Datent No.                                   | Semionae 44                                    | tr anienhac                               | o acinemas                                                                                                                                                                                                                                                                     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| Sequence 15                              | Semence 12                               |                                         | sednence 17                              | Sequence 12                              |                                           | sednence TS                               | Seguence 12                              | CL engines                               | פבלתבווכב דק                                            | sednence 17                              | Sequence 30                             | Semence 3                               | Company 2                      | sednemes                                                                                                                                                                                                                                                                                                                                                                                                 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    | Sequence 11                             | R donathan                 | C Compression                                              |                                       | sednence 4'                            | Sequence 66                             | Sequence 31                             | Semience 7                              | to opening                             | seducince or                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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                                                                         | Sednence 1                               | Seguence 21                              | Dated No.            | Faccus no.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Facent No. :                      | Sequence 13                             | Sequence 13                             |                                       | sednence 4,                             | Patent No. 5270178                 |   |
| Sequence 16<br>Sequence 6,                                                                                          | Sequence 10<br>Patent No. 9                                                   | Semience 9                                                                     | Sequence 11                              | Patent No.                        | Sequence 5,                            | Patent No.                      | Patent No. 5                      | Patent No.                                           | Datent No.                                                    | Datent No.                                   | Semionae 44                                    | tr anienhac                               | o acinemas                                                                                                                                                                                                                                                                     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| Sequence 15                              | Semence 12                               |                                         | sednence 17                              | Sequence 12                              |                                           | sednence TS                               | Seguence 12                              | CL engines                               | פבלתבווכב דק                                            | sednence 17                              | Sequence 30                             | Semence 3                               | Cecinon 2                      | re aniranhae                                                                                                                                                                                                                                                                                                                                                                                             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    | Sequence 11                             | R donathan                 | C Compression                                              |                                       | sednence 4'                            | Sequence 66                             | Sequence 31                             | Semience 7                              | to opening                             | seducince or                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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| 4 US-09-402-515A-16 Sequence 16<br>1 US-08-684-862-6 Sequence 6,<br>1 US-08-684-862-5 Sequence 5,                   | 2 US-08-738-413B-10 Sequence 10<br>6 5223425-8 Patent No. 5                   | 6 5223425-8 Patent No. 5<br>4 US-09-949-016-9575 Semience 95                   | 2 US-08-738-413B-11 Sequence 11          | 6 5223425-4 Patent No. 5          | 3 US-09-261-416-5 Sequence 5,          | 6 5223425-5 Patent No. 5        | 6 5223425-5 Patent No. 5          | 6 5223425-2<br>6 5223425-2<br>Detent No. 6           | 6 3223423-2<br>6 5233435-10<br>6 5233435-10                   | 6 5223423-10<br>6 5223425-10<br>Datont No. 8 | 3 11C-08-044-483-44 Company A                  | 2 100 000 000 000 00 00 00 00 00 00 00 00 | 4 110 00 011 430 00                                                                                                                                                                                                                                                            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| 231 4 US-09-402-515A-16 Sequence 16<br>234 1 US-08-684-862-6 Sequence 6,<br>236 1 US-08-684-862-5 Sequence 5,       | 28.3 236 2 US-08-738-413B-10 Sequence 10<br>28.2 253 6 5223425-8 Patent No. 9 | 28.2 253 6 5223425-8 Patent No. 5<br>28.1 267 4 US-09-949-016-9575 Semience 95 | 28.0 232 2 US-08-738-413B-11 Sequence 11 | 28.0 250 6 5223425-4 Parent No. 3 | 27.5 154 3 US-09-261-416-5 Sequence 5, | 27.3 238 6 5223425-5 Patent No. | 27.3 238 6 5223425-5 Patent No. 5 | 27.3 239 6 5223425-2 Parent No. 37.3 259 6 5223425-2 | 27.3 23.9 6 3223423-2 FALCHL NO. 3                            | 27.2 200 G 3223437-10 Facell NO. 3           | 27.2 200 3 110-08-044-403-44 Comions 44        | 23.00                                     |                                                                                                                                                                                                                                                                                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| 01A-2<br>61A-8<br>63-4<br>177-2<br>771A-21                                                                                                                       | 5-11123<br>5-9238<br>5-9239                                                                            | 5-11539<br>1-2<br>18-2                                                            | 2-2                                                      | 9-10<br>9-10<br>1-51                                        | 3-48<br>3-48<br>3-6                     | 2 2 2                                                              | 3-8<br>3A-1                            | 111                                   | 3-1<br>3B-1                                            | 1 T T                               | 2 - 3 - 1<br>- 3 - 1                 | IA-12                              | IA-6<br>1B-1                        | 8-1<br>1A-13            | 1-4                   | 2-12                                       | 0A-9<br>1A-9               | 3A-7<br>1-26       | 9-22<br>1-2      | 1-2               | 1-3<br>18-11     | 8-2                                  | 1 - 4<br>1 - 4                          | 8-14<br>42-4           | 2A-3              | 1-3                                     | 57-3<br>7-8         | 2-42<br>6-6458      | 9-3                |
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| 258<br>333<br>333<br>4461<br>461<br>161                                                                                                                          | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                  | 637<br>230<br>230                                                                 | 230<br>261<br>261                                        | 308                                                         | 267<br>235<br>406                       | 423                                                                | 437<br>812                             | 812                                   | 812                                                    | 812                                 | 812                                  | 812                                | 435                                 | 415                     | 446                   | 562<br>316                                 | 316                        | 290<br>302         | 302              | 415               | 638              | 295                                  | 579<br>579                              | 579                    | 615               | 615                                     | 615                 | 622                 | 260                |
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|                                                                                                                                                                  |                                                                                                        | 338.5<br>338.5                                                                    | 338.5                                                    | 338.5                                                       | 337.5<br>337<br>337                     | 337                                                                | 337                                    | 337                                   | 337                                                    | 337                                 | 337                                  | 337                                | 336.5                               | 336                     | 334.5                 | 334.5                                      | 334                        | 333.5              | 333.5            | 333               | 332.5            | 331                                  | 331<br>331                              | 331                    | 331               | 331                                     | 331                 | 331                 | 330.5              |
| 467<br>468<br>469<br>470<br>471<br>472                                                                                                                           | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                  | 478<br>480<br>481                                                                 | 4882<br>483                                              | 486<br>486<br>487                                           | 4 8 8 4 4 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 | 491<br>492                                                         | 4 4 4<br>0 0 0 0<br>4 4 0 0            | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 498                                                    | 501                                 | 503                                  | 505                                | 507                                 | 509                     | 511                   | 513                                        | 515                        | 517                | 519              | 521               | 523              | 525                                  | 526<br>527                              | 528                    | 530               | 532                                     | 533                 | 535                 | 5.50<br>5.00       |
| Sequence 111, App<br>Sequence 111, App<br>Sequence 111, App<br>Sequence 111, App<br>Sequence 111, App<br>Sequence 111, App<br>Sequence 111, App                  | Sequence 21, Appl<br>Sequence 16, Appl<br>Sequence 3, Appli<br>Sequence 3, Appli<br>Patent No. 5270178 | Patent No. 5270178 Patent No. 5270178 Patent No. 5270178 Patent No. 5270178       | Patent No. 5270178 Patent No. 5270178 Patent No. 5270178 | Sequence 7, Appli<br>Sequence 7, Appli<br>Sequence 7, Appli | ., ., .                                 | •                                                                  | 0. 0                                   |                                       |                                                        |                                     |                                      | .,                                 | •                                   |                         |                       | Patent No. 5270178 Patent No. 5270178      |                            |                    |                  | Sequence 47, Appl |                  |                                      |                                         |                        |                   |                                         |                     |                     |                    |
| 3 US-08-906-616-111<br>3 US-08-817-795-111<br>3 US-08-639-075A-111<br>3 US-09-012-431-111<br>3 US-09-012-692-111<br>3 US-08-906-613-111<br>5 PCT-US95-14442A-111 | US-09-016-366A-21<br>US-08-978-404B-16<br>US-08-978-404B-3<br>5270178-13                               | 5270178-14<br>5270178-15<br>5270178-16<br>5270178-13                              | 5270178-14<br>5270178-15<br>5270178-16                   | US-09-387-375-7<br>US-10-041-400A-7<br>US-10-042-091A-7     | US-09-032-215-37<br>US-09-079-970A-5    | 5200340-6<br>5200340-6<br>5200340-6                                | US-09-949-016-9983<br>US-08-469-486-54 | US-08-469-658-54<br>US-09-131-995-1   | US-09-132-154-1<br>US-09-132-154-1<br>US-08-991-761A-6 | US-08-924-287A-1<br>US-07-854-603-2 | US-08-14/-000B-29<br>US-09-086-514-1 | US-09-192-012-5<br>US-09-403-736-1 | 5200340-8<br>5200340-8<br>5200340-8 | US-08-684-862-3         | US-08-978-404B-14     | 5270178-19<br>5 5270178-19<br>5 5270178-20 | 5270178-19<br>5 5270178-20 | 5270178-21         | US-09-386-642-53 | US-08-456-840-47  | US-08-892-544-47 | US-08-766-982-12<br>US-08-944-483-53 | 3 US-09-296-219-12<br>4 US-09-601-318-4 | 1 US-09-601-318-5      | 1 US-09-601-318-7 | 3 US-09-079-970A-6<br>4 US-09-601-318-1 | 2 US-09-016-366A-23 | 1 US-09-917-254-101 | 3 US-08-705-875A-6 |
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| 34455.5<br>34455.5<br>34455.5<br>3455.5<br>5                                                                                                                     | 344<br>343<br>343<br>343<br>343<br>343<br>343<br>343<br>343<br>343                                     | 343.5<br>343.5<br>343.5<br>43.5                                                   | 343.5<br>343.5                                           | 343<br>343<br>343                                           | 342.5                                   | 342.5<br>342.5                                                     | 342.5                                  | 342.5                                 | 342.5<br>342.5                                         | 342.5                               | 342.5                                | 342.5                              | 342.5                               | 342                     | 342                   | 341.5                                      | 341.5                      | 341                | 341              | 340.5             | 340.5            | 340.5                                | 340.5                                   | 340.5                  | 340.0             | 340.5                                   | 340.5               | 340.5               | 340.5              |
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| Patent No. 5185259 Patent No. 5200340 Patent No. 5244676 Patent No. 5344773 Patent No. 5185259 Patent No. 5200340 Patent No. 5244676 Patent No. 5244676                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Sequence 11501, A<br>Sequence 7815, Ap<br>Sequence 4, Appli                                                                                         | Sequence 4, Appil<br>Sequence 10661, A<br>Sequence 53, Appl                                                        | Sequence 67, Appl<br>Sequence 55, Appl                                       | Sequence 1, Appli<br>Sequence 4, Appli                                          | Sequence 51, Appl                                                             | Sequence 2, Appli<br>Sequence 3, Appli                                          | Sequence 41, Appl<br>Sequence 14, Appl                       | Sequence 14, Appl<br>Sequence 14, Appl | Sequence 14, Appl                                                             | Sequence 14, Appl                                                      | Sequence 14, Appl<br>Sequence 10662, A        | Patent No. 5520913<br>Patent No. 5520913    | Sequence 24, Appl<br>Sequence 1. 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| 758<br>759<br>760<br>761<br>762<br>763                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                     |                                                                                                                    | 772<br>773                                                                   |                                                                                 | 776                                                                           | 778<br>779                                                                      | 780<br>781                                                   | 782                                    | 784                                                                           | 786                                                                    | 787                                           | 789                                         | 791        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819                                        | 821                                                                   | 823<br>823                               | 824                               | 826                                                            | 823<br>828                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          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                                               | Sequence 1, Applia<br>Sequence 2, Applia<br>Sequence 2, Applia<br>Sequence 2, Applia                                                                |                                                                                                                    |                                                                              |                                                                                 | m m                                                                           | min                                                                             | m -1                                                         | ì air                                  | - ਦਾ                                                                          | 49,                                                                    | 91                                            | 190                                         | 9 6                                                                                        | Sequence 19, Appl<br>Sequence 2, Appli<br>Sequence 22 Appli                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            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8                                          | ä                                                                     | N W                                      | , ., .                            | 41                                                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     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| Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence<br>Sequence                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   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| 296.5 21.6 411 1 US-08-186-748B-18 Sequence 1, 296.5 21.6 411 1 US-08-153-799-18 Sequence 1, 296.5 21.6 411 1 US-08-153-799-18 Sequence 1, 296.5 21.6 411 2 US-08-560-098A-48 Sequence 3, 296.5 21.6 411 2 US-09-880-503-3 Sequence 3, 296.5 21.6 430 6 5219569-2 Sequence 3, 296.5 21.6 431 6 5219569-2 Sequence 1, 296.5 21.6 431 6 5219569-2 Sequence 1, 296.5 21.6 431 6 5219569-1 Sequence 1, 296.5 21.6 431 8 Sequence 1, 296.5 21.6 431 8 Sequence 1, 296.5 21.5 283 3 US-09-715-994-2 Sequence 1, 296.5 21.4 431 4 US-09-715-32 Sequence 2, 292 21.3 237 4 US-09-704-731-2 Sequence 2, 292 21.3 237 4 US-09-004-729-22 Sequence 2, 292 21.3 237 4 US-09-004-729-22 Sequence 893 292 21.3 256 3 US-08-96-616-89 292 21.3 256 3 US-08-96                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 253 3 US-08-944-483-73 Sequence 73, 216-14 235 3 US-08-900-846-2 Sequence 27, 215 2 US-09-100-846-2 Sequence 27, 215 2 US-09-154-144 Sequence 27, 215 2 US-09-154-144 Sequence 37, 215 3 US-08-944-483-42 Sequence 37, 215 3 US-08-944-483-42 Sequence 37, 217 US-09-976-991 Sequence 41, 217 US-09-976-991 Sequence 41, 217 US-09-976-991 Sequence 41, 217 US-08-976-991 Sequence 91, 225 3 US-08-906-769-91 Sequence 91, 225 3 US-08-906-769-91 Sequence 91, 225 3 US-08-906-763-91 Sequence 91, 226 3 US-08-906-763-91 Sequence 10, 226 3 US-08-906-763-91 Sequence 11, 225 3 US-08-906-763-907-91 Sequence 11, 225 3 US-08-906-763-91 Sequence 11, 226 3 US-08 |

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                                     | US-08-906-616-149                                     | US-09-012-431-149                      |                                         |                                                                                 | US-08-978-404B-46                    | US-09-270-767-4802                   | US-09-163-951-16                      |                                        |                                                                 | US-08-639-075A-14                     |                                        |                                      |                                                             |                                     |                                                                              |                                     |                                   |                                  |                             |                                  |                                   |                                                                |                                   |                                   | PCT-US95-14442A-1                                                     |                                  |                                       |                                                                          |                                     |                                     | US-09-796-110-2<br>US-09-270-767-6200                                      | US-08-944-483-31                   |                                    |                                     | US-09-518-046-25                    | US-09-518-046-23                       |                              |                              |                                     |                                     |
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              |                                     |                                   |                                  |                             |                                  |                                   |                                                                |                                   |                                   |                                                                       |                                  |                                       |                                                                          |                                     |                                     |                                                                            |                                    |                                    |                                     |                                     |                                        |                              |                              |           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 28.   28.   28.   28.   28.   28.   28.   28.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 16.4<br>16.4<br>16.4                                                                                                                                               | 16.4                                  | 16.4                                  | 16.4                                   | 16.4<br>16.4                                                                        | 16.4                                    | 16.4                                                          | •                                      |                                                                               | •                                      |                                                       |                                        |                                         |                                                                                 | •                                    | •                                    |                                       | •                                      |                                                                 | 15.7                                  | 15.7                                   | 15.7                                 | 15.7                                                        | 15.7                                | 15.7                                                                         | 15.7                                | 15.7                              |                                  | •                           |                                  | •                                 | •                                                              |                                   | •                                 | •                                                                     | ٠.                               | •                                     |                                                                          | •                                   | •                                   |                                                                            |                                    | •                                  | •                                   |                                     |                                        |                              | •                            | ٠      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| 18.   27.   18.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   28.   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     | 226                                     | 226<br>226                                                    | 226                                    | 223                                                                           | 222                                    | 222                                                   | 222                                    | 222                                     | 222                                                                             | 220.5                                | 220                                  | 217.5                                 | 217.5                                  | 216                                                             | 216                                   | 216                                    | 216                                  | 216                                                         | 216                                 | 216<br>216                                                                   | 216                                 | 216                               | 216                              | 216                         | 216                              | 216                               | 211                                                            | 211                               | 211                               | 211                                                                   | 211                              | 211                                   | 211                                                                      | 211                                 | 211                                 | 210.5                                                                      | 10.                                | 10.                                | 95                                  | 206                                 | 4 6                                    | 04.                          | 4:                           | 94.    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 17.   17.   17.   17.   17.   17.   17.   17.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                    |                                                      |                                    |                                    |                                                                           |            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          |                               |                                                                         |                                    |                                   |                                  |                                       |                                                          |                                       |                                    |                                    |                                     |                                      |                                     |                                    |                                    |                                   |                                                    |                             |            |
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       |                               |                                                                         |                                    |                                   |                                  |                                       |                                                          |                                       |                                    |                                    |                                     |                                      |                                     |                                    |                                    |                                   |                                                    |                             |            |
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· · ·                            | TO.4                               | 10.4                                | 10.4                               | 10.4                               | 10.4                               | 10.4                               | 10.4                               |            |                                     | 10.4                                | 10.4                             | 10.4                                 | 10.3                               | 10.3                               | 10.1                                | 10.1                               | 101                           | 101                           | 1.                                                                      |                                    | 1.01                              | 10.1                             | 10.1                                  | 101                                                      | 1.01                                  | 1.01                               | 10.1                               | 10.1                                | 0.01                                 |                                     | D .                                | 9.6                                | 9.4                               |                                                    | 9.3                         |            |
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                                           | Δ.<br>V.                           | 149                                | 149                                 | 149                                 | h (                              | 149                                | 149                                 | 149                                 | 149                                | 149                                |                                        | ю.                                 | ъ.                                 | e.                                  | ~                                    | •                                        |                                    | ;                                  |                                     | ÷.                                 | ش                                  | 'n                                 | ď                                  |                                    |            |                                     |                                     | 'n                               | ď                                    | ä                                  | ä                                  | 13                                  | 139                                | 139                           | 501                           | 000                                                                     | n c                                | 139                               | 139                              | 139                                   | 120                                                      | 000                                   | 7.3                                | 139                                | 139                                 | 138                                  | 0 5                                 | 134                                | 134                                | 129                               | 1 6                                                | 128                         | 11         |
| 14.9   178   178   178   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.0   18.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                                                                    | 200                                                  | 201                                | 202                                | 202                                                                       | -                                  | -                                  | _                                   |                                  | _                                | _                                  |                                     | 212                                 |                                     |                                   |                                    |                                    |                                    |                              |                              |                                     |                                    |                                   |                                   |                                       |                                               | 577                                | 225                                | 226                                 | 200                                 | 1 2 2                            | 228                                | 229                                 | 230                                 | 231                                | 232                                |                                        |                                    |                                    |                                     |                                      |                                          |                                    |                                    |                                     |                                    |                                    |                                    |                                    |                                    |            |                                     |                                     |                                  |                                      |                                    |                                    |                                     | 252                                | 253                           | 25.4                          | 100                                                                     | 0 10                               | 256                               | 257                              | 258                                   | 0 40                                                     | 0 0                                   | 790                                | 261                                | 262                                 | 263                                  | 200                                 | 764                                | 265                                | 266                               | 9 10                                               | 267                         |            |
| 1122.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               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| 11222222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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                     | equence                            | equence                             | equence                          | equence                          | equence                            | Panence                             | edience                             | Sacra                               | eduente                           | Sequence 139, App                  | Sequence 139, App                  | Sequence 1151, Ap                  | Patent No. 5200340           | Patent No. 5200340           | Sequence 57991, A                   | equence                            | a Dual ma                         | emience                           | 90000000                              | cducince                                      | ednence                            | equence                            | equence                             | o de la                             | edneme                           | ednence                            | equence                             | ednence                             | ednence                            | equence                            | operation of                           | ednence                            | equence                            | equence                             | egnence                              | מיניינייניינייניינייניינייניינייניינייני | edneuce                            | equence                            | ednence                             | ednence                            | equence                            | eguence                            | egnence                            |                                    | מלוכיונים  | ednerice                            | equence                             | ednence                          | equence                              | equence                            | equence                            | egnence                             | equence                            | o due tue              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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        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US-09-012-692-129 Semience         | US-08-906-613-129 Sequence         | US-09-949-016-7265 Sequence         | US-09-411-977-3 Seguence         | US-10-057-951-3 Sequence         | US-08-906-769-139 Seguence         | IS-08-906-616-139 Semience          | IIS-08-639-075A-139 Semience        | 110-00-013-0131-130 Sequence        | 02-03-017-431-139 Sequence        | US-09-012-692-139 Sequence         | US-08-906-613-139 Sequence         | US-09-205-258-1151 Sequence        | 5200340-4 Patent No.         | 5200340-4 Patent No.         | US-09-270-767-57991 Sequence        | US-09-636-382A-15 Sequence         | IIS-10-067-422-9 Semience         | 11S-09-618-259-5 Semience         | 110-09-270-767-44375                  | 02-02-10-00-00-00-00-00-00-00-00-00-00-00-00- | US-08-906-769-123 sequence         | US-08-906-616-123 Sequence         | US-08-639-075A-123 Sequence         | TIC-09-012-602-123 Company          | 10 00 00 01 123 203 3eduence     | US-08-906-613-123 Sequence         | US-09-621-976-5522 Sequence         | US-09-949-016-7471 Sequence         | US-09-012-431-123 Sequence         | US-09-020-956-178 Sequence         | 00000000000000000000000000000000000000 | US-09-030-607-178 Sequence         | US-09-439-313-178 Sequence         | US-09-352-616A-178 Sequence         | IIS-09-232-149A-178 Semience         | 10 00 150 010 170 010 000000             | US-US-129-81Z-178 Sequence         | US-09-636-215-178 Sequence         | US-09-685-166A-178 Sequence         | US-09-115-453-178 Sequence         | US-09-688-489-178 Sequence         | US-09-679-426-178 Sequence         | US-09-759-143-178 Segmence         | 110-09-651-336-178 Gemense         |            | US-03-949-016-910-0 Seduence        | US-09-949-016-6979 Sequence         | US-09-578-303-6 Sequence         | US-09-270-767-44299 Sequence         | US-08-906-769-135 Sequence         | US-08-906-616-135 Sequence         | US-08-639-075A-135 Segmence         | US-09-012-431-135 Seguence         | 110-00-013-452-135 Semiono    | TC-09-006-613-135 Segmente    | 110 00 - 10E - 0163 - 0                                                 | 08-08-703-873A-8 Sequence          | US-09-220-731-23 Sequence         | US-09-242-999-8 Sequence         | TIS-09-270-767-4434A Semience         | 0.011 (2) 0.12 (2) 0.01                                  | CS-03-343-0T9-TTOT3                   | US-08-906-769-133 seguence         | US-08-906-616-133 Sequence         | US-08-639-075A-133 Sequence         | TG-09-012-431-133 Semience           | no-09-012-123 Seducince             | US-09-012-692-133 Sequence         | US-08-906-613-133 Sequence         | US-08-845-998-4 Semience          |                                                    | US-09-206-537-4 Sequence    |            |
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                          | Sequence 27, Appl<br>Sequence 41542, A<br>Sequence 41, Appl<br>Sequence 26, Appl<br>Sequence 32342, A<br>Sequence 1375, App                                                                                                                                                                                  | Sequence 137, App<br>Sequence 137, App<br>Sequence 79, Appl<br>Sequence 137, App<br>Sequence 137, App<br>Sequence 137, App<br>Sequence 137, App<br>Sequence 137, App                                                                                                                                                                                                                                                                                                                                                     | Sequence 59, Appl                                                                                                                                                                                                                     | Sequence 59, Appl<br>Sequence 59, Appl<br>Sequence 59, Appl<br>Sequence 52, Appl<br>Sequence 3317, A<br>Sequence 47534, A<br>Sequence 33002, A                                                                                                                                                                                                                                                                                                                                                                                               | Sequence 48119, A Sequence 6965, Ap Sequence 22, Appl Sequence 77, Appl                                                                                                                                                                                                                                                                                                       | equence                              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| US-09-004-729-81<br>US-09-800-729-86<br>US-09-270-767-32323<br>US-09-270-767-47540<br>US-08-485-4550-69<br>US-08-481-130C-69<br>US-08-484-211C-69<br>US-09-270-767-32670                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | US-09-270-767-61091<br>US-08-906-769-69<br>US-08-906-616-69<br>US-08-817-795-69<br>US-08-483-69<br>US-08-639-0755-69<br>US-09-012-431-69                                                                                                                                                                                                                                | US-09-012-692-69<br>US-08-906-613-69<br>PCT-US95-14442A-69<br>US-09-270-767-31777<br>US-09-270-767-46994<br>US-08-906-769-93                                                                                                                                                                                  | US-08-817-795-93<br>US-08-639-075A-93<br>US-09-012-431-93<br>US-09-012-692-93<br>US-08-906-613-93<br>PCT-US95-14442A-93                                                                                                                                                                       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US-08-485-4550-59<br>US-08-482-130C-59<br>US-08-482-131C-59<br>US-08-906-769-59<br>US-08-906-616-59<br>US-08-817-795-59<br>US-08-485-4438-59<br>US-08-639-075A-59                                                                                                                                                                                                                     | US-09-012-431-59<br>US-09-012-692-59<br>US-08-906-613-59<br>PCT-US95-14442A-59<br>US-09-270-767-32317<br>US-09-270-767-3334<br>US-09-270-767-33002                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                   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Appl<br>Sequence 81, Appl                                                                                                                                                                                                                                                                                                                                     | 15                                                                                 |
| Sequence 335k<br>Sequence 155k<br>Sequence 155k<br>Sequence 155k<br>Sequence 155k<br>Sequence 155k<br>Sequence 155k<br>Sequence 155k<br>Sequence 155k                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Sequence 155, Sequence 83, Sequence 97, Sequence 97, Sequence 97, Sequence 97, Sequence 97, Sequence 97,                                                                                                                                                                                                                                                                | Sequence 97<br>Sequence 97<br>Sequence 97<br>Sequence 48<br>Sequence 35<br>Sequence 54<br>Sequence 54                                                                                                                                                                                                         | Sequence 53<br>Sequence 53<br>Sequence 53<br>Sequence 53<br>Sequence 53                                                                                                                                                                                                                       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| 102 3 US-08-639-075A-125<br>102 3 US-09-012-431-125<br>102 3 US-09-012-629-125<br>102 3 US-08-906-613-125<br>64 1 US-08-482-135<br>64 2 US-08-482-130C-75<br>64 2 US-08-482-130C-75<br>64 3 US-08-906-616-75<br>64 3 US-08-906-616-75<br>64 3 US-08-906-616-75<br>64 3 US-08-906-616-75<br>64 3 US-08-906-616-75<br>64 3 US-08-906-616-75<br>64 3 US-08-817-795-75<br>64 3 US-08-817-795-75<br>64 3 US-08-817-795-75                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | RESULT 1 US-09-949-016-8151 Sequence 8151, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF TITLE OF INVENTION WITH HUMAN DISEASE, METHODS OF TITLE OF INVENTION WITH HUMAN DISEASE, METHODS OF TITLE OF INVENTION WINBER: US/09/949,016 CURRENT FILING DATE: 2000-04-14 FILE REFERENCE: 2000-10-20 PRIOR PELING DATE: 2000-10-20 PRIOR PELING DATE: 2000-10-03 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012 SEQ ID NO 8151 LINGUTH: 249 TYPE: PRI TYPE: PRI HUMAN US-09-949-016-8151                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 98.9%; Score 1359.5; DB 4; 99.6%; Pred. No. 3.1e-124; vative 0; Mismatches 0; CVLGLSQAATPKIFNGTECGRNSQPWQVGLF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| 88<br>88<br>88<br>88<br>88<br>88<br>88<br>87<br>77<br>77                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 6-8151<br>6812339<br>6812339<br>FORMATION:<br>INVENTION:<br>INVENTION:<br>INVENTION:<br>INVENTION:<br>INVENTION:<br>INVENTION:<br>INVENTION:<br>INVENTION:<br>INVENTION:<br>INVENTION:<br>INTERNIT ON INTERNIT ON ING DATE:<br>ING DATE | Ch<br>1 Similarity<br>247; Conser<br>1 MGLSIFLLL<br>3 MGLSIFLLL<br>61 AHCSGSRYW<br>63 AHCSG-RYW<br>21 TSNVQPLPI<br>22 TSSQPLPI<br>22 TSSQPLPI<br>24 TSNWVCAGG<br>81 TSNWVCAGG<br>82 TSNWVCAGG<br>84 TSNWVCAGG<br>84 TSNWVCAGG<br>85 TSNWVCAGG<br>86 TSNWVCAGG<br>87 TSNWVCAGG<br>87 TSNWVCAGG<br>86 TSNWVCAGG<br>87 TSNWVCAGG<br>86 TSNWVCAGG<br>87 TSNWVCAGG<br>86 TSNWVCAGG<br>87 TSNWVCAGG<br>87 TSNWVCAGG<br>88 TSNWVCAGG<br>89 TSNWVCAGG<br>80 TSNWVCAGG<br>80 TSNWVCAGG<br>81 TSNWVCAGG<br>81 TSNWVCAGG<br>81 TSNWVCAGG<br>82 TSNWVCAGG<br>83 TSNWVCAGG<br>84 TSNWVCAGG<br>86 TSNWVCAGG<br>86 TSNWVCAGG<br>87 TSNWVCAGG<br>87 TSNWVCAGG<br>88 TSNWVCAGG<br>86 TSNWVCAGG<br>87 TSNWVCAGG<br>86 TSNWVCAGG<br>87 TSNWVCAGG<br>87 TSNWVCAGG<br>88 TSNWVCAGG<br>88 TSNWVCAGG<br>88 TSNWVCAGG<br>89 TSNWVCAGG<br>80 TSNW                                                                                                                                                                                                             |
| 1488<br>1489<br>1490<br>1491<br>1492<br>1493<br>1495<br>1496<br>1496<br>1499<br>1499<br>1500                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | RESULT 1 US-09-949-016 Sequence 81 Patent No. GENERAL INF TITLE OF I FILTE OF I FILT OF I FILTE OF I FILT OF I                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Query Match Best Local Simil Matches 247; C Qy 1 MGLS Qy 61 AHCS Qy 61 AHCS Qy 121 TSSV Qy 122 TSSV Qy 181 TSNW Qy 182 TSNW Qy 241 IRMI Db 182 CSNM Qy 241 IRMI Db 242 IRMI Db 242 IRMI Db 269-949-016-6948 ; Sequence 648, A ; Patent No. 68123 ; GENERAL INFORMATA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
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| Sequence 77 Sequence 77 Sequence 10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    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| 2-77<br>42-77<br>42-77<br>42-77<br>42-101<br>5-101<br>5-101<br>5-101<br>1-101<br>1-101<br>1-101<br>1-101<br>5-99                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       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5.613-109<br>-0.0442A-109<br>-0.0442A-109<br>-0.01-14<br>-0.01-14<br>-1.07-14<br>-1.07-14<br>-1.07-14<br>-1.07-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1.09-14<br>-1. |
| 5.09-012-693<br>-08-906-611<br>-08-906-764<br>-08-906-764<br>-08-906-611<br>-09-012-431<br>-09-012-693<br>-09-012-693<br>-09-012-693<br>-09-012-693<br>-09-012-693<br>-08-906-765<br>-08-906-765                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 7.00 - 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| 1415<br>1416<br>1417<br>1418<br>1420<br>1421<br>1423<br>1426<br>1426<br>1426                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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121 TSSVOPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI 180
 95 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW 154
 62 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGPSVTHPGYLGAST-SHEHDLRLLRLRLPVRV 120
 73 HCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLLQLRDQASL 132
 181 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW 240
 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 5 IFLLL --- CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
 GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: O'Brien, Timothy J.

APPLICANT: Underwood, Lowell J.

TITLE OF INVENTION: NO. 6442013el Extracellular Serine Protease
FILE REFERENCE: D6020CIP2

CURRENT APPLICATION NUMBER: US/09/618,259

CURRENT FILING DATE: 2000-07-18

PRIOR PILING DATE: 1998-08-21

NUMBER OF SEQ ID NOS: 72

LENGTH: 260
 Query Match 45.9%; Score 630.5; DB 4; Length 260; Best Local Similarity 50.2%; Pred. No. 2.5e-53; Matches 123; Conservative 24; Mismatches 93; Indels 5;
 ; FEATURE:
; OTHER INFORMATION: Amino acid sequence of TADG-14 protein
US-09-618-259-7
 GENERAL INFORMATION:
APPLICANT: SOUTHAN, CHRISTOPHER
APPLICANT: CLINKENBEARD, HELEN
APPLICANT: BURGESS, NICOLA
TITLE OF INVENTION: No. 6100059el Compounds
 Sequence 7, Application US/09618259 Patent No. 6642013
 Sequence 2, Application US/09070526; Patent No. 6100059
 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & E
STREET: P.O. BOX 980
 TYPE: PRT
ORGANISM: Homo sapiens
 241 IRMIMRNN 248
 155 IRMIMRNN 162
 241 IRMIM 245
 |: |:
252 IKKII 256
 US-09-618-259-7
 US-09-070-526-2
 181
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
 61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV 120
 61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV 120
 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI 180
 180
 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV 120
 9
 9
 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA 60
 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
 181 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYIC 235
 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYIC 235
 APPLICANT: Mi, et al.
TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides
TITLE REPERENCE: PP391
CURRENT APPLICATION WHERE: US/09/244,111
CURRENT FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 60/073,961
EARLIER APPLICATION NUMBER: 60/073,961
SARLIER OF FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
 59.0%; Score 811; DB 4; Length 162;
64.1%; Pred. No. 3.8e-71;
iive 0; Mismatches 3; Indels 86;
 ö
 Length 254;
 0; Indels
 94.7%; Score 1301; DB 4; I 100.0%; Pred. No. 1.5e-118; ive 0; Mismatches 0;
 CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 06/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 6948
 ; Sequence 6, Application US/09244111; Patent No. 6566498; GENERAL INFORMATION:
 Matches 235; Conservative
 Query Match
Best Local Similarity 64.1;
Matches 159; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
US-09-244-111-6
 Query Match
Best Local Similarity
 ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6948
 SEQ ID NO 6
LENGTH: 162
 121
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13 HCKKKYSVRLGDHSLQSRDQPEQEIQVAQSIQHPCYNNSNPEDHSHDIMLIRLQNSANL 132
 192
 181 TSNMYCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYYDW 240
 62 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-TSHEHDLRLLRLRLPVRV 120
 13 ILLILEWGAWAGLIRAQGSKILBGRECI PHSQPWQAALFQGERLICGGVLVGDRWVLTAA 72
 133 GDXVKPVQLANLCPKVGQKCIISGWGTVTSPQENFPNTLNCAEVKIYSQNKCERAYPGKI
 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 5 IFLLLCV----LGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
 Length 260;
 Indels
 Query Match
45.3%; Score 622.5; DB 3;
Best Local Similarity 49.0%; Pred. No. 1.5e-52;
Matches 121; Conservative 28; Mismatches 93;
 TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
FILING DATE:
 PF-0481 US
 APPLICANT: Bandman, Olga
Hillman, Jennifer L.
 Sequence 7, Application US/09008271A Patent No. 6203979 GENERAL INFORMATION:
 CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER:
FILING DATE:
NAME: Bilings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ.0555
TELEX:
INFORMATION FOR SEQ ID NO: 3:
INFORMATION FOR SEQ ID NO: 3:
 Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
 COUNTR.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 SEQUENCE CHARACTERISTICS:
LENGTH: 260 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
 241 IRMIMRN 247
 252 IKKTMDN 258
 LIBRARY: GenBank
CLONE: 1020091
Palo Alto
 US-09-008-271A-7
 US-09-025-059-3
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 62 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAST-SHEHDLRLLRLRLPVRV 120
 73 HCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLLQLRDQASL 132
 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI 180
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 5 IFLLL---CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
 Query Match
45.6%; Score 626.5; DB 3; Length 260;
Best Local Similarity 50.4%; Pred. No. 6.2e-53;
Matches 122; Conservative 23; Mismatches 92: Indels 5
 US-09-025-059-3

Sequence 3, Application US/09025059

Patent No. 6075136

GENERAL INFORMATION:

APPLICANT: Corley, Neil C.

APPLICANT: Guegler, Karl J.

TILLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
 OCHEVIES TAND CONDUCTOR OF CONTROLL OF CONTROLS AND CONTROLS AND CONTROLS AND CONTROLS OF CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,526
FILING DATE: 30-APR-1998
CLASSIFICATION NUMBER: GB 9711952.3
APPLICATION NUMBER: GB 9711952.3
APPLICATION NUMBER: BP 97309646.4
FILING DATE: 1-DEC-1997
APPLICATION NUMBER: BP 97309646.4
FILING DATE: 1-DEC-1997
APPRICATION NUMBER: BP 97309646.4
FILING DATE: 1-DEC-1997
APPRICATION NUMBER: BP 97309646.4
FILING DATE: 1-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
TELEPHONE: 610-407-0701
 TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
 LENGTH: 260 amino acids TYPE: amino acid
 STREET: 3174 Porter Dr
 TOPOLOGY: linear MOLECULE TYPE: protein
VALLEY FORGE
 STRANDEDNESS:
 241 IR 242
 252 İK 253
 19482
 US-09-070-526-2
 181
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Gaps

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62 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-TSHEHDLRLLRLRLPVRV 120
 73 HCKKOKYSVRLGDHSLQSRDQPEQEIQVAQSIQHPCYNNSNPEDHSHDIMLIRLQNSANL 132
 181 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW 240
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 5 IFLLLCV---LGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
 Amino acid sequence of mouse neuropsin homologous to TADG-14; accession no. D30785
 DB 4; Length 260;
 Query Match 45.3%; Score 622.5; DB 4; Length Best Local Similarity 49.0%; Pred. No. 1.5e-52; Matches 121; Conservative 28; Mismatches 93; Indels
 APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
 APPLICATION NUMBER: PCT/US98/11422
FILING DATE: 1998-06-04
 CURRENT APPLICATION NUMBER: US/09/205,258
 PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR FILING DATE: 1998-08-21
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 8
 EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,880
 APPLICATION NUMBER: 60/048,896
FILING DATE: 1997-06-06
 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,884
 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
 APPLICATION NUMBER: 60/048,971
FILING DATE: 1997-06-06
 APPLICATION NUMBER: 60/049,020
 APPLICATION NUMBER: 60/048,895
 APPLICATION NUMBER: 60/048,964
 Sequence 427, Application US/09205258 Patent No. 6525174
2000-07-18
 FILING DATE: 1997-06-06
 FILING DATE: 1997-06-06
 FILING DATE: 1997-06-06
 APPLICATION NUMBER: 60/
 241 IRMIMRN 247
 252 İKKTMDN 258
CURRENT FILING DATE:
 OTHER INFORMATION:
OTHER INFORMATION:
US-09-618-259-8
 TYPE: PRT ORGANISM: Mus sp.
 US-09-205-258-427
 FEATURE
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 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW 240
 62 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAST-SHEHDLRLLRLPVRV 120
 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI 180
 72
 5 IFLLL----CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
 .,
 Sequence 8, Application US/09618259
Patent No. 6642013
GENERAL INFORMATION:
APPLICANT: Underwood, Lowell J.
APPLICANT: Underwood, Lowell J.
APPLICANT: Underwood, Lowell J.
APPLICANT: Underwood, Lowell J.
APPLICANT: UNDERWOOD, LOWELL J.
FILE REFERENCE: D60201P2 CURRENT APPLICATION NUMBER: US/09/618,259
 Length 260;
 94; Indels
 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
 CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: «Unknown>
FILING DATE: «Unknown>
ATTORNEY/ABONT INFORMATION:
NAME: MOHAN-PETEREON, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
 Score 622.5; DB Pred. No. 1.5e-52
 24; Mismatches
 CLONE: 1798496
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 LENGTH: 260 amino acids
TYPE: amino acid
STRANDEDNESS: single
 MEDIUM TYPE: Diskette
 INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS
 Query Match
Best Local Similarity 49.8%;
SEQUENCES: 24
 LIBRARY: COLNNOT27
 ZIP: 94304
COMPUTER READABLE FORM:
 Matches 122; Conservative
 COPOLOGY: linear
 CITY: Palo Alto
STATE: CA
 COUNTRY: USA
 IMMEDIATE SOURCE:
 241 IRMIM 245
 ikkii 256
NUMBER OF
 US-09-008-271A-7
 RESULT 8
US-09-618-259-8
 181
 252
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183 TDTWVCASVQEGGKDSCQGDSGGPLVCNQSLQGIISWGQ-DPCAITRKPGVYTKVCKYVD 241
63 CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSI 122
 181 TSNMVCAG-GVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVD 239
 63 CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPVRV 120
 3 LSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 45.0%; Score 618.5; DB 3; Length 282;
48.2%; Pred. No. 4.1e-52;
tive 35; Mismatches 89; Indels 5.
 Sequence 1, Application US/09025059
Patent No. 6075136
GENERAL INFORMATION
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TILLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 SOFTWARE: FASTEM: DOS SOFTWARE: PASTESO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/025 new
 STREET: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto STATE: CA COUNTRY: USA ZID.
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHRACATERISTICS: LENGTH: 282 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE:
 IBM Compatible
 Best Local Similarity 48.23
Matches 120; Conservative
 TELEFAX: 650-845-4166
TELEX:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 PRIOR APPLICATION DATA: APPLICATION NUMBER:
 240 WIRMIMRNN 248
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242 WIQETMKNN 250
 RY: LUNGTUT10
: 2723646
 COMPUTER: IBM CON OPERATING SYSTEM:
 FILING DATE:
CLASSIFICATION:
 94304
 LIBRARY:
 US-09-025-059-1
 US-09-025-059-1
 Query Match
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 CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPVRV 120
 62
 3 LSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
 2,
 45.0%; Score 618.5; DB 4; Length 250; 48.2%; Pred. No. 3.5e-52;
 Indels
 3.5e-52
 ; Pred. No. 3.5e
35; Mismatches
 EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,893
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,900
FILING DATE: 1997-06-06
 APPLICATION NUMBER: 60/049,374
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,917
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,949
 PLICATION NUMBER: 60/048,882
LING DATE: 1997-06-06
 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,915
 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,019
 PILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,883
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,897
FILING DATE: 1997-06-06
 PLICATION NUMBER: 60/048,970
 APPLICATION NUMBER: 60/048,972
FILING DATE: 1997-06-06
 LICATION NUMBER: 60/048,916
 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,373
 APPLICATION NUMBER: 60/048,875
FILING DATE: 1997-06-06
 APPLICATION NUMBER: 60/048,898
FILING DATE: 1997-06-06
 APPLICATION NUMBER: 60/048,962
FILING DATE: 1997-06-06
 APPLICATION NUMBER: 60/048,963
FILING DATE: 1997-06-06
 APPLICATION NUMBER: 60/048,877
FILING DATE: 1997-06-06
 PLICATION NUMBER: 60/048,899
 APPLICATION NUMBER: 60/048,901
FILING DATE: 1997-06-06
 PLICATION NUMBER: 60/048,892
 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,974
 ILING DATE: 1997-06-06
 LING DATE: 1997-06-06
 SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 427
 Best Local Similarity 48.2
Matches 120; Conservative
 ORGANISM: Homo sapiens
 US-09-205-258-427
 63
 Query Match
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847/938-2623
 TELEFAX:
 US-08-944-483-24
 138
SEQ ID NO 14
 Query Match
 FEATURE:
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 180
 ECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVPGQDACQG 198
 171 KCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQITDGWVCAGSSKGADTCQG 230
 51 KIVGGYNCLEPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQN 110
 80 LDWTEQIRHSGFSVTHPGYLGAST-SHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGT 138
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSI 154
 79
 TSNMVCAG-GVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVD
 21 KIFNGTEC-GRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQ
 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 Gaps
 OTHER INFORMATION: Description of Artificial Sequence: Fusion gene OTHER INFORMATION: with homo sapien serine protease catalytic domain
 3;
 Query Match 43.9%; Score 602.5; DB 4; Length 288; Best Local Similarity 51.1%; Pred. No. 1.5e-50; Matches 116; Conservative 21; Mismatches 87; Indels 3.
 DSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIM 245
 APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
APPLICANT: Andreade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386, 642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
 APPLICANT: Darrow, Andrew
APPLICANT: Oi. Jenson
APPLICANT: Qi. Jenson
APPLICANT: Andrade-Gordon, Patricia
TILE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
NUMBER OF SEQ ID NOS: 60
 sequence 13, Application US/09386642
Patent No. 6420157
 Sequence 14, Application US/09386642; Patent No. 6420157; GENERAL INFORMATION:
 ORGANISM: Artificial Sequence
 SOFTWARE: Patentin Ver. 2.0
 WIRMIMRNN 248
 ||: |:||
274 WIQETMKNN 282
 GENERAL INFORMATION:
 US-09-386-642-14
 US-09-386-642-13
 SEQ ID NO 13
95
 121
 155
 240
 111
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 181
 TYPE: PRT
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USEFUL FOR DETECTING AND TREATING DISEASES
 51 XIVGGYNCLEKKIQQPWQAALFEKTRLLCGATLIAPRWLLTAAHCLKPRYIVHLGQHNLQK 110
 TECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAG-GVPGQDAC 196
 80 LDWTEQIRHSGFSVTHPGYLGA - STSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAG
 21 KIFNGTEC-GRNSOPWOVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQ
 ; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-14
 197 QGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMINRNN 248
 43.6%; Score 598.5; DB 4; Length 289; 49.1%; Pred. No. 3.8e-50; Live 34; Mismatches 79; Indels 5.
 NOVEL SERINE PROTEASE REAGENTS
 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
 NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION:
TELEPHONE: 847/935-1729
 TITLE OF INVENTION: NOVEL SERINE PRO
TITLE OF INVENTION: AND METHODS USE:
TITLE OF INVENTION: OF THE PROSTATE
 NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: 1L
COUNTRY: USA
 Sequence 24, Application US/08944483 Patent No. 6232456
 APPLICANT: COLPITTS, TRACEY L.
APPLICANT: REBOMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
 COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GRANADOS, EDWARD N.
TYPE: PRT
ORGANISM: Artificial Sequence
 FILING DATE: ATTORNEY/AGENT INFORMATION:
 Best Local Similarity 49.18
Matches 114; Conservative
 ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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protein
 241 IRMIMRNN 248
 240 IQQTIAAN 247
MOLECULE TYPE:
 TYPE: PRT
ORGANISM: Human
 US-09-949-016-8166
 US-09-949-016-8166
 , rose-956-267A-2
 62
 122
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 180
 61 CLKPRYIVHLGQHNLQKEGGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSI 120
 239
 AUUKESSEE: No. 59453280 No. 5945328disk of No. 5945328th America, Inc. STREET: 405 Lexington Avenue CITY: New York
 CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPVRV 120
 62
 9
 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
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 Gaps
 7;
 DB 3; Length 248;
 Indels
 Sequence 2, Application US/08956267A
Patent No. 5945328
GENERAL INFORMATION:
APPLICANT: WOLDIKE, Helle Fabricius
APPLICANT: KJELDSEN, Thomas Borglum
TITLE OF INVENTION: A Process For Producing Trypsin
TITLE OF EQUENCES: 6
CORRESPONDENCE ADDRESS:
 Query Match
43.5%; Score 597.5; DB 3;
Best Local Similarity 47.8%; Pred. No. 3.9e-50;
Matches 119; Conservative 36; Mismatches 87;
 COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 22-OCT-1997
 4500.204-US
 ATTORNEY AGENT INFORMATION:
NAME: Rozek, Carol
REGISTRATION NUMBER: 36,993
 REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION:
TELEPHONE: 212-867-0123
 ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
US-08-944-483-24
 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 247 amino acids TYPE: amino acid
 INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
 ESS: single
linear
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 212-878-9655
 WIRMIMRNN 248
 ||: |:||
240 WIQETMKNN 248
 TYPE: amino acid
STRANDEDNESS: sin
 TYPE: amino acid
TOPOLOGY: linear
 CLASSIFICATION:
 USA
 10174
 COUNTRY:
 63
 121
 240
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JAPELCANTE VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PLING DATE: 2000-10-20

PRIOR PPLICATION NUMBER: 60/237,768

PRIOR PPLICATION NUMBER: 60/231,498

PRIOR PPLICATION NUMBER: 60/231,498

PRIOR PPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

SEQ ID NOS: 207012

SOFTWARE: PSESEQ for Windows Version 4.0

LENGTH: 290
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 240
 182 GNMICVGFLEGGKDSCQGDSGGPVVCNGQLQGIVSWGY--GCAQKNKPGVYTKVCNYVNW 239
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 90 CLKEGLKYYLGKHALGRVEAGEQVREVVHSIPHPEYRRSPTHLNHDHDIMLLELQSPVQL 149
 121 TSSVQPLPLP-NDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGR 179
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 61
 63
 6 FLLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
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 10;
 Length 247;
 Length 290;
 Indels
 41.7%; Score 573; DB 2; Le 45.6%; Pred. No. 9.3e-48; tive 42; Mismatches 83;
 80;
 41.3%; Score 567; DB 4;
46.8%; Pred. No. 4.4e-47;
iive 36; Mismatches 80
 Sequence 8166, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
Query Match
Best Local Similarity 45.6
Matches 113; Conservative
 Query Match
Best Local Similarity 46.8
Matches 116; Conservative
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239 DWIRMIMR 246 ||| :| 269 LWIRETIR 276 S &

Search completed: March 5, 2005, 20:45:52 Job time : 51 secs

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venombin A (EC 3.4
tissue kallikrein
chymase (EC 3.4.21
crogulation factor
plasmin (EC 3.4.21
granzyme A (EC 3.4
chymotrypsin (EC 3
coagulation factor
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pancreatic elastas
chymotrypsin (EC 3
coagulation factor
mast cell proteina
pancreatic elastas
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mast cell proteina
pancreatic elastas
 probable serine pr
complement factor
pancreatic elastas
chymotrypsin (EC 3
venombin A (EC 3.4
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trypsin (EC 3.4.21.1
tissue kallikrein
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kallikrein, glandu
venombin B (EC 3.4
snake venom factor
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Compugen Ltd.
 Total number of hits satisfying chosen parameters:
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 version :
 summaries
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TRBOTR

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| trypsin (EC 3.4.21 tensacin precursor Doc4 protein, stre streptogrisin C (E MEGF8 protein - hu nonstructural poly fibrillin 1 precur probable pepetidas hypothetical prote nerve growth facto                                                                                                                                                              | kallikrein - mouse<br>kallikrein - mouse<br>kallikrein-like se<br>differentiated ker<br>G surface protein<br>acetate kinase - b<br>probable secreted<br>G surface protein<br>hypothetical prote<br>IgG Fc binding pro<br>fibrillin I - bovi<br>hypothetical prote                                                                                      | hypothetical prote<br>integrin beta-6 ch<br>bullous pemphigoid<br>hypothetical prote<br>Putative protease<br>hypothetical prote<br>alpha-amlyase - De<br>hypothetical prote<br>proteinase (EC 3.4<br>hypothetical prote<br>staphylolytic prot<br>Lash proteinase pr<br>gelatin-binding 28<br>hypothetical prote<br>callaga proteinase pr                                                                                                                                                                                 | hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote collagen COLFI - 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bovin<br>alpha-2-macroglobu<br>secreted serine pr<br>hypothetical prote<br>thypothetical prote<br>thypothetical prote<br>hypothetical prote                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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| hypothetical prote<br>scavenger receptor<br>hypothetical 20k p<br>virk protein - Shi<br>probable regulator<br>imidazolonepropion<br>hypothetical prote<br>transcription fact<br>interleukin enhanc<br>adenine deaminase | adenine deaminase adenine deaminase hypothetical prote hypothetical prote outer membrane pro hypothetical prote collagen alpha 5(I epidermal growth genome polyprotein notch protein homo hypothetical prote CPY protein midg osmotin-like prote fructokinases homo GTP-binding protei probable GTP-bindia hypothetical prote cysteine protein probable GTP-bindia hypothetical protei grobable GTP-bindia collagen short cha alpha-lytic protei proteines cysteine proteines                                             | probable transcrip probable transcrip polyketide hydroxy hypothetical protection collagen alpha 1(v kinase-related tra collagen alpha 2(1 collagen alpha 1(1 collagen alpha 2 t chlorophyll a/b-bi collagen alpha 2 t chlorophyll a/b-bi collagen alpha 2 t chlorophyll a/b-bi collagen alpha cha hypothetical protehypothetical protehypothetical protehypothetical protehypothetical protehypothetical protehypothetical protehemagglutinin - 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| collagen alpha 1(I protein-tyrosine k hypothetical prote collagen alpha 3(I xin protein, stage hypothetical prote hypothetical prote hypothetical prote hypothetical prote cysteine proteinas                           | cysteine proteinas arylaulfatase acti succinate-semialde succinate-semialde cellulose 1,4-beta collagen alpha 1(X antigen Em100 - Ei iron-regulated out collagen alpha 1(X cerastocytin (EC 3 hypothetical prote probable secreted probable transmemb metalloproteinase melanoma-associate tryptophan synthas transcription acti hypothetical prote nitrate reductase 230k bullous pemph epidermal growth f collagen alpha 1(I genome polyprotein                                                                         | genome polyprotein intrinsic factor-B trypsin/factor XII probable chaperone probable chaperone molecular chaperone molecular chaperone dihydrodipicolinat hypothetical prote 2-nitrotoluene red probable secreted Regulator of chrom PF20 protein, micr telomerase catalyt procollagen type V glutamate synthase hypothetical prote probable (O-methylt hypothetical prote probable (O-methylt hypothetical prote Ubx protein - frui                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | integrin beta-6 ch protein F25E5.7 [i probable bacteriop receptor kinase-11 hypothetical prote jagged protein pre genome polyprotein genome polyprotein genome polyprotein genome polyprotein genome polyprotein collagen homolog A hypothetical prote chymotrypsin-like probable thigsulfa hypothetical prote probable infagilfa hypothetical prote probable indoleace cruciferin F2009.2 hypothetical prote env polyprotein pr                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
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| Ig heavy chain V4. probable galactosy mannose-binding le pulmonary surfacta osmotin precursor endonuclease IV [i hypothetical prote hypothetical prote hemaglutinin - in collagen alpha 1(I                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | collagen alpha 3(V ABC transporter (p cysteine proteinas hypothetical prote NR3-dependent NAD integrin beta-5 ch phosphoribosylform trophinin - human collagen alpha 1(X DNA-directed DNA p collagen alpha 1(I collagen alpha 1(I collagen alpha 1(I collagen alpha 1(I collagen alpha 1(I collagen alpha 1(I collagen alpha 1(I collagen alpha 1(I collagen alpha 1(I collagen alpha 1(I collagen alpha 1(I collagen alpha 1(I collagen alpha 1(I)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | tenascin-C human pseudo-kallikrein finger protein (cl mannose-binding le hypothetical prote hypothetical prote hypothetical prote hypothetical prote guanine nucleotide molybdopterin bios cytochrome c-type hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote beta transducin - 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sm<br>collagen alpha 1 (I<br>hypothetical prote<br>laminin beta-1 cha                               | genome polyprotein genome polyprotein protein-tyrosine-p ALR protein - huma ALR protein - huma ALR protein - huma ALR protein - huma Erredoxin XF1964 vasotoin 2 / neur pathogenesis-relat comotin-like prote collagen alpha 1 (v hypothetical prote fructokinases homo hypothetical prote hypothetical prote probable aryl alco conserved hypothet                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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| beta-glucuronidase<br>hypothetical prote<br>Delta-4 protein -<br>nitrate reductase<br>arginine decarboxy<br>hypothetical prote<br>hypothetical prote<br>probable N-methyl-<br>collagen alpha cha | mucin - rac<br>collagen alpha 2 c<br>fibropellin ia - s<br>DNA-binding protei<br>major DNA-binding<br>collagen alpha 2{I<br>collagen alpha 1(I<br>probable ctpI prot | adenylate cyclase collagen alpha 1(X collagen type I(Y collagen alpha 1(X collagen alpha 1(X collagen alpha 1(X collagen alpha 1(X denome polyprotein Xotch protein - Af hemagglutinin-like complement factor pancreatic ribonuc | ig heavy chain V r Ig heavy chain V r Ig heavy chain V r hypotherical prote osmotin - common t mannose-binding le hypotherical prote hypotherical prote hypotherical prote conserved hypotherical prote hypotherical prote hypotherical prote hypotherical prote hypotherical prote hypotherical prote hypotherical prote hypotherical prote hypotherical prote probable DMA-bindichtinase (BC 3-2.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | circumsporozoite p<br>hypothetical prote<br>hypothetical prote<br>sodium/proline sym<br>serine proteinase<br>hypothetical serin<br>probable membrane<br>alpha-glucosidase<br>maltooligosyltreha<br>metalloproteinase<br>growth arrest-spec<br>collagen alpha 3(1<br>Delta-4 protein -<br>hypothetical prote                                                                                                                                                                                                                                                                                                                                                                                                   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| beta-lact                | 1490<br>1491                         | 629                    | v v               | 552                | 0 0<br>0 0     | C86171<br>S69889                                                                   | hypothetical prote<br>hemagglutinin prec                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| ical prote               | 1492                                 |                        | ιύn               |                    |                | 20885                                                                              | hydrogenase-2 larg                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
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| ical prote dinitrifi     | 1495<br>1496                         |                        | vίν               |                    |                | JN0877<br>T51880                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| rrest-spec               | 1497<br>1498                         |                        |                   |                    |                | AB0548<br>JC7705                                                                   | PrpE protein [impo<br>death receptor-6 -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| polyribon                | 1499                                 | 62                     |                   |                    |                | S22293                                                                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ke 1 - mou               |                                      | ,<br>,                 |                   |                    |                | 1                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| procein -<br>precursor   |                                      |                        |                   |                    |                | ALIGNMENTS                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Deta-5 cn<br>  salt-indu |                                      |                        |                   |                    |                |                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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| te-Peyer's               | neuropsin -                          | - mouse                | :                 |                    |                |                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ical prote<br>unc-52 [im | C;Species:<br>C:Date: 26-            | Mus musc<br>Jul-1996   | ulus (?<br>#seque | ouse               | mou<br>revi    | se)<br>sion 26-Jul-1996 #1                                                         | C;Species: Mus musculus (house mouse)<br>C:Date: 26-Jul-1996 #seguence revision 26-Jul-1996 #text change 09-Jul-2004                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| precursor                | C; Accession                         | 1: I56559              |                   | 1                  |                |                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| dependent                | J. Neurosci                          | .,; rosni<br>[. 15, 50 | 88-5097           | , 19               | 4<br>6<br>6    | ; Momota, I.; suz                                                                  | uki, U.; idnaka, I.; iCO, U.; Nishin                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| dependent                | A; Title: Ex                         | cpression              | and ac            | tivi               | ty-d           | ependent changes of                                                                | f a novel limbic-serine protease gene                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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| like growt               | A;Status: F                          | relimina               | iry; tra          | nsla               | red            | from GB/EMBL/DDBJ                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ical prote               | A; Residues:                         | 1-260 <                | RES>              |                    |                |                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| e (EC 3.4.               | A; Cross-ref                         | erences:               | UNIPRC            | T:06:              | 1955           | , GB:D30785; NID:g                                                                 | 1648847; PIDN:BAA06451.1; PID:g10200!                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| chain V r                | C; Superrami<br>F; 33-252/Dc         | ly: cryp<br>main: tr   | ypsin h           | ypsi               | 04 <u>7</u> 60 | mology<br><try></try>                                                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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| secretory                | Matches                              | 121; Cc                | ğ                 | ive                | ₩.             | Mismatc                                                                            | ; Indels 5; Gaps 3;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| ion-relace               | δλ                                   | S IFLL                 | CVLG              | LSOA               | ATPK           | IFNGTECGRNSQPWQVGL                                                                 | IFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA 61                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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| ical prote               | 3                                    |                        | or recording      |                    | Š              | T TROUBELL FINS OF TRANSPORT                                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ical prote               | Š                                    | 62 HCSGS               | RYWVRLO           | EHSL               | SOLD<br>-      | WTEQIRHSGFSVTHPGYL(                                                                | HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-ISHEHDLRLLRLRLPVRV 120                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| d hypothet               | qq                                   | 73 HCKK                | KYSVRLO           | DHSL(              | SRD            | PEQEIQVAQSIQHPCYN                                                                  | HCKKÇKYSVRLGDHSLQSRDQPEQEIQVAQSIQHPCYNNSNPEDHSHDIMLIRLQNSANL 132                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| B22C12.24                |                                      | 121 TSSVC              | INd'Id'Id         | CATA               | REC            | HVSGWGI TNHPRNPFPDL                                                                | TSSVOPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLOCLNLSIVSHATCHGVYPGRI 180                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| transcrip                |                                      |                        |                   | ģ                  | ;              | :          :                                                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ical prote               | Dp 1                                 | 133 GDKVR              | PVQLANI           | CPKV               | SKG            | I I SGWGTVTS PQENF PNT)                                                            | GDKVKPVQLANLCPKVGQKCIISGWGTVTSPQENFPNTLNCAEVKIYSQNKCERAYPGKI 192                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| ical prote               | ,<br>%                               | 181 TSNMV              | CAGGVPC           | ODAC               | SGDS           | SGPLVCGGVLQGLVSWGS                                                                 | TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW 240                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| ical prote<br>transport  | Db 1                                 | <br>193 TEGMV          | <br> CAGSSNO      | ADTC(              |                |                                                                                    | TEGWYCAGSSNGADTCOGDSGGPLVCDGMLOGITSWGS-DPCGKPEKPGVYTKICRYTTW 251                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| tein - Eme               |                                      |                        |                   |                    |                |                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| CDF-6-deo                | à                                    | 241 IKMIMKN            | KN 247            |                    |                |                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ical prote               | Dp                                   | 252 IKKTMDN            | IDN 258           |                    |                |                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| chain (5.                |                                      |                        |                   |                    |                |                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| troyemase<br>tein D pre  | RESULT 2                             |                        |                   |                    |                |                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| oacyl-[ACP               | SSSOG6                               | 1 3 4 21               | 4) TT r           | יניספר             | raor           | pancreatic (clone                                                                  | e 2-P29) - chicken                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|                          | N, Alternate                         | names:                 | trypsir           | ogen               | H              |                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ical prote               | C,Species:<br>C:Date: 23-            | Gallus g<br>Aug-1995   | allus (           | chic               | ken)<br>revi   | sion 19-Oct-1995 #1                                                                | text change 09-Jul-2004                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| naj pe                   | C, Accession                         | 355066                 | , \$7234          | 7                  |                | •                                                                                  | 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|                          | R; Wang, K.;<br>Biochem. J.          | 307, 47                | ; Lee,<br>1-479,  | I.; I<br>1995      | 900H           | i                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|                          | A, Title: IE                         | solation               | and cha           | ract               | eriz           | ation of the chicken                                                               | en trypsinogen gene family.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|                          | A; Accession                         | : S55066               | 390448            | Σ                  | 5.01           | A; Reference number: S55065; MUID: 95251611; FMID: //33865<br>A; Accession: S55066 | 688                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|                          | A; Molecule                          | type: mR               | INA<br>WAN1       |                    |                |                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Tycerate m               | A; ACBICACO                          | 0 2 2 1                | V TATEM.          |                    |                |                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |

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40.8%;
 236 KYVDWIRMIMRNN 248
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236 NYVSWIKTTMSSN 248
 Query Match
Best Local Similarity
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A;Cross-references: UNIPROT:Q90629; EMBL:U15157; NID:g603906; PIDN:AAA79914.1; PID:g6039
A;Experimental source: clone 2-P29
A;Accession: S72347
 trypsin (EC 3.4.21.4) I precursor, pancreatic - chicken
NyAlternate names: trypsingen I
C,Species: Gallus gallus (chicken)
C,Species: Gallus gallus (chicken)
C,Species: Gallus gallus (chicken)
C,Species: Gallus gallus (chicken)
C,Species: Gallus gallus (chicken)
C,Species: Gallus gallus (chicken)
C,Species: Gallus gallus (chicken)
C,Species: Gallus gallus
R,Wang, K.; Gan, L.; Lec.
Biochem. J. 307, 471-479, 1955
Biochem. J. 307, 471-479, 1955
A;Title: Isolation and characterization of the chicken trypsinogen gene family.
A;Reficueron number: SSSO65; MUID:95251611; PMID:7733885
A;Residues: 1-248 «WAMA)
A;Residues: 1-248 «WAMA>
A;Residues: 1-248 «WAMA>
A;Residues: 1-248 «WAMA>
A;Residues: 1-248 «WAMA>
A;Residues: 1-248 «WAMA>
A;Residues: 1-248 «WAMA>
A;Residues: 1-248 «WAMA>
A;Residues: 1-248 «WAMA>
A;Residues: 1-248 «WAMA>
A;Residues: 1-29, VV., 11-12, Tr., 14-102, A,,104-214, Tr.,216-248 «WAMA>
A;Residues: 1-3, VV.,11-12, Tr.,14-102, A,,104-214, Tr.,216-248 «WAMA>
A;Residue: 1-3, VV.,11-12, Tr.,14-102, A,,104-214, Tr.,216-248 «WAMA>
A;Re
 Afforcation of the state of the
 238
 60 AAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVR 119
 63 AAHCYKSRIQVRLGEYNIDVQEDSEVVRSSSVIIRHPKY--SSITLNNDIMLIKLASAVE 120
 120 VTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGR 179
 181 ITSNMICVGFLEGGKDSCQGDSGGPVVCNGELQGIVSWG-IG-CALKGYPGVYTKVCNYV 238
 62
 180 ITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYV
 5 IFLLLCVLGLS-----QAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT
 Gaps
 11;
 Query Match
41.4%; Score 569.5; DB 2; Length 248;
Best Local Similarity 47.5%; Pred. No. 6e-39;
Matches 116; Conservative 39; Mismatches 78; Indels 11.
 239 DWIR 242
 239 DWIQ 242
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Trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)

N;Contains: trypsinogen
C;Species: Sus scrotd domestica (domestic pig)
C;Species: Sus scrotd domestica (domestic pig)
C;Species: Sus scrotd domestica (domestic pig)
C;Species: Na; Rovery, M.; Guidoni, A.; Desnuelle, P.
Biochim. Biophys. Acta 69, 115-12, 1963
A;Title: Su le trypsinogene et la trypsine de porc.
A;Reference number: A90641
A;Accession: A90641
A;Accession: A90641
A;Reference number: Lo CHA>
A;Cross-references: UNIPROT:P00761
A;Reference number: A90369, M.H.; Neurath, H.; Walsh, K.A.
Biochemistry 12, 3146-3153, 1973
A;Title: Determination of the amino acid sequence of porcine trypsin by sequenator analys
A;Reference number: A90368, MUID:73258692; PMID:4738933
A;Accession: A90368
A;Molecule trype: protein
A;Residues: 9-231 - HER>
A;Note: at position 20, Ile and Val occur alternatively
C;Superfamily: trypsin, trypsin demology
C;Superfamily: trypsin fastuus experimental - APT>
F;1-231/Product: trypsin sequence experimental - APT>
F;2-231/Product: trypsin secuence experimental - APT>
F;2-231/Product: trypsin sequence experimental - APT>
F;2-231/
 9
A,Accession: S71155
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Cross-references: 1-102,'A',104-248 cWAN5>
A,Cross-references: EMBL:U15156; NID:g603904; PIDN:AAA79913.1; PID:g603905
A,Experimental source: clone 1-P38
C,Superfamily: trypsin homology
C,Superfamily: trypsin process; protein digestion; serine proteinase; zymogen
F,1-15/Domain: signal sequence #status predicted <SIG>F,16-25/Domain: activation peptide #status predicted <APT>F,26-244/Product: trypsin pemology <TRX>
F,26-244/Domain: trypsin homology <TRX>
F,56-241/Domain: trypsin homology <TRX>
F,56-241/Domain: Appsin Mathematical Asp, Ser #status predicted
 60 VLSAAHCYKSSIQVKLGEYNLAAQDGSEQTISSSKVIRHSGY--NSNTLNNDIMLIKLSK 117
 57 VLTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRL 116
 17 PVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVY 176
 177 PGRITSNMVCAGGV-PGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYIC 235
 23
 1 MKFLVLVAFLGVAVAFPISDEDDDKIVGGYSCARSAAPYQVSLNSGYHF-CGGSLISSQW
 3 LSIFLLLCVLG-----LSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRW
 12; Gaps
 Length 248;
 Length 231;
 Query Match
41.3%; Score 567; DB 2; Length 24:
Best Local Similarity 45.5%; Pred. No. 9.6e-39;
Matches 115; Conservative 38; Mismatches 88; Indels
 Score 561; DB 1;
Pred. No. 2.7e-38;
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C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A5368
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J;Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Acession: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Atatus: preliminary
A;Molecule type: mRNA
A;Kesidues: 1-253 cHAN>
A;Coss-references: UNIFROT:P49862; GB:L33404; NID:g521214; PIDN:AAC37551.1; PID:g532504
C;Genetics: PRESS SCCE
A;Coss-references: GDB:37730
A;Coss-references: GDB:37730
A;Map position: 7q35-7q35
C;Superfamily: trypsin homology cTRY>
F;30-245/Domain: trypsin homology cTRY>
 Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cibate: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
Ciscession: B2528
Ristevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A; Ritle: Sequence organisation and transcriptional regulation of the mouse elastase II an A; Reference number: A93646; MUD:87066713; PMID:3641189
A; Reference number: A93646; MUD:87066713; PMID:3641189
A; Residues: 1-246 <STE>
A; Residues: 1-246 <STE>
A; Residues: In-246 <STE>
A; Residues: Calcium binding; hydrolase; protein digestion; serine proteinase
C; Superfamily: trypsin, homology or RYA>
C; Superfamily: trypsin #status predicted <SIG>
F; 24-2346/Product: trypsin #status predicted <AMAT>
F; 24-2346/Product: trypsin #status predicted <AMAT>
F; 24-2346/Product: trypsin #status predicted <AMAT>
F; 24-2346/Ardive site: His, Asp, Ser #status predicted
F; 30-160, 48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F; 75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
 ..
 9
 DHRWVLTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLL 112
 RLRLPVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATC 172
 234
 9
 HGVYPGRITSNMVCAGGVPG--QDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGV
 -----QAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLI
 Gaps
 14; Gaps
 16;
 Length 253;
 90; Indels
 40.2%; Score 553; DB 2; 44.7%; Pred. No. 1.3e-37;
 40.4%; Score 555; DB 2;
44.6%; Pred. No. 9.2e-38;
iive 37; Mismatches 90
 45; Mismatches
 trypsin (EC 3.4.21.4) precursor - mouse
 YTYICKYVDWIRMIMRNN 248
 YTQVCKFTKWINDTMKKH 252
 Best Local Similarity 44.6
Matches 115; Conservative
 1 MGLSIFLLLCVLGLS-
 Matches 113; Conservative
 Local Similarity
 23
 113
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 A; Molecule Lype: mRNA
A; Residues: 1-243 <5H15
A; Residues: 1-243 <5H15
A; Cross-references: UNIPROT: P19799; EMBL: X53458; NID: g65162; PIDN: CAA37538.1; PID: g65163
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin digestion; serine proteinase
F; 1-15/Domain: signal sequence #status predicted <5IG>
F; 16-20/Domain: activation peptide #status predicted <APT>
F; 12-236/Domain: trypsin homology <ffree firsts.
 trypsin (EC 3.4.21.4) precursor, pancreatic - African clawed frog C;Species: Xenopus laevis (African clawed frog)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C;Accession: A55871; S12117
R;Shi, Y.B.; Brown, D.D.
Genes Dev. 4, 1107-1113, 1990
A;Title: Developmental and thyroid hormone-dependent regulation of pancreatic genes in A;Reference number: A35871; MUID:91007255; PMID:2210372
A;Accession: A35871
 140
 124
 184
 CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTS 122
 CYKASIQVRLGEHNIALSEGTEQPISSSKVIRHSGY--NSYTLDNDIMLIKLSSPASLNA 118
 182
 241
 HVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVP-GQDACQGD 199
 179 NMICVGYMEGGKDSCQGDSGGPVVCNGQLQGVVSWGY--GCAMRNYPGVYTKVCNYNAWI 236
 99
 62
 9
 FLLLCVL-LGAAAAFDDDKIIGGATCAKSSVPYIVSLNSGYHF-CGGSLIINQWVVSAAH
 SVQPLPLPNDCATAGTECHVSGWGITNHPRNPPPDLLQCLNLSIVSHATCHGVYPGRITS
 DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLRLPVRVTSSVQPLPLPNDCATAGTEC
 KI FNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL
 FLLLCVLGLSQAAT - - - PKI FNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
 NMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWI
 Gaps
 Gaps
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 10;
 SGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
 Length 243;
 Indels
 serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
 77;
 Query Match 40.4%; Score 555; DB 2; Best Local Similarity 45.7%; Pred. No. 8.8e-38; Matches 113; Conservative 42; Mismatches 82.
 Mismatches
 39;
 RMIMRNN 248
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 101;
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Cispecies: Bos primigentus taurus (cattle)
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Cispecies: Dos primigentus taurus (cattle)
Cispecies: Dos-Doc-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
Cispecies: Dischem: Si3813
Rile Huerou, I.; Wicker, C.; Guilloteau, P.; Toullec, R.; Puigserver, A.
Bur. J. Biochem. 193, 767-773, 1990
A; Hitle: Isolation and mucleotide sequence of cDNA clone for bovine pancreatic anionic to A; Reference number: Si3813; MUD:91065383; PMID:1701147
A; Reference number: Si3813
A; Reference number: Si3813
A; Reference number: Si3813
A; Residues: J-247 - HUE>
A; Residues: J-247 - HUE>
A; Residues: J-247 - HUE>
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 C,Accession: A26273
R,Pinsky, S.D.; LaForge, K.S.; Scheele, G.
R,Pinsky, S.D.; LaForge, K.S.; Scheele, G.
A) Call. Biol. 5, 2669-2676, 1985
A,Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA sequer A;Reference number: A26273; MUID:86284628; PMID:3841794
 A;Molecule type: mRNA
A;Residues: 1.247 <PIN>
A;Cross-references: UnlPNDOT:P06872; GB:M11589; NID:g164094; PIDN:AAA30899.1; PID:g164095
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
 5
199
 239
 63 CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLRVRVTS 122
 64 CYQYHIQVRLGEYNIDVLEGGEQFIDASKIIRHPKY--SSWTLDNDILLIKLSTPAVINA 121
 123 SVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITS 182
 181
 63
 trypsin (EC 3.4.21.4) precursor, anionic - dog
NyAlternate names: cationic trypsinogen
C.Species: Canis lupus familiaris (dog)
C.Species: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
 141 HVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVP-GQDACQGD
 183 NAVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWI
 7 LLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
 Gaps
 10;
 200 SGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
 183 SGGPVVCSGKLQGIVSWGS--GCAQKNKPGVYTKVCNYVSWIKQTIASN 229
 84; Indels
 Length
 Query Match

40.0%; Score 550; DB 2;
Best Local Similarity 45.7%; Pred. No. 2.3e-37;
Matches 113; Conservative 40; Mismatches 84,
 242 RMIMRNN 248
 240 QETIAAN 246
 RESULT 10
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 R;Bode, W.; Schwager, P.

Woll Biol. 98, 693-717, 1975

A;Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom resolution A;Reference number: A92954; MUID:76072097; PMID:512

A;Reference number: A92954; MUID:76072097; PMID:512

A;Reference number: A92954; MUID:76072097; PMID:512

A;Reference number: A92954; MUID:76072097; PMID:512

A;Reference number: A92954; MUID:76072097; PMID:512

C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.
C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.
C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.
C;Comment: Autocatalytic cleavage after Lys-6 leads to beta-trypsin by releasing a termis special pylocology greater after Arg-105.
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen F;1-220/Product: trypsinogen appetide apperimental <APV>
F;1-220/Promain: trypsin homology <TRY>
F;1-220/Product: alpha-trypsin #status experimental <APV>
F;7-131,132-230/Product: alpha-trypsin #status experimental <APV-F;6-7/Cleavage site: Lys-11e (enteropeptidase) #status experimental F;8:40,90,183/Active site: His-119-120/Disulfide bonds: #status experimental F;8:60,63,68/Bsinding site: calcium (Glu, Asn, Val) & St. #status experimental F;8:8:60,63,68/Bsinding site: Lys-16 (autolytic) #status experimental
 remaining amides
 175
 PGRITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYIC 235
 81 DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGTEC 140
 65 EGNEQFISASKSIVHPSY--NSNTLNNDIMLIKLKSAASLNSRVASISLPTSCASAGTQC 122
 RVTSSVQPLPLPLPNDCATAGTECHVSGWG--ITNHPRNPFPDLLQCLNLSIVSHATCHGVY 176
 80
 6 KIVGGYTCGANIVPPYQVSLNSGYHF-CGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVV 64
 ;Species: Bos primigenius taurus (cattle)
bate: 24-Apr-1984 #sequence_revision 28-Feb-1986 #text_change 18-Jul-1997
jAccession: A90164; A00946; S08774
;Mikes, O.; Holeysovsky, V.; Tomasek, V.; Sorm, F.
inchem. Biophys. Res. Commun. 24, 346-352, 1966
j'ittle: Covalent structure of bovine trypsinogen. The position of the remains Reference number: A90164; MUID:67168848; PMID:5967094
 : : | :|||: || |||||: || TINARVASVPLPSSCAPAGTQCLISGWGNTLSNGVNN--PDLLQCVDAPVLPQADCEASY
TAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPV
 21 KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL
 Gaps
 9
 A,Molecule type: protein
A,Residues: 1-57,'Q',59-67,'Q',69-150,'N',152-176,'N',178-229 <MIK>
R,Hartley, B.S.
Philos. Trans. R. Soc. Lond. B257, 77-87, 1970
 ; Score 552; DB 1; Length 229;
; Pred. No. 1.4e-37;
40; Mismatches 77; Indels
 A, Reference number: A93755
A, Contents: annotation; revisions
R, Titeni, K.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.
Blochemistry 14, 1358-1366, 1975
A; Title: Amino acid sequence of dogfish trypsin.
A, Reference number: A00950; MUID:75146445; PMID:1092332
 Note: the sequence agrees with that shown Bode, W.; Schwager, P.
 (EC 3.4.21.4) precursor - bovine
 A; Contents: annotation; revisions
 46.3%;
 |||||| : :|
234 NYVDWIQNTIADN 246
 236 KYVDWIRMIMRNN 248
 Query Match
Best Local Similarity 46.39
Matches 106; Conservative
 trypsin (EC 3.4.21.4) p.
N;Contains: trypsinogen
 Accession: A90164
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Cispecies: Rattus norvegicus (Norway rat)
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Cibate: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
Cibacession: A2754
RiPletcher, T.S.; Alhadeff, M.; Craik, C.S.; Largman, C.
Biochemistry 26, 3081-3086, 1987
A; Pletcher, T.S.; Alhadeff, M.; Craik, C.S.; Largman, C.
Biochemistry 26, 3081-3086, 1987
A; Pletcher, T.S.; Alhadeff, M.; Craik, C.S.; Largman, C.
A; Pletcher, T.S.; Alhadeff, M.; Craik, C.S.; Largman, C.
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NyAlternate names: trypsinogen I
Cypecies: Rattus norvegicus (Norway rat)
Cypecies: Rattus norvegicus (Norway rat)
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Cybecies: Rattus norvegicus (Norway rat)
Cyaccession: B22657; A00948
RyCraik, C.S.; Choo, O.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984
A;Reference number: A22657; MUID:85054880; PMID:6094547
A,Recession: B22657
A,Rocession: B22657
A,Rocession: B22657
A,Rocession: B22657
A,Rocession: A;Reference: UNIPROT:P00762; GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
A,Cross-references: UNIPROT:P00762; GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
A,Roche: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 17(
B. MacDonald, R.J.; Stary, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982
 237
 118 VRVTSSVQPLPLDPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYP 177
 GRITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICK 236
 58 LTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLP 117
 59
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 (EC 3.4.21.4) precursor,
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 109; Conservative
 248
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 VDWIRMIMRNN
 Similarity
 238
 178
 Query Match
 Local
 Best Loca
Matches
 RESULT 13
 trypsin
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 A; Accession: B26273
A; Molecule type: mRNA
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A; Cross-references: 1-246 cPIN.
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 Ripinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2659-2676, 1985
A;Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA seque
A;Reference number: A26273; MUID:86284628; PMID:3841794
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 TINSRVSAIALPKSCPAAGTQCLISGWGNTQSIGQNYPDVLQCLKAPILSDSVCRNAYPG 1777
 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVT 121
 RVTSSVQPLPLPUDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPG 178
 61
 5 LILAFLG-AAVATPTDDDDKIVGGYTCEENSVPYQVSLNAGYHF-CGGSLISDQWVVSAA 62
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 53
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C;Species: Canis lupus familiaris (dog)
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 239 IQSTIAAN 246
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 Query Match
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5, 2005, 20:46:44
 238 VDWIRMIMRNN 248
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 Search completed: March
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 59
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A;Reference number: A00948; MUID:82265624; PMID:6896710
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C; Salace: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C; Accession: S6657; 831779
R; Male, R.; Lorens, J.B.; Smalas, A.O.; Torrissen, K.R.
Eur. J Biocchem. 23, 677-685, 1995
A; Title: Molecular cloning and characterization of anionic and cationic variants of A; Reference number: S66657; MUID:96035908; PMID:7556223
 Ajuntons: 14/1; 67/2; 152/1; 197/3
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 KYVDWIR 242
 234 NFVGWIQ 240
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Best Local Similarity
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 A; Accession: A00948
 A; Reference number: A; Accession: S66657
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A;Molecule type: mRNB
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A;Rosidues: 1-247 <LUB-
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 119 VLNSQVSTVSLPRSCASTDAQCLVSGWGNTVSIGGKYPALLQCLEAPVLSASSCKKSYPG 178
 236
 131
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 TAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPV 118
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C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
 119 RVISSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPG
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 1 MKISIFFAFLGAAVALPVNDDDKIVGGYTCPKHLVPYOVSLHDGISHQCGGSLISDQWVL
 RITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKY
DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGTEC
 1 MGLSIF--LLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVL
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 C,Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Ju
C,Accession: S05494
R,Luetcke, H.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.F.
Nucleic Acids Res. 17, 6736, 1989
A,Title: A fourth trypsinogen (P23) in the rat pancreas induced by CC
A,Reference number: S05494; MUID:89386010; PMID:2780302
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N;Alternate names: 23K protein; trypsinogen IV precursor
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|----------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------|--------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|-----------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------|----------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|---------------------------------------------------------------------------|-------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------|---------------------------------------|------------------------------------------------------------|
| 32 563 41.0 248 2 Q7SZT1<br>33 562 40.9 255 2 Q6GNU2<br>34 561 40.8 231 1 TRYP_PIG<br>35 561 40.8 243 1 TRYI_BOVIN<br>36 561 40.8 244 1 KLKF_HUMAN | 557 40.5 237 2<br>555 40.4 243 1<br>555 40.4 243 2<br>555 40.4 253 2<br>553 40.3 246 2                                                                      | 553.5 40.3<br>553 40.2<br>550.5 40.1<br>550 40.0                           | 546.5 39.7 247.1 546.2 39.7 247.1                                                    | 544.5 39.6 247 1<br>544.3 39.6 247 1<br>544.3 30.6 253 2                                                 | 543 39.5 246 2<br>541.5 39.4 247 2                           | 540 59.3 246 2 Q792Y<br>540 39.2 249 2 Q91VE<br>536 39.0 246 2 Q71TT4             | 535.5 39.0 246 2<br>535.5 39.0 245 2<br>535.5 39.0 261 2<br>534.5 38.9 245 2        | 533.5 38.8 247 1<br>533 38.8 246 1<br>533 38.8 246 2                                                                                                                                               | 532 38.7 246<br>528 38.4 246<br>528 38.4 263 | 527.5 38.4 261 1<br>525 38.2 240 2<br>523 5 38.1 246 2   | 521.5 38.0 244 2<br>521.5 38.0 246 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 520.5 37.9 258<br>519 37.8 246<br>519 37.8 246                                       | 518 37.7 261 1<br>514.5 37.4 242 2                                        | 513.5 37.4 239 1<br>513.5 37.4 239 1                                                      | 513.5 37.4 243 2<br>513.5 37.4 261 2<br>513 5 37.4 278 2                                                 | 512 37.3 279 2<br>512 37.3 279 2<br>511.5 37.2 261 2                                 | 510.5 37.2 238 2<br>510.5 37.2 261 1<br>509.5 37.1 222 2       | 509.5 37.1 235 2<br>508 37.0 242 1                                               | 508 37.0 242<br>507 36.9 244<br>507 36.9 259                                                                    | 98 506 36.8 245 2<br>99 505 36.8 242 2<br>00 505 36.8 249 2                                                      | 505 36.8 260 1<br>505 36.8 260 1      | 03 504.5 36.7 269<br>04 503 36.6 241                       |
| GenCore v Copyright (c) 1993                                                                                                                       | OM protein - protein search, using sw model Run on: March 5, 2005, 20:42:30 ; Search time 174 Seconds (without alignments) 729.860 Million cell updates/sec | IMRN                                                                       | coring table: BLOSUW62 Gapop 10.0 , Gapext 0.5                                       | Searched: 1612378 segs, 512079187 residues<br>Total number of hits satisfying chosen parameters: 1612378 | Minimum DB seq length: 0<br>Maximum DB seq length: 200000000 | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1500 summaries | Database : UniProt_03:* 1: uniprot_sprot:* 2: uniprot_trembl:*                      | Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. |                                              | Result Query<br>No. Score Match Length DB ID Description | 1374 100.0 248 1 KLKC HUMAN Q9ukr0 homo 952.5 69.3 234 2 09C976 Q9cv76 Q9cv76 Q9cv76 mus 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 09C976 quas 1 2 0 |                                                                                      | 618 5 45 0 250 1 KLKB HUKAN Q94DX7 homo 88 618 1 44.5 255 2 Q7JJG6 gaguin | 9 610 44:4 250 2 Q83.2K2 Q83.2K2 Q83.2K2 GAUCY<br>1 601 43.7 275 2 Q81.XD7 Q81.Xd7 home 1 | 2 599 43.6 255 2 QGISIO QGISIO<br>3 599 43.6 256 1 KLKP HUMAN Q9DAZKS<br>6 67 6 74 6 740 7 000VXI OCUMEN | 5 597.5 43.5 276 2 Q9QXN3 Q9QXD3 miles<br>6 595 43.3 255 2 Q9GRQ0 Q96RQ0 Q96RQ0 homo | 7 588.5 42.8 293<br>8 588 42.8 276<br>9 586 42.6 250           | 0 578 42.1 242 2 Q80VS4 Q80VS4 mus mus<br>1 576 41.9 246 2 Q6P3Z0 Q6p3z0 mus mus | 2 569.5 41.4 248 1 TRY3 CHICK Q90629<br>3 569.5 41.4 251 1 KKE HUMAN Q9p0g3<br>4 569.5 41.4 251 2 Q6B089 Q6b089 | 5 568.5 41.4 250 1 KLK9_HUMAN Q9ukq9<br>6 557 41.3 277 1 KLKD_HUMAN Q9ukr3<br>7 566 41.9 248 1 TPV2_CHTCK C00629 | 565 41.1 293 1 KLK5_HUMAN Q99337 homo | 0 564 41.0 276 1 KLKA HUMAN<br>1 563 41.0 244 1 TRY2_XENLA |

| 1 nomo sapien<br>14 trimeresuru<br>29 bothrops ja<br>kl agkistrodon<br>16 trimeresuru                     | is trimeresuru<br>19 trimeresuru<br>19 trimeresuru | f grant morne<br>klagkistrodon<br>18 bothrops ja               | 34 trimeresuru<br>j8 agkistrodon | 11 vipera lebe<br>08 trimeresuru | lu trimeresuru<br>51 agkistrodon | 55 praomys nat<br>37 trimeresuru        | 11 trimeresuru<br>17 trimeresuru | 57 trimeresuru 56 trimeresuru | <pre>51 trimeresuru i9 trimeresuru</pre> | jo trimeresuru<br>iz aqkistrodon | 10 4       |              | ~ —              |                      | 71 mus musculu<br>50 trimeresuru |                      | ez homo sapien<br>17 mus musculu         | 53 trimeresuru<br>i0 trimeresuru | c3 crotalus at<br>32 aqkistrodon | 52 trimeresuru<br>k2 agkistrodon | <pre>j3 trimeresuru e1 homo sapien</pre> |                    | k2 crotalus ad     | xenopus 1                                |                                          |                  | 82 trimeresuru<br>55 daboia russ | 94 dicentrarch  | 18 ciimetesuu<br>j2 agkistrodon | 59 trimeresuru<br>el gloydius sa | 20 trimeresuru<br>89 lachesis mu | 10 gloydius sh | 17 trimeresuru<br>13 gallus gall | 40 vipera lebe<br>62 vipera lebe         |
|-----------------------------------------------------------------------------------------------------------|----------------------------------------------------|----------------------------------------------------------------|----------------------------------|----------------------------------|----------------------------------|-----------------------------------------|----------------------------------|-------------------------------|------------------------------------------|----------------------------------|------------|--------------|------------------|----------------------|----------------------------------|----------------------|------------------------------------------|----------------------------------|----------------------------------|----------------------------------|------------------------------------------|--------------------|--------------------|------------------------------------------|------------------------------------------|------------------|----------------------------------|-----------------|---------------------------------|----------------------------------|----------------------------------|----------------|----------------------------------|------------------------------------------|
| 0719j                                                                                                     | Qedy / e                                           | 0918X<br>0918X<br>09ptu                                        | 09498<br>09ygj                   | O9pt4<br>O9150                   | O9151<br>O9pt5                   | 00395                                   | 09151<br>071gi                   | O9df6<br>O9df6                | 01306<br>071qi                           | 071qj<br>09vqj                   | P1896      | 09ygi        | 07380<br>096je   | 0714j<br>06h32       | P0407<br>01306                   | 08ay8<br>09105       | 096je<br>Q8k5d                           | 01306<br>Q71qi                   | Q8qhk<br>09350                   | 01306<br>Q918x                   | 0714j<br>096je                           | P8117              | Ognak<br>Ognak     | 066h0                                    | 0/141<br>08uuj                           | 08ghk<br>071gi   | Q8ay8<br>P1896                   | 09359           | O8uuj                           | 01305<br>Q782e                   | P0562                            | Q6t51          | 071qn<br>07820                   | 227.<br>28jh6                            |
|                                                                                                           |                                                    |                                                                |                                  |                                  |                                  |                                         |                                  |                               |                                          |                                  |            |              |                  |                      |                                  |                      |                                          |                                  |                                  |                                  |                                          |                    |                    |                                          |                                          |                  |                                  |                 |                                 |                                  |                                  |                |                                  |                                          |
| Q71QJ4<br>Q7T229<br>Q8UVX1<br>VSP1_TRIST                                                                  | QSAI/8<br>Q71QI5<br>VSP3_TRIMU                     | VSP2_AGKAC<br>VSP3_BOTJA                                       | VSP7_TRIMU<br>Q9YGJ8             | VSP1 VIPLE<br>VSP2 TRIMU         | VSP4 TRIMU<br>Q9PT51             | Q03955<br>VSP1_TRIMU                    | VSP5_TRIMU<br>Q71QT7             | VSP2_TRIJE<br>VSP3_TRIJE      | VSPB_TRIGA<br>0710 <u>1</u> 9            | Q71QJO<br>VSP1 AGKHP             | VSPA_DABRU | VSP2_AGKHP   | 073800<br>Q96JE0 | Q71QJ1<br>KLK2_HORSE | KLKG MOUSE<br>VSPA_TRIGA         | QBAYB1<br>VSP1_AGKCA | Q96JE2<br>Q8K5D7                         | VSP3_TRIGA<br>Q71Q <u>T</u> 0    | Q8QHK3<br>O93502                 | VSPC_TRIGA<br>VSP1_AGKAC         | Q71Q√3<br>O96√E1                         | VSP1 AGKHA         | QBUUK2             | Q66H01                                   | Q71Q18<br>Q8UUJ1                         | Q8QHK2<br>Q71Q16 | Q8AY82<br>VSPG DABRU             | 0935 <u>9</u> 4 | 0710H8<br>0800J2                | VSP1_TRIGA<br>Q7S2 <u>E</u> 1    | VSP1_TRIFL                       | Q6T5L0         | <b>3</b> 1 O                     | VSP2_VIPLE<br>Q8JH62                     |
| 260 2 260 2 258 1                                                                                         |                                                    |                                                                |                                  |                                  |                                  |                                         |                                  |                               |                                          |                                  |            |              |                  |                      |                                  |                      |                                          |                                  |                                  |                                  |                                          |                    |                    |                                          |                                          |                  |                                  |                 |                                 |                                  |                                  |                |                                  |                                          |
| 32.8<br>32.8<br>32.7                                                                                      | 32.5                                               | 32.2                                                           | 32.0                             | 31.9                             | 31.8                             | 31.8<br>31.8                            | 31.8<br>31.7                     | 31.7<br>31.6                  | 31.6                                     | 31.6                             | 31.4       | 31.4         | 31.4             | 31.4<br>31.4         | 31.4                             | 31.4<br>31.4         | $\frac{31.3}{31.2}$                      | 31.2<br>31.2                     | 31.2                             | 31.0                             | 30.9                                     | 30.8               | 30.7               | 30.7                                     | 30.5<br>30.5                             | 30.5<br>30.5     | 30.4                             | 30.2            | 30.1                            | 30.1<br>30.1                     | 30.1                             | 29.9           | 0.00                             | 29.8<br>29.7                             |
| 4 4 4 4 4 5 5 1 2 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                         | 446.5<br>445.5                                     | 4443<br>443                                                    | 439.5                            | 437.5                            | 437.5                            | 436.5<br>436.5                          | 436.5                            | 435<br>434                    | 434<br>434                               | 433.5                            | 4.4        | 432          | 432<br>431.5     | 431.5                | 431.5                            | 431<br>431           | 429.5                                    | 429<br>429                       | 428.5                            | 426.5                            | 424.5                                    | 423<br>422 5       | 422.5              | 421.5                                    | 420.5<br>419.5                           | 419<br>418.5     | 418                              | 415.5           | 415.5                           | 413<br>413                       | 413                              | 411            | 411                              | 408.5                                    |
| 173<br>180<br>181                                                                                         |                                                    |                                                                | ,                                |                                  |                                  |                                         |                                  |                               |                                          |                                  |            |              |                  |                      |                                  |                      |                                          |                                  |                                  |                                  |                                          |                    |                    |                                          |                                          |                  |                                  |                 |                                 |                                  |                                  |                |                                  |                                          |
| F32824 praomys nat<br>Q9w6k0 notothenia<br>P36376 rattus norv<br>Q91515 fugu rubrip<br>Q93266 pseudopleur | pa<br>ga(                                          | Vanicy nomo sapien<br>Q788vo dissostichu<br>Q9y5k2 homo sapien | rai                              | homo e<br>mus mu                 | para<br>petr                     | 042608 petromyzon<br>Q86u61 homo sapien | mace                             | home                          | home                                     | P06870 home sapien               | gadı       | squi         | mus              | rat                  | mus<br>taut                      | mus m<br>mus m       | Q8n2u3 homo sapien<br>P15948 mus musculu |                                  | ratt                             | mus                              | O9xsn6 sus scrofa                        | P33619 macaca mula | Occurs maraca rase | O93265 pseudopieur<br>Q6ie12 rattus norv | P00755 mus musculu<br>Q61754 mus musculu |                  | dia                              | fuguı           | xenop                           | homo<br>trime                    | mus                              | ratt           | mus<br>trim                      | Q8k0c6 mus musculu<br>P07647 rattus norv |
| 2 09W6K0<br>1 KLKC RAT<br>2 091515<br>2 093266                                                            |                                                    |                                                                |                                  |                                  |                                  |                                         |                                  |                               |                                          |                                  |            |              |                  |                      | 2 Q9DBQ8<br>2 Q6RI79             |                      |                                          |                                  |                                  |                                  |                                          |                    |                    |                                          |                                          |                  |                                  |                 |                                 |                                  |                                  |                | 1 KLKQ_MOUSE<br>2 Q71QH6         |                                          |
| 22222                                                                                                     |                                                    |                                                                |                                  |                                  |                                  |                                         |                                  |                               |                                          |                                  |            |              |                  |                      |                                  |                      |                                          |                                  |                                  |                                  |                                          |                    |                    |                                          |                                          |                  |                                  |                 |                                 |                                  |                                  |                |                                  |                                          |
| 30.000                                                                                                    |                                                    | 36.2                                                           |                                  |                                  |                                  |                                         |                                  |                               |                                          |                                  |            |              |                  |                      |                                  |                      |                                          |                                  |                                  |                                  |                                          |                    |                    |                                          |                                          |                  |                                  |                 |                                 |                                  |                                  |                | 34.0                             |                                          |
| 502<br>502<br>501.5<br>501.5                                                                              | 501<br>499.5                                       | 4 4 4<br>2 0 0<br>2 0 0                                        | 497                              | 496.5                            | 496<br>496                       | 4 4<br>9 6<br>9 6                       | 495.5<br>495.5                   | 4<br>4<br>9<br>5<br>5         | 494.5                                    | 4.93<br>6.04                     | 491.5      | 491<br>490.5 | 489.5            | 489                  | 487.5                            | 485.5                | 484.5                                    | 484.5                            | 483.5                            | 482                              | 481                                      | 479                | 478.5              | 478.5                                    | 477.5                                    | 476.5            | 476.5                            | 472.5           | 471<br>470.5                    | 470.5                            | 469.5                            | 463.5          | 467.5                            | 462.5<br>461.5                           |
| 96586                                                                                                     | 5446                                               | 3 4 R                                                          | 16                               | 8 6                              | 0 1                              | 3 5                                     | 4.0                              | 926                           | 80 6                                     | 225                              | 100        | 2 4          | 9.2              | 18                   | 60                               | 42                   | 13                                       | 5 9                              | 7 8                              | 6.0                              | 11.0                                     | 105                | # LO !             | 27.0                                     | ω σ.                                     | 0.1              | 25                               | . <del></del> . | 5 9                             | 23                               | 0.5                              | 25             | 72 ,                             | 4 <sub>10</sub>                          |

| Q78251 brachydanio<br>Q6wgrl ictalurus p<br>Q64061 xenopus lae<br>Q61aus homo sapien<br>Q61aus homo sapien<br>P35036 anopheles g<br>Q9esdl mus musculu<br>Q6p326 xenopus tro<br>Q80x23 rattus norv<br>Q804x0 fugu rubitp                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                                  | hon<br>tac<br>tac<br>hon                                                                                                                                                 | 496728 nome Sapren<br>Q9734 drosophila<br>P21845 mus musculu<br>Q9887 rattus norv<br>Q6GX59 lepeophthei<br>Q8wmm5 trichoderma<br>Q80X17 mus musculu<br>Q80X17 mus musculu       | Q9w_pp paralichtny P05208 mus musculu P47796 gadus morhu P50342 meriones un Q7dgz6 anopheles g P50343 rattus norv Q9y6m0 homo sapien Q20278 canis famil                      | 0994.ps aus scrota<br>06pgs4 xenopus lae<br>06gnk3 xenopus lae<br>06gnk2 homo sapien<br>P11032 mus musculu<br>07c0t6 xenopus lae<br>083748 rattus norv<br>0966v4 halocynthia<br>P33587 mus musculu<br>099gyz9 mus musculu |                                                                                                                                                                                              | P08217 nomo sapren<br>O61cv2 homo sapren<br>O96899 scolopendra<br>O8cj16 rattus norv<br>Q8cj17 rattus norv<br>Q61711 rattus norv<br>Q7qim7 anopheles g<br>Q26422 carcinoscor<br>Q56423 carcinoscor<br>Q6avb0 brachydanio<br>Q8avb0 brachydanio<br>Q8pye4 mus musculu<br>Q9dbi0 mus musculu                                                                      |
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| 361.5 26.3 267 2 361 361 26.3 267 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2 369 2  | 358.5 26.1 245 1 358.5 26.1 444 1 358 26.1 812 1 357.5 26.0 371 2 357.5 26.0 643 2                                               | 357 26.0 262 1<br>357 26.0 263 1<br>357 26.0 271 1<br>357 26.0 271 1<br>357 26.0 1019 1<br>357 26.0 1019 1<br>356.5 25.9 261 2                                           | 355.5 25.9 321<br>355.5 25.9 276<br>355.5 25.9 276<br>354.5 25.8 342<br>354.5 25.8 311<br>354.5 25.8 331                                                                        | 354 25.8 250 2<br>354 25.8 271 1<br>353.5 25.7 263 1<br>353.5 25.7 270 1<br>353 25.7 274 1<br>353 25.7 314 1<br>353 25.7 314 1                                               | 353 25.7 459 1<br>352.5 25.7 263 2<br>352 25.6 111 2<br>352 25.6 211 2<br>352 25.6 277 3<br>352 25.6 277 3<br>352 25.6 277 3<br>352 25.6 277 3<br>351 25.6 460 1<br>351 25.5 460 1                                        | 351 25.5 456 1<br>350.5 25.5 265 2<br>350.5 25.5 274 2<br>350.5 25.5 274 2<br>350.5 25.5 274 2<br>350 25.5 268 2<br>350 25.5 268 2<br>350 25.5 268 2<br>350 25.5 268 2                       | 384 349.5 25.4 269 1 ELZA HOMAN<br>385 349.5 25.4 269 1 ELZA HOMAN<br>386 349.5 25.4 277 2 096892<br>387 349.5 25.4 371 2 08C016<br>388 349.5 25.4 445 2 08C017<br>390 349.5 25.4 130 2 06C017<br>391 349.5 25.4 1130 2 07QIM7<br>392 348.5 25.4 1083 2 026423<br>393 348.5 25.4 429 2 08AVE4<br>394 348.5 25.4 593 2 08AVE4<br>395 348.5 25.4 811 1 TMSE_MOUSE |
| 042207 agkistrodon<br>Q8ay79 trimeresuru<br>013057 trimeresuru<br>07057 trimeresuru<br>071435 trimeresuru<br>071431 trimeresuru<br>078ze2 agkistrodon<br>06.wf1 bothrops al<br>P81824 bothrops ja                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | P04971 bothrops at<br>Q9df68 trimeresuru<br>Q9dg93 trimeresuru<br>P82981 agkistrodon<br>Q802f0 agkistrodon<br>Q8qg86 bothrops in | 07472 trimeresuru<br>Q90z47 agkistrodon<br>Q74q4 trimeresuru<br>Q9er05 mus musculu<br>Q74qb trimeresuru<br>Q1369 bothrops ja<br>Q907p8 mus musculu<br>Q918w9 agkistrodon | QVequal cultureresuru<br>Q9equal cuttus norv<br>Q8wzb4 homo sapien<br>P00746 homo sapien<br>Q8jh85 vipera lebe<br>Q13058 trimeresuru<br>P08419 sus scrofa<br>Q8mfy7 homo sapien | Q86V)5 nomo sapien<br>Q98tt5 agkistrodon<br>Q918x0 agkistrodon<br>P81661 bothrops ja<br>Q91961 agkistrodon<br>Q9W781 agkistrodon<br>Q6C687 bitis gabon<br>P15950 rattus norv | P40313 homo sapien<br>Q90960 mus musculu<br>Q81uw0 homo sapien<br>Q07277 homo sapien<br>Q91674 xenopus lae<br>P32038 rattus norv<br>Q8n4e0 homo sapien<br>Q6538 symphysodon<br>Q7sy86 xenopus lae<br>Q6ncw4 homo sapien   | QGGMG9 brachydanio P03953 mus musculu QGfhw3 homo sapien QGcjf4 rattus norv P00774 rattus norv QG6vi7 homo sapien P51779 sus scrofa P04813 canis famil P26324 agkietrodon QGi9p2 aplysina fi | Q661477 Xenopus tro Q16651 homo sapien O93267 pseudopleur O60235 homo sapien P03952 homo sapien P47797 agkistrodon Q9w7q3 paralichthy Q9xy60 ctenocephal Q7sx97 brachydanio Q99144 mus musculu Q8bjv6 mus musculu P50340 meriones un                                                                                                                            |
| 9.6 258 1 9.6 258 1 9.6 258 2 9.6 251 1 1 9.6 251 2 9.6 231 2 257 2 9.5 257 2 9.5 231 2 231 2 231 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 257 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9.3 2 9. | 9.3 255 1<br>9.3 260 1<br>9.1 234 1<br>257 2                                                                                     | 888.9<br>88.9<br>8.9<br>8.7<br>8.8<br>8.6<br>7.0<br>8.6<br>7.0<br>8.6<br>7.0<br>8.6<br>9.6<br>9.6<br>9.6<br>9.6<br>9.6<br>9.6<br>9.6<br>9.6<br>9.6<br>9                  | 88.55 25.84 2 2 25.84 2 2 25.84 2 2 25.84 2 2 25.84 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                       | 88.1 2558 2 258 8.1 2558 2 1 2558 2 1 2568 2 1 2568 2 1 2568 2 1 2568 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3                                                                  | 8.1 264 1<br>8.1 264 2<br>8.1 269 2<br>8.0 195 2<br>7.7 263 1<br>7.7 263 2<br>7.7 255 2<br>7.7 456 2                                                                                                                      | 7.5 261 2 261 2 261 2 261 2 261 2 261 2 261 2 2 2 2                                                                                                                                          | 26.9 330 1 PSSB HUMAN 26.8 343 1 PSSB HUMAN 26.8 418 1 HATT HUMAN 26.6 258 1 YAL HUMAN 26.6 258 1 VAL HUMAN 26.6 258 2 Q9W7Q 26.6 263 2 Q9W7Q 26.5 339 2 Q99L44 26.4 340 2 Q9BJV6 26.4 387 2 Q9XY57                                                                                                                                                             |
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| Q03238 rattus norv Q80324 brachydanio P80009 canis famil Q61600 rattus norv Q8vif2 mus musculu Q28661 oryctolagus P00740 homo sapien Q95nd7 pan troglod P03951 homo sapien Q01177 rattus norv Q18599 drosophila                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Ogynnia nomo saplen<br>Ogynnia nomo saplen<br>Ogorade homo saplen<br>Ogorade homo saplen<br>Ogorade homo saplen<br>Ogorade mus musculu<br>Ogorade homo saplen<br>Ogorade homo saplen<br>Ogorade homo saplen<br>Ogorade nomohales sex<br>Organia anopheles sex<br>Ogorade nomo saplen<br>Ogorade mus musculu<br>Ogorade anties saries<br>Ogorade anties<br>Ogorade anties<br>Ogorade anties<br>Ogorade onopheles g<br>Ogorade onopheles g<br>Ogorade anties<br>Ogorade onopheles<br>Ogorade o | O9jis9 rattus norv<br>O86chm8 rattus norv<br>O70500 rattus norv<br>O70500 mus musculu<br>O7962 equus cabal<br>O9bye1 homo sapien<br>O9bye2 homo sapien<br>O15096 homo sapien<br>O15096 komopus lae<br>Q8mgf6 xenopus lae |
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| 339.5 24.7 258 1<br>339.5 24.7 271 2<br>339.5 24.7 331 1<br>339 24.7 321 2<br>339 24.7 458 1<br>339 24.7 461 1<br>339 24.7 625 1<br>338.5 24.7 625 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 335 24.4 701 2<br>334.5 24.3 24.3 24.3<br>334.5 24.3 263 1<br>334.5 24.3 263 1<br>334.5 24.3 263 1<br>334.5 24.3 275 2<br>334.5 24.3 581 2<br>334 24.3 284 2<br>334 24.3 264 2                                           |
| O6pba6 brachydanio P35041 anopheles g G6isn8 homo sapien Q7pufe anopheles g G640f8 xenopus lae G6fbb8 homo sapien P04070 homo sapien Q3bk47 luidia foli Q29461 bos taurus G46507 papio hamad G8i6k0 holotrichia g9966507 papio hamad G8i6k0 holotrichia                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Ogyrab mus musculu Ogyrab anopheles g Ogyab anopheles g Ogyab anopheles g Dyagab anopheles g Dyagab anopheles g Dyagab anopheles g Dyagab rattus norv Og864w7 fugu rubxip Ogyal mus musculu Ogyos mus musculu Ogyos mus musculu Ogyos panio hamad Ogyos panio hamad Ogyos mus musculu Ogyos mus musculu Ogyos panio homo sapien Ofyal homo sapien Ofyal homo sapien Ofyal homo sapien Ofyal homo sapien Ofyal homo sapien Ofyal homo sapien Ogyal lepeophthei Pyolos mus musculu Ogyal mus musculu Ogyal mus musculu Ogyal mus musculu Ogyal mus musculu Ogyal pom capien Offay bom capien Offay bom capien Offay bom capien Offay bom capien Offay bom capien Offay bom capien Offay bom capien Offay bom capien Offay bom capien Offay bom capien Offay mus musculu Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio Ogykl brachydanio                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | P21812 mus musculu P35035 anophales g Q8k3u6 rattus norv Q9dat3 mus musculu Q9smal ovis aries Q8n171 homo sapien O88781 rattus ratt O17489 anophales g O08732 mesocricetu P54625 drosophila                              |
| 25.2 2 269 255.2 269 255.3 3 269 255.3 3 269 255.3 3 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 269 255.2 260 | 346.5 2.5.2 445 1 1 NASA MOUSE 346.5 2.5.2 446 1 PAY MOUSE 346.5 2.5.2 446 1 PAY MOUSE 346.5 2.5.2 446 1 PAY MOUSE 346.5 2.5.2 461 2 090RYZ 30 346.5 2.5.2 461 2 060RYZ 30 346.5 2.5.2 461 2 060RYZ 30 346.5 2.5.2 311 1 TAYG MOUSE 346.5 2.5.1 312 1 TAYG MOUSE 346.5 2.5.1 312 1 TAYG MOUSE 346.5 2.5.1 467 2 0920Z 3 344 5 2.5.1 25.1 25.1 25.1 25.1 25.1 25.1 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 24.8 246 1<br>24.8 446 1<br>24.8 624 2<br>24.7 273 2<br>24.7 290 2<br>24.7 290 2<br>24.7 291 2<br>24.7 291 2<br>24.7 291 2                                                                                               |

| Q7q1d1 anopheles g<br>Q7ax4 brachydanio<br>Q6gnk4 xenopus lae<br>Q6gnk4 xenopus lae<br>Q7x10 lampetra ja<br>Q8mxh5 drosophila<br>Q0x319 drosophila<br>Q9xyey6 drosophila<br>Q9vey6 drosophila<br>Q6bea2 rattus norv<br>P19540 cantus famil<br>Q9dgr2 xenopus lae<br>P56415 macaca fasc<br>Q9ty16 penaeus van                                                                                                                                                                                    | Qédimé homo sapien Qédimé xenopus lae P49275 dermatophag Q78484 xenopus lae Q278242 dermatophag Q77872 dermatophag Q77872 xenopus lae P08882 mus musculu Q669177 sus scrofa Q91873 mus musculu Q660712 sus scrofa Q91874 anopheles g Q74110 anopheles g Q74114 anopheles g Q74114 anopheles g Q7414 anopheles g Q7414 anopheles g Q81760 mus musculu Q94081 pacisatacu Q94175 homo sapien Q94032 homo sapien Q94032 homo sapien Q94032 homo sapien Q94032 homo sapien Q94032 homo sapien Q94037 homo sapien Q94037 homo sapien Q94037 homo sapien Q94037 rattus norv Q95047 struthio ca P5730 homo sapien Q94037 mus musculu Q94087 drosophila Q80176 mus musculu Q94087 mus musculu Q94087 mus musculu Q94097 mus musculu Q84037 mus musculu Q84037 mus musculu Q84037 mus musculu Q84048 mus musculu Q84048 mus musculu Q84048 mus musculu Q84048 mus musculu Q84048 mus musculu Q84048 mus musculu Q84104 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 mus musculu Q84048 mus musculu Q84048 mus musculu Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q8410 homo sapien Q84 | Q96pg8 homo sapien<br>P80219 bos taurus  |
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| Q8sxz4 drosophila Q7pnf7 anopheles g Q9bqr3 homo sapien Q6iccz homo sapien Q6iccz homo sapien P00766 bos taurus Q9r0k0 mus musculu P16295 cavia porce Q7f0vz xenopus lae Q7pev7 anopheles g Q7pev7 anopheles g Q8t497 aedes aegyp Q8t4p6 lepeophthei                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | P80010 eguus cabal<br>Q9nas9 anopheles g |
| 333.5 24.3 253<br>333.5 24.3 275<br>333.5 24.3 275<br>333.5 24.3 290<br>333 24.2 245<br>333 24.2 245<br>333 24.2 245<br>333 24.2 256<br>332.5 24.2 256<br>332.5 24.2 254                                                                                                                                                                                                                                                                                                                        | 558         332.5         24.2         264         2         7VSS9           559         332.5         24.2         490         1         TMS2         AMOUSE           561         332.5         24.2         490         1         TMS2         AMOUSE           562         332.5         24.2         24.0         1         PLMM         MACMU           564         332         24.2         24.7         2         OVD942           566         332         24.2         251         2         OVD942           566         332         24.2         251         2         OVD944           568         332         24.2         251         2         OVD944           568         332         24.2         251         2         OVD944           570         331         24.1         256         2         OVD944           571         331.5         24.1         254         2         OMPWE           573         331.5         24.1         254         2         OMPWE           574         331.5         24.1         254         2         OMPWE           574         331.5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 328.5 23.9 338 1<br>328.5 23.9 364 2     |

| Q6azs7 xenopus lae Q9y5y6 homo sapien O97370 euroglyphus Q80y38 mus musculu Q9d9m0 mus musculu Q9i7v4 drosophila Q804x7 gallus gall Q9i712 drosophila Q8cir9 mus musculu Q905711 xenopus lae Q8C3711 xenopus lae Q8C343 rattus norv                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Q7qkl2 anopheles g<br>Q6ie06 rattus norv<br>O35164 mus musculu<br>Q6vpu6 sarcoptes s<br>Q804g0 sphoeroides |
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| 314 22.9 629 313.5 22.8 321 313.5 22.8 321 313.5 22.8 321 313.5 22.8 326 313.5 22.8 364 313.5 22.8 241 313 22.8 241 313 22.8 336 313 22.8 697                                                                                                                       | 776 313 22.8 855 2 Q9JUIT7 779 312.5 22.7 241 1 TRYS_ANOGA 780 312.5 22.7 241 1 TRYS_ANOGA 780 312.5 22.7 271 2 QBTTRE 779 312.5 22.7 370 2 Q9TTRE 781 312.5 22.7 300 2 Q9TTRE 783 312.5 22.7 300 2 Q9TTRE 784 312.5 22.7 310 2 Q9TTRE 784 312.5 22.7 3132 2 QPTRE 785 312.5 22.7 3132 2 QPTRE 786 312.5 22.7 3132 2 QPTRE 788 312 22.7 3132 2 QPTRE 789 312 22.7 3132 2 QPTRE 789 312 22.7 324 2 QBTRE 789 312 22.7 374 311.5 22.7 374 2 QBTRE 789 311.5 22.7 597 2 QBTRE 793 311.5 22.7 597 2 QBTRE 793 311.5 22.7 597 2 QPTRE 793 311.5 22.7 561 1 DRTR MOUSE 799 311 22.6 431 1 DRTR MOUSE 799 311 22.6 431 1 DRTR MOUSE 799 311 22.6 431 1 DRTR MOUSE 801 311 22.6 431 1 DRTR MOUSE 802 311 22.6 431 1 DRTR MOUSE 803 311 22.6 431 1 DRTR MOUSE 803 310 22.6 471 1 DRTR MOUSE 803 310.5 22.6 471 1 DRTR MOUSE 803 310.5 22.6 471 1 DRTR MOUSE 803 310.5 22.6 471 1 DRTR MOUSE 811 310.5 22.6 471 1 DRTR MOUSE 812 310.5 22.6 471 1 DRTR MOUSE 813 310.5 22.6 471 1 DRTR MOUSE 814 310.5 22.6 471 1 DRTR MOUSE 814 310.5 22.6 471 1 DRTR MOUSE 814 310.5 22.6 471 1 DRTR MOUSE 814 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.6 471 2 QPTP 74 818 310.5 22.5 471 2 QPTP 74 818 310.5 22.5 471 2 QPTP 74 818 310.5 22.5 471 2 QPTP 74 818 310.5 22.5 471 2 QPTP 74 818 310.5 22.5 246 2 QPTP 74 818 310.5 22.5 246 2 QPTP 74 82 310.5 22.5 246 2 QPTP 74 82 310.5 22.5 246 2 QPTP 74 82 310.5 22.5 246 2 QPTP 74 82 310.5 22.5 246 2 QPTP 74 82 310.5 22.5 246 2 QPTP 74 82 310.5 22.5 246 2 QPTP 74 82 310.5 22.5 246 2 QPTP 74 82 310.5 22.5 246 2 QPTP 74 82 310.5 22.5 246 2 QPTP 74 82 310.5 22.5 246 2 QPTP 7 | 309 22.5 404 2 308.5 22.5 240 2 308.5 22.5 246 1 308.5 22.5 260 2 308.5 22.5 260 2 308.5 22.4 125 2        |
| Q6iel3 rattus norv<br>P50341 meriones un<br>P18291 rattus norv<br>P19236 canis famil<br>Q9vuf0 drosophila<br>Q04186 homo sapien<br>P04187 mus musculu<br>Q7m755 mus musculu<br>Q9w7q1 paralichthy<br>Q7q432 anopheles g<br>Q7px72 anopheles g<br>Q6gng0 xenopus lae | O'DFÉT anophales g<br>Q81py7 drosophila<br>Q641di anophala<br>Q641di anthonomus<br>Q641di anthonomus<br>Q85nde pan troglod<br>P98074 sus scrofa<br>P81286 ovis aries<br>Q61615 rattus norv<br>Q920k3 rattus norv<br>Q920k3 rattus norv<br>Q920k3 ratus pipie<br>Q18488 penaeus van<br>P16293 sus scrofa<br>P16291 ovis aries<br>Q65267 culex pipie<br>Q18488 penaeus van<br>P16291 ovis aries<br>Q65267 homo sapien<br>P19221 mus musculu<br>P00767 bos taurus<br>P16291 mus musculu<br>P00767 bos taurus<br>Q65361 rattus norv<br>Q9xy9 rhyzopertha<br>P54627 drosophila<br>P11034 mus musculu<br>Q9xy9 rhyzopertha<br>Q63636 rattus norv<br>Q5367 recephal<br>Q63636 rattus norv<br>Q54001 gallus gall<br>Q94101 gallus gall<br>Q94101 mus musculu<br>Q94719 mus musculu<br>Q6755 noulex quinq<br>Q6525 mus musculu<br>Q6625 mus musculu<br>Q6612 rattus norv<br>Q6522 rattus norv<br>Q6522 rattus norv<br>Q66124 homo sapien<br>P1362 drosophila<br>Q66224 rattus norv<br>Q66144 drosophila<br>Q66144 drosophila<br>Q66144 drosophila<br>Q66144 drosophila<br>Q66144 drosophila<br>Q66144 drosophila<br>Q66144 drosophila<br>Q66144 mus musculu<br>Q87410 mus musculu<br>Q86141 mus musculu<br>Q86141 mus musculu<br>Q86141 mus musculu                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | bran<br>anop<br>anop<br>cani<br>homo                                                                       |
| 23.4<br>23.4<br>23.4<br>23.4<br>23.4<br>23.4<br>23.3<br>23.3                                                                                                                                                                                                        | 319 23.2 241 2 07PFF7 319 23.2 264 2 07PFF7 319 23.2 264 2 08PFF7 319 23.2 264 10.2 20 64101 319 23.2 20 2 064101 319 23.2 20 2 064101 318.5 23.2 1034 1 ENTK PIG 318.5 23.2 1034 1 ENTK PIG 318.5 23.2 1034 1 ENTK PIG 318 23.1 259 2 0920K3 318 23.1 259 2 0920K3 318 23.1 265 2 016488 23.1 265 2 016488 23.1 265 2 016488 23.1 265 2 016488 23.1 265 2 016488 23.1 265 2 016488 23.1 265 2 016488 23.1 265 2 016488 23.1 265 2 016488 23.1 265 2 016488 23.1 265 2 016488 23.1 266 2 016488 23.1 266 2 016488 23.1 266 2 016488 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 23.1 266 2 01688 2 01688 23.1 266 2 01688 2 01688 23.1 266 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 2 01688 | 4.5 22.9 680 2<br>314 22.9 275 1<br>314 22.9 275 2<br>314 22.9 280 2<br>314 22.9 422 2                     |

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| anopheles<br>homo sapie<br>desmodus r<br>desmodus r<br>m mus musc<br>tachypleus                                               | Q. Q. Q. Q. V. Algorians groups and P. P. P. P. P. P. P. P. P. P. P. P. P.               | Q95v22 lumbricus b<br>Q8vhk8 mus musculu<br>Q8vdv1 mus musculu<br>P98121 desmodus ro | Q96rs4 homo sapien<br>Q7tzhi xenopus lae<br>Q91894 arenicola m<br>Q68fn6 brachydanio<br>Q81924 bombyx mori |                                                                                      | Q8wril paralithode<br>Q8iq89 drosophila<br>Q8hhj4 rattus norv<br>Q9pu71 xenopus lae                           | 000356 mus musculu<br>Q6dbs8 brachydanio<br>019023 macaca mula<br>Q17025 anopheles g                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Q7pt16 anopheles g<br>O15344 sarcophaga<br>Q9w2c8 drosophila<br>Q6ruj3 trichinella<br>P23378 mus musculu | Q81zz5 homo sapien<br>Q90wd8 bufo japoni<br>P97435 mus musculu<br>Q6v1q1 verticilliu<br>P22293 rattus norv<br>Q91004 gecko gecko | Q9vq98 drosophila P21842 canis famil Q7dky0 anopheles g P22457 bos taurus Q8t3a2 ciona intes Q9vxx9 drosophila Q20731 oryctolagus |                                                                                                                                    | Q'QqB'S anopheles g<br>Q9vw19 drosophila<br>P05049 drosophila<br>Q'Q482 anopheles g<br>Q'Dx74 anopheles g<br>Q815a3 ciona intes<br>097507 sus screfa<br>P00765 astecus flu<br>P21844 mus musculu<br>Q9xy51 ctenocephal                                                                                              |
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| Q9vka8 drosophila<br>Q8mkp4 drosophila<br>Q9v513 drosophila<br>Q8sy35 drosophila<br>O97099 anopheles d        | Q9vsj2 drosophila<br>Q61096 mus musculu | Q17004 anopheles g | anopneles<br>drosophila | P83370 hoplocephal | xenopns   | Q6dkq2 elsenia toe<br>O8clq8 mus musculu |        | Q6nlm5 drosophila<br>O9v5x9 drosophila | Ost out aedes aegyp | Q17035 anopheles g<br>O25082 hypoderma l | drosophil | Q7z0g3 phlebotomus<br>OgaveR venomis lae | Q7q619 anopheles g | Oschp7 cavia porce | P15156 mesocricetu | 09cd78 m mus muscu |        | P43430 mus musculu | Q8k597 rattus norv | P54629 drosophila        | Q17800 caenorhabdi<br>Ogvem8 drosophila | P79343 bos taurus | Q9gmel ornithorhyn<br>P42279 drosophila | O7px30 anopheles g | P29598 rattus norv | Q804w8 fugu rubrip | 001310 botryllus s | P42278 drosophila | Q8sx49 drosophila | P25155 gallus gall | V/Zi55 CHITOMANICES<br>P09871 homo sapien | Oscies mus musculu | Q8is83 aedes albop | Q9nb91 agrotis ips |                  | 096442 strongyloce |        |        | O7pi75 anopheles q |        | P11033 mus musculu<br>P35046 manduca sex | Q7q235 anopheles g | Ol8440 nelicoverpa<br>O7d6u4 anopheles q | 070542 rattus norv |
|---------------------------------------------------------------------------------------------------------------|-----------------------------------------|--------------------|-------------------------|--------------------|-----------|------------------------------------------|--------|----------------------------------------|---------------------|------------------------------------------|-----------|------------------------------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------------|-----------------------------------------|-------------------|-----------------------------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------------------------------|--------------------|--------------------|--------------------|------------------|--------------------|--------|--------|--------------------|--------|------------------------------------------|--------------------|------------------------------------------|--------------------|
| Q9VKA8<br>Q8MKP4<br>Q9V513<br>Q8SY35<br>O97099                                                                | J2<br>MOUSE<br>E4                       | ANOGA              | 70                      | HOPST              | R1        | 0.02                                     | 2 E    | .X9                                    | ne<br>ne            | 35                                       | 10        |                                          | 119                | IP7                | CASP MESAU         | <u>17</u> 8        | IF7    | MCT8_MOUSE         | 76.                | DROER                    | 00                                      | 43                | E1<br>I DROME                           | Q7 PX30            | RAT                | ¥8                 | 10                 | DROME             | 64.9              | CHICK              | HUMAN                                     | 128                | 83                 | 191                | .S3              | 42                 | 20     | B4     | 7.5                | 156    | MOUSE                                    | Q7Q235             | 40<br>U4                                 | 42                 |
| 2 Q9VK<br>2 Q8MK<br>2 Q9V5<br>2 Q8SY<br>2 Q9SY                                                                |                                         |                    |                         |                    |           |                                          |        |                                        |                     |                                          |           |                                          |                    |                    |                    |                    |        |                    |                    |                          |                                         |                   |                                         |                    |                    |                    |                    |                   |                   |                    |                                           |                    |                    |                    |                  |                    |        |        |                    |        |                                          |                    |                                          |                    |
| 273<br>398<br>1629<br>1674<br>257                                                                             |                                         |                    |                         |                    |           |                                          |        |                                        |                     |                                          |           |                                          |                    |                    |                    |                    |        |                    |                    |                          |                                         |                   |                                         |                    |                    |                    |                    |                   |                   |                    |                                           |                    |                    |                    |                  |                    |        |        | 219                |        |                                          |                    |                                          |                    |
| 20.5<br>20.5<br>20.5<br>20.5<br>20.5<br>20.5                                                                  | 202                                     | 20.1               | 20.1<br>20.1            | 20.1               | 20.1      | 20.1                                     | 20.1   | 20.1                                   | 20.1                | 20.0                                     | 20.0      | 20.0                                     | 20.0               | 20.0               | 20.0               | 19.9               | 19.9   | 19.9               | 6.61               | 19.9                     | 19.9                                    | 19.9              | 9.6                                     | 19.8               | 19.8               | 19.8               | 19.8               | 19.8              | 19.8              | 19.8               | 19.8                                      | 19.8               | 19.8               | 19.8               | 19.8             | 19.8               | 19.7   | 19.7   | 19.7               | 19.7   | 19.7                                     | 19.7               | 19.7                                     | 19.7               |
| 277<br>277<br>277<br>277 ·                                                                                    | 276.5                                   | 276                | 276<br>276              | 276                | 276       | 275.5                                    | 275.5  | 275.5                                  | 275.5               | 275                                      | 275       | 275                                      | 275                | 275                | 274.5              | 274                | 274    | 273                | 273                | 273                      | 273                                     | 273               | 272.5                                   | 272.5              | 272.5              | 272.5              | 272                | 272               | 272               | 272                | 272                                       | 272                | 271.5              | 271.5              | 271.5            | 271.5              | 271    | 271    | 270.5              | 270.5  | 270.5                                    | 270.5              | 270                                      | 270                |
| 1200<br>1201<br>1202<br>1203                                                                                  |                                         |                    |                         |                    |           |                                          |        |                                        |                     |                                          |           |                                          |                    |                    |                    |                    |        |                    |                    |                          |                                         |                   |                                         |                    |                    |                    |                    |                   |                   |                    |                                           |                    |                    |                    |                  |                    |        |        |                    |        |                                          |                    |                                          |                    |
| Q6t776 homo sapien<br>Q6dkq3 eisenia foe<br>OVIN P05805 bos taurus<br>Q7rtz1 homo sapien<br>Q6b4r4 bos taurus | 001309 bot<br>086p18 aed                | 0x6be0             | P35048 str<br>Q7qkl3 an | Q76h11             | ul ogi7po | 09v1f5<br>09v929                         | Q6r558 | 069dk8<br>061kf3                       | 018600              | Q9nb92                                   | Q6q1q9    | Q868h4                                   | Q8mlc5<br>Q8mlc5   | Q7z1f0             | 072095<br>072095   | Q9va66             | 07qb72 | Q7phb4             | 097100             | Q/qune and<br>Q9y1k7 and | Q7qj44<br>064559                        | 08bhm9            | Q7pqb3<br>p51588                        |                    | 02539              | Q7rty              | Derei<br>Oevid     |                   | Q9208.            | Q9va67             |                                           | Q9vrs5             | 099110<br>025101   | Q8r099             | Vepeti<br>Q7zt69 |                    | 061e62 | P98140 | Qynkcs<br>O7ozh7   | 019045 | Q7qcv0                                   |                    | 076519<br>09dar1                         | 076498             |
| Q6T776<br>Q6DKQ3<br>CAC3 BOVIN<br>Q7RTZ1<br>Q6B4R4                                                            |                                         |                    |                         |                    |           |                                          |        |                                        |                     |                                          |           |                                          |                    |                    |                    |                    |        |                    |                    |                          |                                         |                   |                                         |                    |                    |                    |                    |                   |                   |                    |                                           |                    |                    |                    |                  |                    |        |        |                    |        |                                          |                    |                                          |                    |
| 172 2<br>245 2<br>253 1<br>264 2<br>235 2                                                                     |                                         |                    |                         |                    |           |                                          |        |                                        |                     |                                          |           |                                          |                    |                    |                    |                    |        |                    |                    |                          |                                         |                   |                                         |                    |                    |                    |                    |                   |                   |                    |                                           |                    |                    |                    |                  |                    |        |        |                    |        |                                          |                    |                                          |                    |
| 20.7<br>20.7<br>20.7<br>20.7<br>20.7                                                                          | 20.7                                    | 20.6               | 20.6<br>20.6            | 20.6               | 20.6      | 20.6                                     | 20.6   | 20.6                                   | 20.5                | 20.5                                     | 20.5      | 20.5                                     | 20.5               | 20.5               | 20.2               | 20.5               | 20.5   | 20.3               | 20.4               | 20.2                     | 20.4                                    | 20.4              | 20.4                                    | 20.0               | 20.2               | 20.4               | 20.4               | 20.3              | 20.3              | 20.3               | 20.3                                      | 20.3               | 20.3               | 20.3               | 20.3             | 20.3               | 20.3   | 20.3   | 20.2               | 20.2   | 20.5                                     | 20.2               | 20.2                                     | 20.5               |
| 284.5<br>284.5<br>284.5<br>284.5<br>284.5                                                                     | 284                                     | 283.5              | 283<br>283              | 283                | 282.5     | 282.5                                    | 282.5  | 282.5                                  | 282                 | 282                                      | 282       | 282                                      | 281.5              | 281.5              | 281                | 281                | 281    | 280.5              | 280.5              | 280.5                    | 280.5                                   | 280.5             | 280                                     | 200                | 780                | 280                | 280                | 279.5             | 279               | 279                | 279                                       | 279                | 279                | 279                | 279              | 278.5              | 278.5  | 278.5  | 278                | 278    | 278                                      | 277.5              | 277.5                                    | 277                |
| 30 5 8 7                                                                                                      | 332                                     | 35                 | 37                      | 38                 | 2.6       | 1 2                                      | 1.6    | 4. 4<br>4. 7.                          | 46                  | 7 4                                      | 0         | 20                                       | 4 22               |                    | a ru               | 9                  | 50     | 0 0                | 0:                 | 7.7                      | e 5                                     | ្រ<br>ព           | 9 6                                     | . 60 '6            | ν 5                | 7.5                | 2 5                | 4.                | n 9               | 7.                 | B 6                                       | ۵:                 | 7 2                | 8.3                | 4 C              | 36                 | . 8    | 6.5    | 2 5                | 25     | e 4                                      | 9 W                | 96                                       | . 8                |

|   | Ogezga drosophila                            | O7pvq3 anopheles g<br>O7q6t1 anopheles g | Qbpgw/ bracnydanio<br>045048 anopheles g | Q7px38 anopheles g<br>O7gnm1 anopheles g | drosophila         | 0/01/0 mus musculu<br>P10323 homo sapien  | Q7pwel anopheles g | P97611 rattus norv | Q7qfw4 anopheles g                       | P83298 lumbricus r | lumbri             | eisenia            | Q7pff6 anopheles g<br>O9vt25 drosophila  | Q7pz90 anopheles g | Q9pvy4 xenopus lae<br>ORigez sedes trise | Q7pvp7 anopheles g | Q8i1g9 drosophila<br>O61388 mis misculi | Q66uc8 culicoides | Q6dhh4 brachydanio<br>O6bd05 drogophila | Q6bd06 drosophila  | Q6bd16 drosophila<br>O9vzh5 drosophila  | Q8sxg6 drosophila | P08884 mus musculu<br>Q9v5x7 drosophila | O7ge41 anopheles g | Q6ie58 rattus norv | 06999/ streptomyce<br>Q9v4w7 drosophila  | Q8mgm9 drosophila<br>O8+3a0 ciona intes  | Oggp27 drosophila  | O7pg95 anopheles g                       | Ol8445 nelicoverpa<br>Q7q6u0 anopheles g | Q7kvm3 drosophila<br>Q7rty4 homo sapien  | Q6vfc8 anopheles g<br>O6ie09 rattus norv | Q01136 metarhizium | galleria m         | 097097 anopheles a<br>Q6dhc9 brachydanio |                   | Qflbb home sapien                        | O18441 helicoverpa<br>O8mlv8 drosophila | Ocjego homo sapien | QevrdO anopheles g<br>Q9bzj3 homo sapien | 6ntb8             | O9xy47 ctenocephal                   | yxyss crenoce<br>9vru0 drosopl          | Q7qcx2 anopheles g<br>Q9ksq6 vibrio chol |    |
|---|----------------------------------------------|------------------------------------------|------------------------------------------|------------------------------------------|--------------------|-------------------------------------------|--------------------|--------------------|------------------------------------------|--------------------|--------------------|--------------------|------------------------------------------|--------------------|------------------------------------------|--------------------|-----------------------------------------|-------------------|-----------------------------------------|--------------------|-----------------------------------------|-------------------|-----------------------------------------|--------------------|--------------------|------------------------------------------|------------------------------------------|--------------------|------------------------------------------|------------------------------------------|------------------------------------------|------------------------------------------|--------------------|--------------------|------------------------------------------|-------------------|------------------------------------------|-----------------------------------------|--------------------|------------------------------------------|-------------------|--------------------------------------|-----------------------------------------|------------------------------------------|----|
|   | 52 19.1 266 2 Q9VWX7<br>52 19.1 272 2 Q8SZG4 | 19.1 390 2                               | 19.0 259 2                               | 19.0 262 2<br>19.0 297 2                 | 19.0 324 2         | 19.0 421 1                                | 19.0 669 2         | 19.0 246 2         | 19.0 262 2                               | 19.0 242 1         | 19.0 242 2         | 19.0 242 2         | 19.0 245 2                               | 19.0 298 2         | 19.0 688 2                               | 18.9 282 2         | 18.9 302 2                              | 18.9 275 2        | 18.9 309 2                              | 18.9 324 2         | 18.9 324                                | 18.9 546 2        | 18.9 248 1<br>18.9 263 2                | 18.9 279 2         | 18.8 248 2         | 18.8 285 2<br>18.8 459 2                 | 18.8 522 2                               | 18.8 267 2         | 18.8 277 2                               | 18.8 295 2<br>18.8 300 2                 | 18.8 352<br>18.8 387                     | 18.7 196 2                               | 18.7 254 2         | 18.7 255 2         | 18.7 259 2<br>18.7 274 2                 | 18.7 286 2        | 18.7 237 2                               | 18.7 256 2                              | 18.7 417 2 0       | 18.7 196 2<br>18.7 235 1                 | 18.7 242 2        | 18.6 245                             | 18.6 265 2<br>18.6 267 2                | 18.6 282 2<br>18.6 403 2                 |    |
|   | 1346 262                                     |                                          |                                          |                                          |                    |                                           |                    |                    |                                          |                    |                    |                    |                                          |                    |                                          |                    |                                         |                   |                                         |                    |                                         |                   |                                         |                    |                    |                                          |                                          |                    |                                          |                                          |                                          |                                          |                    |                    |                                          |                   |                                          |                                         |                    |                                          |                   |                                      |                                         |                                          |    |
| · | Q6bda8 penaeus jap<br>Q9gtk7 aedes albop     | Qumwrb dermatophag<br>Qonas8 anopheles g | Q/qgn4 anopheles g<br>Q7q956 anopheles g | P98159 drosophila<br>O6df10 xenopus tro  | 09y842 metarhizium | Q/2094 phitebocomus<br>Q00344 cochliobolu | P54628 drosophila  | Q70w31 oncorhynchu | Q6plj6 penaeus jap<br>P24158 homo samien | Ogvkag drosophila  | Q6wn60 branchiosto | 044332 manduca sex | Q6glkl xenopus lae<br>O6plis neogaridina | Q8szg7 drosophila  | O7pia2 anopheles g                       | Q7sig2 solenopsis  | P52905 drosophila                       | Ogvem9 drosophila | Q8mtu7 drosophila<br>Q8mlc4 drosophila  | Q9grg2 tenebrio mo | Q7pr64 anopheles g<br>O6bd01 drosophila | 09v7s7 drosophila | Q9v4w6 drosophila<br>Q9vq99 drosophila  | Q7qkr3 anopheles g | POSO11 SUS SCROFA  | Q29015 sus sp. pre<br>Q7pff5 anopheles g | P35049 fusarium ox<br>P35045 manduca sex | Q07943 bombyx mori | Qoqoss carrinectes<br>Qopvyz triakis scy | Q15098 homo sapien<br>Q96a30 homo sapien | Q7pxg5 anopheles g<br>P20160 homo sapien | Q6r561 ostrinia nu<br>O9vmx9 drosophila  | P54630 drosophila  | Oft775 home sapien | Q7q5e4 anopheles g<br>Q8ire2 drosophila  | Q9vzt0 drosophila | Q/qins anopheres g<br>Q945t9 phytophthor | Q9n6c6 heliothis z                      | Q8sz60 drosophila  | Q61t09 pseudonaja<br>P35047 manduca sex  | Q9vrs6 drosophila | Qeyps arcsopnia<br>Qeqwf2 rattus sp. | Q9v519 drosophila<br>Q9cvu2 mus musculu | fenn<br>dros                             |    |
|   | 2 Q6BDA8<br>2 Q9GTK7                         |                                          |                                          |                                          |                    |                                           |                    |                    |                                          |                    |                    |                    |                                          |                    |                                          |                    |                                         |                   |                                         |                    |                                         |                   |                                         |                    |                    |                                          |                                          |                    |                                          |                                          |                                          |                                          |                    |                    |                                          |                   |                                          |                                         |                    |                                          |                   |                                      |                                         |                                          |    |
|   | .6 339                                       | ٠٠٠                                      | و و                                      | φ. ri.                                   | ı.                 | ūν                                        | n, n               | ່ ພ່               | v. r                                     | i ri               | ri. r              | in.                | ر. 4                                     | 4.                 | 4.4                                      | 4.                 | 4.4                                     | 4.                | 4. 4                                    | . <del>4</del> .   | 4.4                                     | . m. c            | m m                                     | w u                | i ui (             | i wi                                     | ת ת                                      |                    | . m. (                                   | N 01                                     | 4.4                                      | 2.5                                      | . 7. 7             | , -i               | -: -:                                    | ٠<br>-            | -<br>-<br>-                              | ٦.                                      | ! ←! •             | - <u>:</u> -:                            | 4.                | 1-1-1                                | -: -:                                   | <del>-</del>                             | ,, |
|   | 269.5 19                                     | 1 1 5                                    | 13                                       | 269 19<br>68.5 19                        | 68.5 19            | 13                                        | 68.5 19            | 68.5 19            | 1 1                                      | 13                 | 268 19<br>67 5 19  | 19                 | 67.5 19<br>267 19                        | 6 1                | 19                                       | 19                 | 9 -                                     | 13                | 13                                      | 13                 | 266 19                                  |                   | 65.5 1<br>265 1                         | -                  |                    | 265 I<br>64.5 I                          | 64.5 1                                   | 1 ~ ~              | 64.5 19                                  | 19                                       | 264 19<br>63.5 19                        | 63.5 19                                  | 19                 | 263 1              |                                          | -                 | 1 1                                      | ٦,                                      |                    | 263 1<br>62.5 1                          | 62.5              | ч гч ,                               | 262 1                                   |                                          |    |
|   | 273                                          | 276                                      | 128                                      | 80                                       | 183                | 83                                        | 84<br>7            | 986                | 787                                      | 68                 | 06.5               | 20                 | 6 9                                      | 92                 | 96                                       | 86                 | ه<br>و 5                                | 10                | 2 6                                     | 40                 | 902                                     | 0.0               | 80                                      | 915                | 175                | 14                                       | 15                                       | 11                 | 166                                      | 27                                       | 22                                       | 2.24                                     | 26                 | 28                 | 30                                       | 31                | 3 6                                      | 4 د<br>1 م                              | 36.                | 38                                       | 66.4              | 41                                   | 43.                                     | 44                                       |    |

| Q80yd5 mus musculu<br>Q9vmz3 drosophila<br>Q61hi7 photobacter<br>Q9u4i4 plodia inte<br>Q6y1y9 lygus lineo<br>Q7m4i3 megabombus<br>Q7q8q5 anopheles g<br>Q9vcj9 drosophila<br>Q9w1x6 drosophila                                                                                          | PRT; 248 AA.  sequence update) annotation update) 3.4.21) (Kallikrein-like protein 5) 3.4.21) (Kallikrein-like protein 5) 3.4.21) (Kallikrein-like protein 5)  is; Catarrhini; Hominidae; Homo.  is; Catarrhini; Hominidae; Homo.  is; Catarrhini; Hominidae; Homo.  is; Catarrhini; Hominidae; Homo.  is; Catarrhini; Hominidae; Homo.  is; Catarrhini; Hominidae; Homo.  is; Catarrhini; Hominidae; Homo.  is; Catarrhini; Hominidae; Homo.  is; Catarrhini; Hominidae; Homo.  is; Catarrhini; Hominidae; Homo.  is; Catarrhini; Hominidae; Homo.  is; Catarrhini; Hominidae; Homo.  is; Catarrhini; Hominidae; Homo.  is; Catarrhini; Hominidae; Homo.  is; Catarrhini; Hominidae; Homo.  is; LaND 2).  is; LaND 2).  is; Land 2.  is; Land 3.  is; Land 3.  is; Land 3.  is; Land 4.  is And 5.  is And 5.  is And 5.  is And 5.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is And 6.  is                                                                                                                                                                                                                                                                                                           | A., Schmutz J.,<br>ouronne O., Tran-Gyamfi M.,<br>E., Black S., Branscomb E.,<br>Y.M., Christensen M.,<br>P., Denys M., Detter J.C.,                                                                                                                                                                                                            |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1492 248 18.0 374 2 Q80YDS<br>1494 248 18.0 392 2 Q9VMZ3<br>1495 247.5 18.0 260 2 Q9U414<br>1496 247.5 18.0 291 2 Q6YLY9<br>1497 247 18.0 243 2 QYGYY9<br>1499 247 18.0 278 2 Q7Q8Q5<br>1499 247 18.0 350 2 Q9WCJ9<br>1500 247 18.0 360 2 Q9WIX6                                        | REMOUTAL RESERVE TO THE STANDARD; PRT; 248 AA.  COUNTRO, COUNTR.; CALLED CREETED.  COUNTRO, COUNTR.; CALLED SEQUENCE Update)  DE 16-CCT-2001 (Rel. 40, Least sequence update)  DE 16-CCT-2004 (Rel. 40, Least sequence update)  DE 16-CCT-2004 (Rel. 45, Least sequence update)  EXALISTECIA 12 PROCEDURES (EX 34.21) (Kallikrein-like protein 5)  KILLIKTCEIN UNGESPROBIOSI)  EXALISTECIA 12 PROCEDURES (EX 34.21) (Kallikrein-like protein 5)  REMINITED 5066;  SHORTOFER FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SEQUENCE FROM N.A. (ISOPORM 1)  EX SECUENCE FROM N.                                                                                                                                                                                                                                                                                                         | Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J., Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M. Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E. Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M., Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C., |
|                                                                                                                                                                                                                                                                                         | K R R R R R R R R R R R R R R R R R R R                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | R R R R R R R R R R R R R R R R R R R                                                                                                                                                                                                                                                                                                           |
| Q6zmr5 homo sapien<br>Q6it10 pseudonaja<br>Q6xx43 drosophila<br>Q18436 helicoverpa<br>Q72163 dermatophag<br>Q7pv05 anopheles g<br>Q7pvq5 anopheles g<br>Q7pvq3 anopheles g<br>Q18434 helicoverpa<br>P91893 arenicola m<br>Q7q92 anopheles g<br>Q7qxx6 anopheles g<br>Q7qxx6 anopheles g | Quenco drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo drosophila Questo droso                                                                                                                                                                                                                                                                                                     | Q945u0 phytophthor<br>Q9vzs9 drosophila<br>Q7q141 anopheles g<br>Q7qmm2 anopheles g<br>Q7qmm2 anopheles g                                                                                                                                                                                                                                       |
| 00000000000000                                                                                                                                                                                                                                                                          | 524 2 QRNR00<br>334 2 QONRR00<br>242 2 QOYEAO<br>242 2 QOYEAO<br>251 2 QOYEAO<br>252 2 QOYEAO<br>253 1 QOYEAO<br>254 2 QOYEAO<br>255 2 QOWIND<br>255 2 QOYEAO<br>265 2 QOYEAO<br>265 2 QOYEAO<br>266 2 QOYEAO<br>266 2 QOYEAO<br>276 2 QOYEAO<br>276 2 QOYEAO<br>276 2 QOYEAO<br>276 2 QOYEAO<br>277 2 QOYEAO<br>278 2 QOYEAO<br>278 2 QOYEAO<br>278 2 QOYEAO<br>279 2 QOYEAO<br>270 2 QOYEAO<br>270 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>272 2 QOYEAO<br>273 2 QOYEAO<br>274 2 QOYEAO<br>274 2 QOYEAO<br>275 2 QOYEAO<br>276 2 QOYEAO<br>277 2 QOYEAO<br>277 2 QOYEAO<br>278 2 QOYEAO<br>278 2 QOYEAO<br>279 2 QOYEAO<br>270 2 QOYEAO<br>270 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>271 2 QOYEAO<br>2 | 00000                                                                                                                                                                                                                                                                                                                                           |
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Nature 409:685-690(2001).
 Best Local Similarity 100.
Matches 248; Conservative
 RIKEN FANTOM Consortium;
 PRELIMINARY;
 241 IRMIMRNN 248
 241 IRMIMRNN 248
 Mus musculus (Mouse)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Q9CV76;
01-JUN-2001
 Name=Klk12;
 61
 121
 181
 Query Match
 9CV76
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 Kallikrein 12.
Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
KYVDWIRMIRMINN -> NSTLVGLGTSWNFNSCQPF (in
Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M., A Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T., Hange W., Israni S., Jett J., Kadner K., Kimball H., Kobayashi A., Larionov V., Leem S.-H., Lopez P., Lou Y., Lowry S., Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J., Popkie A.P., Predki P., McCready P.M., Medina C., Morgan J., Popkie A.P., Predki P., Salamov A., Salazar A., She X., Smith D., Slezak T., Solovyev V., Thayer N., Tie G., Yang J., Dubchak I., Slezak T., Solovyev V., Thayer N., Tie G., Yang J., Dubchak I., Ne Furey T.S., DeJong P., Dickson M., Gordon D., Bichler E.E., Myers R.M., Rubin E.M., Lucas S.M.;
Rubin E.M., Lucas S.M.;
The DNA sequence and biology of human chromosome 19.";
Hature 428:529:331(2004).

-I- SUBCELLULAR LOCATION: Secreted (Probable).
 Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
 Isold=Q9UKR0-2; Sequence=VSP 005403;
SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 MIM; 605539; -
60 GO:0005576; C:extracellular; NAS.
GO; GO:0004525; F:serine-type endopeptidase activity; NAS.
GO; GO:0004508; P:proteolysis and peptidolysis; NAS.
InterPro; IPR00903; Peptidase_STE_CYS.
InterPro; IPR001254; Peptidase_S1.
 isoform 2).
/FIId=VSP_005403.
BB473E9@F8BAF703 CRC64;
 Event=Alternative splicing; Named isoforms=2;
 IsoId=Q9UKR0-1; Sequence=Displayed;
 PEAM; PF00089; TYYPSIN; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; TYP, SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN ES; 1.
 EMBL, AF135025, AAF06065.1; --
EMBL, AF43524; AG3365.1; --
EMBL, AY356524; AAQ8888.1; --
EMBL, AC011473; AAG23258.1; --
HASP, POOT60; LEZX.
MEROPS, SO1.020; --
Genew, HGNC:6360; KLK12.
 EMBL; AF135025; AAD26426.2; -.
 248 AA; 26733 MW;
 248
622
108
161
161
161
222
222
248
248
 140
172
196
24
163
236
 18
62
62
200
28
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 subfamily
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ACT_SITE
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DISULFID
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 Signal.
SIGNAL
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 CARBOHYD
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 180
 240
 240
 9
 SECTRAIN=CS7BL/6J; TISSUE=Tongue;

STRAIN=CS7BL/6J; TISSUE=Tongue;

The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:563-573(2002).
 STRAIN=CS7BL/60; TISSUB=Tongue;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFBGTSLRCGGVLIDHRWVLTA
 61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRV
 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
 TSSVQPLPLPNDCATAGTECHVSGWG1TNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 STRAIN=C57BL/6J; IISSUE=Tongue;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
 Gaps
 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
 "Functional annotation of a full-length mouse cDNA collection.";
 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male tongue cDNA, RIKBN full-length enriched
library, clone:2310008B01 product:similar to KALLIKREIN 12 (EC
3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (KLK-L5) (Fragment).
 ö
Length 248;
 Indels
 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Score 1374; DB 1;
Pred. No. 3.5e-102;
Mismatches 0;
 234 AA
 (TrEMBLrel. 17, Created)
 PRT;
100.0%; Sco
100.0%; Pro
 Meth. Enzymol. 303:19-44(1999)
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akanira S., Akimura T., Arai A., Aono H.,

Adachi J., Aizawa K., Akanira S., Akimura T., Bukunishi Y., Furuno M.,

Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Managaki T., Hara A., Hayatawi N., Hirancka T., Kato H.,

Kawai J., Kojima Y., Konon H., Kouda M., Koya S., Kurihara C.,

Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Muramatsu M., Hayashizaki Y.,

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK009217; BAB26143.1; -.

BRBS; PROFFOR DELLAMARIYER BELONGS to peptidase family SI.

REMBL; AK009217; BAB26143.1; -.
 74 EHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPNDC 133
 60 EHSLIKLDWIEQLRHITFSIIHPSYQGAYQNHEHDLRLLRLARINRPIHLTRAVRPVALPSSC 119
 134 ATAGTECHVSGWGITNHPRNPFPDLLQCLALSIVSHATCHGVYPGRITSNMVCAGGVPGQ 193
 120 VTTGAMCHVSGWGTTTNKPWDPFPPDRLQCLNLSTVSNETCRAVFPGRVTENMLCAGGEAGK 179
 1 LSQADREKIYNGVECVKNSQPWQVGLFHGKYLRCGGVLVDRKWVLTAAHCR-DKYVVRLG 59
 73
SEQUENCE FROM N.A.

C STRAIN=C57BL/6J; TISSUE=Tongue;

X MEDLINE=C57BL/6J; TISSUE=Tongue;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

M. Somi N., Ishii T., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto N., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
 LSQAATPKI FNGTECGRNSQPWQVGLFEGTSLRCGGVLI DHRWVLTAAHCSGSRYWVRLG
 Gaps
 DACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
 180 DACQGDSGGPLVCGGVLQGLVSWGSVGPCGQKGIPGVYTKVCKYTDWIRIVIRNN 234
 ij
 DB 2; Length 234;
 41; Indels
 MGD; MGI:1916761; KIk12.

MGD; MGI:1916761; KIk12.

GO; GO:0008233; F:ehymotrypsin activity; IEA.

GO; GO:0008233; F:epeptidase activity; IEA.

GO; GO:0008295; F:trypsin activity; IEA.

GO; GO:000508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR001254; Peptidase S1.

InterPro; IPR001314; Peptidase S1.

InterPro; IPR001314; Peptidase S1A.

PRONOTE: PR00099; Trypsin, 1.

PRINTS; PR00022; CHYMOTRYPIN.

SMART; SM00020; Tryp SPC; 1.

PROSITE; PS00240; TRYPSIN DOM.

PROSITE; PS00134; TRYPSIN INS; UNKNOWN.1.
 234 AA; 25888 MW; 6D81E609EDD39110 CRC64;
 69.3%; Score 952.5; DB 2 70.6%; Pred. No. 1.9e-68;
 27; Mismatches
 Hydrolase; Protease; Serine protease.
 Matches 166; Conservative
 MEROPS; S01.020; -
 Similarity
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 194
 Query Match
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RESULT 3 KLK8\_HUMAN

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MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; A. Clark H.F., Gurney A.L., Abaya E. Baker K., Baldwin D., Brush J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., A. Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vi S., Yu G., Yuan J., Zhang M., Zhang K., Xie M.-H., Yansura D., A. Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;

"The secreted protein discovery initiative (SPDI), a large-scale fefort to identify novel human secreted and transmembrane proteins: a transmembrane proteins: a
KLK8 HUMAN STANDARD; PRT; 260 AA.
060259; Q9HCB3; Q9UIL9; Q9UQ47;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Ovasin) (Serine protease TADG-14) (Tumor-associated differentially expressed gene-14 protein) (UNQ283/PRO322).
Name=KLK8; Synonyms=NRPN, PRSS19, TADG14;
 O'Brien T.J.; "Cloning of tumor-associated differentially expressed gene-14, a novel
 Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
 Yoshida S., Taniguchi M., Hirata A., Shiosaka S.; "Sequence analysis and expression of human neuropsin cDNA and gene."; Gene 213:9-16 (1998).
 Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.; "A novel form of human neuropsin, a brain-related serine protease, is generated by alternative splicing and is expressed preferentially in human adult brain.";
 TISSUE=Hippocampus; MEDLINE=98372070; PubMed=9714609; DOI=10.1016/S0378-1119(98)00232-7;
 SEQUENCE FROM N.A. (ISOFORM 1).

Gan L., Gelinas R., Gown A.M., Moss P., Smith R., Wang K.;

"Molecular cloning and characterization of a novel serine protease,
ovasin, a potential molecular marker for ovarian carcinomas.";
submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 MEDLINE=99413504; PubMed=10485494;
Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 SEQUENCE FROM N.A. (ISOFORM 1).

PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;

Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.
Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";

Gene 257:119-130(2000).
 serine protease overexpressed by ovarian carcinoma.";
Cancer Res. 59:4435-4439(1999).
 SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1)
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 Eur. J. Biochem. 260:627-634(1999).
 MEDLINE=99203457; PubMed=10102990;
 Genome Res. 13:2265-2270(2003).
 SEQUENCE FROM N.A. (ISOFORM 1).
 SEQUENCE FROM N.A. (ISOFORM 1).
 Homo sapiens (Human).
 NCBI_TaxID=9606;
 TISSUE=Brain;
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 Potential.

By similarity.

Neuropsin.

Charge relay system (By similarity).

Charge relay system (By similarity).

Charge relay system (By similarity).

By similarity.

By similarity.

By similarity.

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By similarity.
 Olsen A.S., Carrano A.V.;
"Sequence analysis of chromosome 19q13.4.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S., Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 Isold=O60259-2; Sequence=VSP 005401;
TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in pancreas while isoform 2 is expressed in adult brain and hippocampus Both forms are also found in fetal brain and placenca. Not detected in kidney, spleen, liver and lung. SIMILARITY: Belongs to the peptidase SI family. Kallikrein
 Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
 hippocampal plasticity.
--- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-,
--- SUBCELLULAR LOCATION: Secreted.
--- ALTERNATIVE PRODUCTS:
 ; 605644; -.
GO:0008236; F:serine-type peptidase activity; TAS.
GO:0007399; P:neurogenesis; TAS.
 Event=Alternative splicing; Named isoforms=2;
 IsoId=O60259-1; Sequence=Displayed;
 InterPro; IPR00903; Pept Ser Cys.
InterPro; IPR00124; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
Pfam; PR00189; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS0240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
 EMBL; AB009849; BAA28673.1; --
EMBL; AB012761; BAA28676.1; --
EMBL; AB010760; BAA88684.1; --
EMBL; AB0008920; BAA82665.1; --
EMBL; AB0008927; BAA82666.1; --
EMBL; AF055992; AAD56050.1; --
EMBL; AF095742; AAD25979.1; --
EMBL; AF095743; AAD25979.1; --
EMBL; AF095743; AAD23974.1; --
EMBL; AF095743; AAD33861.1; --
EMBL; AY359036; AAQ89395.1; --
EMBL; AC011473; AAG23254.1; --
HSSP; P00760; HEXX.
MEROPS; S01.244; --
GENEW; HGNC:6369; KLK8.
 29
33
33
212
212
212
23
26
28
20
21
23
 .gnal; Zymogen
 subfamily.
 Name=1
 ACT_SITE
ACT_SITE
 ACT_SITE
DISULFID
 CARBOHYD
 DISULFID
 DISULFID
 DISULFID
 DISULFID
 DISULFID
 SIGNAL
 PROPEP
 MIM;
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 62 HCSGSRYWVRLGEHSISQLDWTEQIRHSGFSVTHPGYLGAST-SHEHDIRLIRRIRLPVRV 120
 251
 61
 72
 133 GSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQ1
 193 TDGMYCAGSSKGADTCQGDSGGPLVCDGALQGITSWGS-DPCGRSDKPGVYTNICRYLDW
 13 MFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAA
 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
 5 IFLLL---CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 2
 DB 1; Length 260;
 45.9%; Score 630.5; DB 1; Length 50.2%; Pred. No. 1.3e-42; ive 24; Mismatches 93; Indels
 Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: Belongs to peptidase family S1.
WRSNPLPPAA (in isoform 2)
 FTId=VSP_005401.
EF439E5B8C83E660 CRC64;
 01-WAR.2003 (TrEMBLrel. 23, Created)
1-WAR.2003 (TrEMBLrel. 23, Last sequence update)
01-WAR.2004 (TrEMBLrel. 26, Last annotation update)
Kallikrein 8, isoform 1 preproprotein.
 Sci. U.S.A. 99:16899-16903(2002)
 260 AA.
 /FTIG=VSP
 28048 MW;
 -!- SIMILARITY: Belongs to p
EMBL, BC040887; AAH40887.1;
 and mouse cDNA sequences.";
 123; Conservative
 PRELIMINARY;
 Local Similarity
 260 AA;
 241 IRMIM 245
 SEQUENCE FROM N.A. TISSUE=Brain;
 SEQUENCE FROM N.A.
 rissum=Brain;
 Name=KLK8
 73
 SEQUENCE
 Query Match
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Q8IW69
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 -!- MASS
 180
 240
 62 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAST-SHEHDLRLLRLRLPVRV 120
 133 GSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQI 192
 61
 72
 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 TSNWYCAGGVPGQDACQGDSGGPLYCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
 5 IFLLL --- CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
 Yoshida S., Hirata A., Inoue N., Shiosaka S.; "Cloning and assignment of mouse neuropsin gene, Prss19 to chromosome
 Gaps
 SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=Hippocampus;
MEDLINE=95.348H; PubMed=7623137;
MEDLINE=95.348H; PubMed=7623137;
MEDLINE=95.348H; S., Kato K., Momota Y., Suzuki J., Tanaka T.,
Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
"Expression and activity-dependent changes of a novel limbic-serine protease gene in the hippocampus.";
J. Neurosci. 15:5088-5097(1995).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
 2
 'Match 45.7%; Score 627.5; DB 2; Length 260; Local Similarity 50.2%; Pred. No. 2.2e-42; les 123; Conservative 24; Mismatches 93; Indels 5;
 Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
 GO; GO:0004265; F:chymotrypsin activity; IEA.
GO; GO:0004256; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
Fram; PR00899; Trypsin; 1.
FRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00020; Tryp_SRF; 1.
FROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
 28090 MW; EF5934EB96295660 CRC64;
 15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8)
Mame=Klk8; Synonyms=Nrpn, Prss19;
Mus musculus (Mouse).
 260 AA
 [3] SEQUENCE FROM N.A. STRAIN=Czech II; TISSUE=Mammary gland;
 Hydrolase; Protease; Serine protease.
 15-JUL-1999 (Rel. 38, Created)
 Matches 123; Conservative
 STANDARD;
 260 AA;
 241 IRMIM 245
 |: |:
252 IKKII 256
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 MOUSE
 181
 SEQUENCE
 Query Match
 NRPN MOL
Q61955;
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.R., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhard N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhard N.K.,
A physina R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A papleton M., Soares M.B., Bonaldon M.F., Carahnof T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toophyuki S., Carahnof P.L., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan R.J., Make J.A., Gupt. Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E.,
Butterfield W.S.N., Krzywinski W.I., Marra M.A.,
Butterfield W.S.N., Krzywinski W.I., Marra M.A.,
Butterfield W.S.N., Krzywinski W.I., Marra M.A.,
Butterfield W.S.N., Krzywinski W.I., Marra M.A.,
Butterfield W.S.N., Krzywinski W.I., Marra M.A.,
Butterfield W.B. Welley W. Marya M.A.,
Butterfield W.B. Welley W. Welley W. Marra M.A.,
Butterfield W.B. Welley W.B. W.,
Butterfield W.B. Welley W.B. W.,
Butterfield W.B. Welley W.B. W.,
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Butterfield W.B. Welley W.B. W.,
Butterfield W.B. Welley W.B. W.,
Butterfiel
 system of
pyramidal
 TISSUE=Hippocampus;

MEDLINE=99134351, PubMed=9933620; DOI=10.1074/jbc.274.7.4220;

Kishi.NE=9134351, PubMed=9933620; DOI=10.1074/jbc.274.7.4220;

Kishi.NE=9134351, PubMed=9933620; DOI=10.1074/jbc.274.7.4220;

Shiosaka S., Hakoshina T.;

"Crystal structure of neuropsin, a hippocampal protease involved in kindling epileptogenesis.";

J. Biol. Chem. 274:4220-4224 (1999).

-I. FUNCTION: Suggested to be involved in kindling epileptogenesis and
 CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
ENZYME REGULATION: Strongly inhibited by disopropyl
fluorophosphate, leupeptin and (4-amidinophenyl)methanesulfonyl 1-
 hippocampal plasticity. Has a strong proteolytic activity against fibronectin.
 STRAIN=BALB/C; TISSUE=Brain;
MEDLINE=9825202; PubMed=9556608; DOI=10.1074/jbc.273.18.11189;
Shimizu C., Yoshida S., Shibbata M., Kato K., Momota Y., Matsumoto K.
Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
"Characterization of recombinant and brain neuropsin, a plasticity-
 SEQUENCE OF N-TERMINUS, CHARACTERIZATION, AND MASS SPECTROMETRY
 NOTE-Ref.4.
SIMILARITY: Belongs to the peptidase S1 family. Kallikrein subfamily.
 TISSUE SPECIFICITY: Expressed specifically in the limbic mouse brain and is localized at highest concentration in neurons of the hippocampal Cal-3 subfields.

MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260;
 SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260;
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
 related serine protease.";
J. Biol. Chem. 273:11189-11196(1998).
 SUBCELLULAR LOCATION: Secreted.
 InterPro; IPR009003; Pept_Ser_Cys.
 EMBL; D30785; BAA06451.1; -.
EMBL; AB032202; BAA92435.1; -.
EMBL; BC055895; AAH55895.1; -.
 PDB; 1NPM; X-ray; A/B=33-256
 mouse cDNA sequences."
 MEROPS; S01.244; -.
MGD; MGI:892018; Klk8.
 PIR; 156559; 156559
 luoride.
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 SEQUENCE FROM N.A.

C STRAIN=Flascher; TISSUE=Brain;

X MEDLINE=99389725; PubMed=972524; DOI=10.1074/jbc.273.36.23004;

MEDLINE=99389725; PubMed=972524; DOI=10.1074/jbc.273.36.23004;

Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;

L "Serine proteases in rodent hippocampus.";

L "Serine proteases in rodent hippocampus.";

L "Serine proteases in rodent hippocampus.";

L "Serine proteases in rodent hippocampus.";

C "I ENUCTION: Suggested to be involved in kindling epileptogenesis and hippocampal plasticity. Has a strong proteolytic activity against fibronecin (By similarity).

C "I CATALYTIC ACTIVITY: Preferential cleavage: Arg., Lys-.

C "I SUBCELLULAR LOCATION: Secreted (By similarity).

C "I SINILARITY: Belongs to the peptidase SI family. Kallikrein subfamily.
 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
 TEGWYCAGSSNGADTCQGDSGGPLVCDGMLQGITSWGS-DPCGKPEKPGVYTKICRYTTW
 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 Name=Klk8; Synonyms=Bspl, Nrpn, Prssl9;
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
 NRPN_RAT STANDARD; PRT; 260 AA.
088780,
115-JUL-1999 (Rel. 38, Created)
115-JUL-1999 (Rel. 38, Last sequence update)
25-GOT-2004 (Rel. 45, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine protease 1).
 (By similarity). (By similarity). (By similarity).
 InterPro; IPR009003; Pept_Gase_S1.
InterPro; IPR001254; Pept_Gase_S1.
InterPro; IPR001214; Pept_Gase_S1.
InterPro; IPR001314; Pept_Gase_S1.
InterPro; IPR001314; Pept_Gase_S1.
INTERPOSE I
 Charge relay system
Charge relay system
Charge relay system
 EMBL; AJ005641; CAA06643.1; -. HSSP; Q61955; 1NPM.
 32
260
73
120
212
 241 IRMIMRN 247
 252 IKKTMDN 258
 MEROPS; S01.244; -
 73
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 193
 ACT_SITE
ACT_SITE
ACT_SITE
 RESULT
NRPN RA
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 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-TSHEHDLRLLRLRLPVRV 120
 72
 61
 13 İLLİLEMGAWAĞLTRAQGSKİLEĞRECIPHSQPWQAALFQĞERLICĞĞVLVGDRWVLTAA
 IFLILCV---LGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
InterPro; IPR001254; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN JER; 1.
PROSITE; PS00135; TRYPSIN JER; 1.
3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
 similarity). similarity). similarity).
 N-linked (GlcNAc. . .) (Potential)
 5;
 45.3%; Score 622.5; DB 1; Length 260; 49.0%; Pred. No. 5.6e-42; ive 28; Mismatches 93; Indels 5.
 256
28523 MW; BESF6F6BE37CD60E CRC64;
 8 (B)
 system
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 Charge relay s
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Charge relay s
 Neuropsin.
 Potential
 Serine protease; Signal; Zymogen
 Query Match
Best Local Similarity 49.0%
Matches 121; Conservative
 245 :
260 AA;
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64 SGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-TSHEHDLRLLRLRLPVRVTS 122
 123 SVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITS 182
 NAVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGTPGVYTY1CKYVDWIR 242
 195 GAVCAGSSNGADICQGDSGGPLVCNGVLQGITTWGS-DPCGKPEKPGVYTKICRYTNWIK 253
 135 KVKPIELANLCPKVGQKCIISGWGTVTSPQENFPNTLNCAEVKIYSQNKCERAYPGKITE 194
 63
 SEQUENCE FROM N.A. (ISOFORM 1).
MEDIJINE=20130117; PubMed=10662548; DOI=10.1006/geno.1999.6072;
Yousef G.M., Socrilas A., Diamandis E.P.;
"Genomic organization, mapping, tissue expression, and hormonal regulation of trypsin-like serine protease (TLSP PRSS20), a new member of the human kallikrein gene family.";
 5 IFLLL-CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWYLTAAHC
 Gaps
 TISSUE=Hippocampus, and Prostate;
MEDLINE=20329229; PubMed=10872828; DOI=10.1006/bbrc.2000.2761;
Mitsui S., Yamada T., Okui A., Kominami K., Uemura H., Yamaguchi N.;
"A novel isoform of a kallikrein-like protease, TLSP/hippostasin,
(PRSS20), is expressed in the human brain and prostate.";
Biochem. Biophys. Res. Commun. 272:205-211(2000).
 TISSUE-Hippocampus;
MEDLINE-984388738; PubMed=9765601; DOI=10.1016/S0167-4781(98)00116-X;
MSDLINE-98438738; PubMed=9765601; DOI=10.1016/S0167-4781(98)00116-X;
MSShida S., Taniquchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;
"CDNA cloning and expression of a novel serine protease, TLSP.";
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2004 (Rel. 45, Last annotation update)
Kallikrein 11 precursor (EC 3.4.21.-) (Hippostasin) (Trypsin-like protase) (UNQ649/PRO1279).
Name=KLK11; Synonyms=PRSS20, TLSP;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 .) (Potential)
 3,
 45.2%; Score 621.5; DB 1; Length 260;
173 By similarity.
74 By similarity.
246 By similarity.
218 By similarity.
198 By similarity.
23 By similarity.
23 By similarity.
23 N-linked (GlCNAc. . .) (Pote N-linked (GlCNAc. .) (Pote N-linked (GlCNAc. . .) (Pote N
 90; Indels
 Pred. No. 6.7e-42;
 32; Mismatches
 250 AA.
 Biochim. Biophys. Acta 1399:225-228(1998)
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 SEQUENCE FROM N.A. (ISOFORM 1).
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SEQUENCE FROM N.A. (ISOFORM 1).
 48.68;
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O9UBX7; 075837; 09NS65;
 Genomics 63:88-96(2000)
 173
74
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233
 Homo sapiens (Human)
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260 AA;
 Local Similarity
 243 MIM 245
 254 KTM 256
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Ratschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhard N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M., Soares M.B., McKernan K.J., Maramson R.D., Mullahy S.J.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rochards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

Rapleton D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

Rapleton B.K., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rochiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Cheerzation and initial analysis of more than 15,000 full-length human

T. "Generzation and initial analysis of more than 15,000 full-length human
 PubMed=15057824, DOI=10.1038/nature02399;

Ry Gordon L.A., Terry A., Schmutz J.,
Ramwood J., Gordon L.A., Terry A., Schmutz J.,
Ramwood J., Gordon L.A., Terry A., Schmutz J.,
Ramwood J., Gordon L.A., Capelen D., Couronne O., Tran-Gyamfi M.,
Rampeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,
Rampeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,
Rampeel S., Carrano A.V., Caoile C., Chan Y.M., Dents M.,
Rampeel S., Carrano A.V., Dalin B., Dehal P., Denys M., Detter J.C.,
Rampina T., Flowers D., Foroquios D., Garcia C., Georgescu A.M.,
Rampina T., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
Robayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
Ramifatti S., Martinaz D., McCready P.M., Medina C., Morgan J.,
Ramifatti S., Martinaz D., McCready P.M., Medina C., Morgan J.,
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Ramirez T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
Ramirez T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
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Ramirez D. Dickson M., Gordon D., Eichler E.E.,
Ramirez D. Stubbs L., Rokhsar D.S., Myers R.M.,
 | SECURIOR FROM N.A. (ISOFORM 1).
| SEQUENCE FROM N.A. (ISOFORM 1).
| SEQUENCE FROM N.A. (ISOFORM 1).
| MEDLINE=22887296; PubMed=1297309; DOI=10.1101/gr.1293003; W.A. Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Baton D., Foster J., Grimaldi C., Gu Q., Hass P.B., Heldens S., Huang A., Kim H.S., Kilmandst L., Jin Y., Johnson S., Lee J., Hawis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J., Senhagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandien R., Watanabe C., Waleand D., Woods K., Xie M.-H., Yansura D., Na. Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.,
| The secreted protein discovery initiative (SPDI), a large-scale of effort to identify novel human secreted and transmembrane proteins: a reference of the content of the con
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Possible multifunctional protease. Efficiently cleaves
bz-Phe-Arg-4-methylcoumaryl-7-amide, a kallikrein substrate, and
weakly cleaves other substrates for kallikrein and trypsin.
 .
.
 Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J. Moss P., Paeper B., Wang K.; Sequencing and expression analysis of the serine protease gene cluster located in Chromosome 19q13 region."; Gene 257:119-130(2000).
 TISSUE=Testis; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 Rubin E.M., Lucas S.M.; "The DNA sequence and biology of human chromosome 19.";
 PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
 bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
 SEQUENCE FROM N.A. (ISOFORM 1).
 and mouse cDNA sequences.";
 Nature 428:529-535(2004).
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-!- SUBCELLULAR LOCATION: Secreted

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63 CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKWASPVSI 122
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 TSSVQPLPLPNDCATAGTECHVSGWG1TNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
 Conservative
 PRELIMINARY;
 240 WIRMIMRNN 248
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242 WIQETMKNN 250
 Local Similarity
es 118; Conserv
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 Query Match
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 IsoId=Q9UBX7-2; Sequence=VSP 005402; ISSUE SPECIFICITY: Expressed in brain, skin and prostate. Isoform 1 is expressed preferentially in brain; isoform 2 in prostate. SIMILARITY: Belongs to the peptidase SI family. Kallikrein
 d -> MQRLRWLRDWKSSGRGLTAAKEPGARSSPLQAM (in jeoform 2).
 similarity).
similarity).
similarity).
 GO, GO:0008236; F:serine-type peptidase activity; TAS.
InterPro; IPR001254; Pept Ser Cys.
InterPro; IPR001254; Peptidase Si.
InterPro; IPR001314; Peptidase Si.
InterPro; IPR001314; Peptidase Si.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
 Activation peptide (Potential).
Kallikrein 11.
Charge relay system (By similarity Charge relay system (By similarity Charge relay system (By similarity By similarity.
By similarity.
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N-linked (GlCNAc. . .) (Potential)
N-linked (GlCNAc. . .) (Potential)
N-linked (GlCNAc. . .) (Potential)
N-linked (GlCNAc. . .) (Potential)
N-linked (GlCNAc. . .) (Potential)
N-linked (GlCNAc. . .) (Potential)
N-linked (GlCNAc. . .) (Potential)
N-linked (GlCNAc. . .) (Potential)
M-> MQRLKWLRDWKSSGRGLTAAKEPGARSSP
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 (Potential)
 (Potential)
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; Pred. No. 1.1e-41;
35; Mismatches 89; Indels 5.
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192D910BBCDC7A56 CRC64;
 Event=Alternative splicing; Named isoforms=2;
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 EMBL, AB012917, BAA33404.1; ALT_INIT.
EMBL, AB041036; BAA88713.1; --
EMBL, AB041036; BAA8677.1; --
EMBL, AP164623; AAA7815.1; --
EMBL, AP243527; AAG33364.1; --
EMBL, AP259014, AAG33334.1; --
EMBL, AC011473; AAG33237.1; --
EMBL, BC022068; AAH22068.1; --
EMSP, POOTGO, IEXX.
MENOPS, S01.257; --
Genew, HGNC.6359; KLKII.
 /FTId=VSP
 27466 MW;
 45.0%;
 Matches 120; Conservative
ALTERNATIVE PRODUCTS:
 H-InvDB; HIX0015375; -.
 250 AA;
 Similarity
 MIM; 604434; -.
 gnal; Zymogen.
 subfamily.
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5
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 of
 20 KLLEGEECAPHSÓPWÓVALYERGRENCGASLISPHWVLSAÁHCOSRFMRVRLGEHNLRKR
 DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLIRLRLPVRVTSSVQPLPLPNDCATAGTEC
 HVSGWGITNH------PRN--PPPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGV
 21 KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL
 14; Gaps
 SEQUENCE FROM N.A.
MEDLINE=21094033; PubMed=11177570; DOI=10.1089/104454900750058080;
Olsson A.Y., Persson A.M., Valtonen-Andre C., Lundwall A.;
Glandular kallikreins of the cotton-top tamarin: molecular cloning the gene encoding the tissue kallikrein.";
DNA Cell Biol. 19:721-727(2000).
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Platyrrhini, Callitrichidae, Saguinus. NCBI TaxID=9490,
 Length 255;
 44.5%; Score 611; DB 2; Length 25
49.4%; Pred. No. 4.6e-41;
ive 31; Mismatches 76; Indels
 SEQUENCE FROM N.A.
Olsson Y., Persson M., Lundwall A.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-! SINILARITY: Belongs to peptidase family S1.
EMBL, AF173845; AAS45302.1; -.
HSSP; P00761; 1AKS.
 GO; GO:000423; F:chymotrypsin activity; IEA.
GO; GO:0004233; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin and peptidolysis; IEA.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR00909; Pept_Ser_Cys.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00022; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_I.
 Hydrolase; Protease; Serine protease.
SEQUENCE 255 AA; 28078 MW; A040914ABC8FEC8D CRC64;
 05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
255 AA
 Saguinus oedipus (Cotton-top tamarin)
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CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPVRV 120

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4 LOLILLALATGLVGGET-RIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH LSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH

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MEDLINE=22325484; PubMed=12437987; DOI=10.1016/S0006-291X(02)02629-3;
 Matches 124; Conservative
 PRELIMINARY;
 HSSP; P00760; 1EZX.
MEROPS; S01.297; -.
 SECUENCE FROM N.A.
 SEQUENCE FROM N.A.
 TISSUE=Prostate;
 NCBI_TaxID=9606;
 Name=KLK11;
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 Query Match
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 66 PHYVILIGEHNLEKTDGCEQRRMATESFPHPGFNNSLPNKDHRNDIMLVKMSSPAFITRA 125
 VQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSN 183
 184 MVCAG-GVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTXICKYVDWIR 242
 66 SRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPVRVTSS 123
 191 -PGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
 FLLLCVLGLSQAATPKI FNGTECGRNSQPWQVGLFEGTSLRCGGVL I DHRWVLTAAHCSG
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 4; Gaps
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 SEQUENCE FROM N.A.

PubMed=1520312; DOI=10.1016/j.ygeno.2004.01.009;
Olsson A.Y., Lulja H., Lundwall A.;
"Taxon-specific evolution of glandular kallikrein genes and identification of a progenitor of prostate-specific antigen.";
Genomics 84:147-156(2004).

-I MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.
 Query Match 44.4%; Score 610; DB 2; Length 250; Best Local Similarity 46.7%; Pred. No. 5.4e-41; Matches 115; Conservative 37; Mismatches 90; Indels
 1 18 Potential.
22 250 glandular kallikrein 11.
250 AA; 27630 MW; 247B29D3F0DEF8F1 CRC64;
 Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
 250 AA
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 25-OCT-2004 (TrEMBLrel. 28, Create 25-OCT-2004 (TrEMBLrel. 28, Last 8 25-OCT-2004 (TrEMBLrel. 28, Last a Glandular kallikrein 11 precursor.
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
 Name=Klk15; Synonyms=KLK15;
 PRELIMINARY;
 Rattus norvegicus (Rat).
 PRELIMINARY;
 243 MIMRNN 248
 EVMRNN 250
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 NCBI_TaxID=10090;
 Name=Klk11;
 198
 124
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 Query Match
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 Q63ZF2;
 Q632F2
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Q8CGR4
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63 CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLRVRVTS 122
 61 CQTRFWRVRLGEHNLRKFDGPEQLRSVSRIIPHPGY--EARTHRHDIMLLRLFKPARLTA 118
 123 SVQPLPLPNDCATAGTECHVSGWGITNHPRNP-----FPDLLQCLNLSIVSHAT 171
 62
 9
 5 IFLLLCVLGLSQAAT -- PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
 Gaps
Olsson A.Y., Lundwall A.; "Organization and evolution of the glandular kallikrein locus in Mus
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 22;
 Length 254;
 77; Indels
 Adams M., Mural R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
-i- SHIMLARITY: Belongs to peptidase family S1.
EMBL; AXISS43; AAN78422.1; -.
HSSP; P00760; 1EZX.
 Nakamura T., Mitsui S., Miki T., Yamaguchi N.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 Hydrolase, Protease, Serine protease.
SEQUENCE 254 AA; 28042 MW; AA9E38BEBDD01861 CRC64;
 MEKCHS; SULLS.,
(G) MG1:244753; Klk15.
(G) GO:0004263; F:chymotrypsin activity; IEA.
(G) GO:0004295; F:crypsin activity; IEA.
(G) GO:0004295; F:crypsin activity; IEA.
(G) GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR009003; Pept_Ser_Gys.
 (TrEMBLrel. 23, Last sequence update) (TrEMBLrel. 26, Last annotation update)
 Biochem. Biophys. Res. Commun. 299:305-311(2002)
 / Match 44.3%; Score 608; DB 2; Local Similarity 49.0%; Pred. No. 7.9e-41; nes 124; Conservative 30; Mismatches 77,
 275 AA
 PERM; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp. SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN HIS; UNKNOWN 1.
 (TrEMBLrel. 23, Created)
 PRT;
 01-MAR-2003 (TrEMBLrel. 23, Cre 01-MAR-2003 (TrEMBLrel. 23, Las 01-MAR-2004 (TrEMBLrel. 26, Las Variant form hippostasin/KLK11.
 GVYTYICKYVDWI 241
 GVYTKVČSÝLEWÍ 247
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64 SGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSS 123
 124 VQPLPLPNDCATAGTECHVSGWGITNH-----PRN--PFPDLLQCLNLSIVSHATCH 173
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; analysis of more than 15,000 full-length human "Generation and initial analysis of more than 15,000 full-length human
 8 LLCVLGLSQAAT----PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHC
 3 LILTLSFILLASTAQDGDKLLEGDECAPHSQPWQVALYERGRFNCGASLISPHWVLSAAHC
 174 GVYPGRITSNMVCAGGV-PGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYT
 PubMed=11010966; DOI=10.1074/jbc.M005432200;
Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis E.P.;
 Craniata; Vertebrata; Euteleostomi;
 SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY
 HSSP, P00761; JAKS.

GO, GO:0004263; F:chymotrypsin activity; IEA.

GO, GO:0004295; F:trypsin activity; IEA.

GO; GO:0006209; F:trypsin activity; IEA.

GO; GO:0006209; F:trypsin activity; IEA.

GO; GO:0006209; F:trypsin and peptidolysis; IEA.

InterPro; IPR00124; Peptidase_S1A.

InterPro; IPR0009003; Pept Ser_Cys.

FFam; PF00099; Trypsin; 1.

PRINTS; PR00722; CTWOOTRYPSIN.

SMART; SM00020; TrypSFC; 1.

RROSITE; PS50240; TRYPSIN DOM; 1.

RROSITE; PS00134; TRYPSIN DOM; 1.

RROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.

HYdrolaes; Procease; Serine procease.

SEQUENCE 255 AA; 28016 MW; 1591B784D4A39C4F CRC64;
 86; Indels
 Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases -! - SIMILARITY: Belongs to peptidase family S1.
 Catarrhini, Hominidae;
 KLKF HUMAN STANDARD; PRT; 256 AA.
O9H2R5; Q15358; Q9H2R3; Q9H2R4; Q9HBG9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2004 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Kallikrein 15 precursor (EC 3.4.21.-) (ACO protease)
 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 43.6%; Score 599; DB 2;
46.9%; Pred. No. 4.2e-40;
iive 32; Mismatches 86;
 EMBL; BC069518; AAH69518.1; -. EMBL; BC069480; AAH69480.1; -.
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 248
 : | |:: | |: | |: | 240 KVCHYLEWIRETMKRN 255
 SEQUENCE FROM N.A.
TISSUE=PCR rescued clones;
Director MGC Project;
 233 YICKYVDWIRMIMRNN
 Best Local Similarity 46.9
Matches 120; Conservative
 Homo sapiens (Human).
 NCBI_TaxID=9606;
 Name=KLK15;
 Query Match
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TISSUB-PCR rescued clones;

TISSUB-PCR rescued clones;

MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Rischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blant N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heibh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Porshyuki S., Carninci P., Prange C.,

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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 98 YLGA--STSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPF 155
 156 PDLLQCLNLSIVSHATCHGVYPGRITSNMVCAG-GVPGQDACQGDSGGPLVCGGVLQGLV 214
 183 PHTLRCANITIIEHQKCENAYPGNITDTWVCASVQEGGKDSCQGDSGGPLVCNQSLQGII 242
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 3 LSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
 Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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GO; GO:0004285; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006289; P:trypsin activity; IEA.
InterPro; IPR001254; Peptidase_SI.
InterPro; IPR001314; Peptidase_SIA.
InterPro; IPR001314; Peptidase_SIA.
InterPro; IPR00903; Pept_Ser_Gys.
Pfam; PF00089; Trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
SNART; SM00020; Tryp_SPS; I.
PROSITE; PS00134; TRYPSIN_DOM; I.
PROSITE; PS00134; TRYPSIN_DIS; UNKNOWN_I.
 275 AA; 30165 MW; 257A42B28F40E2C4 CRC64;
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
-1- SIMILARITY: Belongs to peptidase family Sl.
EMBL, AB078780; BAC54105.1; -.
HSSP; P00760; 1EZX.
 215 SWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
 255 AA
 Kallikrein 15, isoform 4 preproprotein.
 Hydrolase, Protease, Serine protease.
SEQUENCE 275 AA; 30165 MW; 257A42
 Best Local Similarity 44.28
Matches 121; Conservative
 PRELIMINARY;
 Homo sapiens (Human).
 NCBI_TaxID=9606
 63
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 018190
 RESULT 12
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 IsoId=Q9H2R5-4; Sequence=VSP_005404; ISSUE SPECIFICITY: Highest expression in the thyroid gland. Also expressed in the prostate, salivary, and adrenal glands and in the colon testis and kidney. SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 IsoId=Q9H2R5-2; Sequence=VSP 005405; Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;
 not yet known
 MEDLINE=94289486; PubMed=8018728; DOI=10.1016/0167-4781(94)90018-3;
 SEQUENCE FROM N.A.
PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
Moss P., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Pagner B., Wang K.;
"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";
Molecular cloning of the human kallikrein 15 gene (KLK15). Up
 Dihanich M.E., Spiess M.; "A novel serine proteinase-like sequence from human brain."; Biochim. Biophys. Acta 1218:225-228(1994).
 GO; GO:0005576; C:extracellular; NAS.
GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
 SPLICE ISOPORM(S) THAT ARE POTENTIAL NWD TARGET(S). Pubmed=14759258; DOI=10.1186/gb-2004-5-2-r8; Hillman R.T., Green R.E., Brenner S.E.; "An unappreciated role for RNA surveillance."; Genome Biol. 5:RESEARCHO08.1-KESEARCHO08.16(2004).
-!- FUNCTION: Protease whose physiological substrate is 1:SUBCELIULAR LOCATION: Secreted (Probable).
 IsoId=Q9H2R5-3; Sequence=VSP_005406, VSP_005407;
Name=4;
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SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00114; TRYPSIN HIS; 1.
PROSITE; PS001135; TRYPSIN HIS; 1.
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 EMBL; AF242195; AAG09469.1; -.
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EMBL; AF243527; AAG33354.1; -.
EMBL; X75363; CAA53145.1; ALT_SEQ.
HSSOP; POO760; 1EZX.
MEROPS; SO1.081; -.
Genew; HGNC;20453; KLK15.
 InterPro; IPR009003; Pept Ser Cys.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
 regulation in prostate cancer."; J. Biol. Chem. 276:53-61(2001).
 Pfam, PF00089, Trypsin, 1.
 Gene 257:119-130(2000).
 TISSUE=Brain;
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63 CQSRFWRVRLGEHNLRKRDGPEQLRTTSRVIPHPRY--EARSHRNDIMLLRLVQPARLNP 120
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 181 DKSYPGRLTNTMVCAGAEGRGAESCEGDSGGPLVCGGILQGIVSWGDV-PCDNTTKPGVY
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MEDLIME=20255460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
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Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.;
"CDNA cloning and tissue-specific splicing variants of mouse hippostasin/TLSP (PRS220).";
hippostasin/TLSP (PRS220).";
Biochim. Biophys. Acta 1494:206-210(2000).
 Gaps
 Potential.
Activation peptide (Potential).
Kallikrein 15.
Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
N-linked (GlcNAc. .) (Potential).
Missing (in isoform 4).
FridevSp DosAd4.
Missing (in isoform 2).
/FTIGeVSp_00540s.
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
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Yamaguoth N., Mitsui S.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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 /FTId=VSP_005405.
V -> G (in isoform 3).
/FTId=VSP_005406.
 Last sequence update)
Last annotation update)
 43.6%; Score 599; DB 1; ilarity 47.1%; Pred. No. 4.2e-40; Conservative 32; Mismatches 88
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 Created)
 PRT;
 TYICKYVDWIRMIMRNN 248
 240 TKVCHYLEWIRETMKRN 256
 160 S
28087 MW;
 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26,
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 16
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106
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206
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 161
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 Best Local Similarity
Matches 121; Conserv
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 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 .gnal; Zymogen.
 162
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 Hippostasin.
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 61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPV 118
 119 RVISSVOPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPG 178
 120 FFTRAVQPLTLSPHCVAAGTSCLISGWGTTSSPQLRLPHSLRCANVSIIEHKECEKAYPG 179
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 180 NITDIMLCASVRKEGKDSCQGDSGGPLVCNGSLQGIISWGQ-DPCAVTRKPGVYTKVCKY 238
 9
 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLJDHRWVLTA
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
25-07-2004 (TrEMBLrel. 28, Last annotation update)
Hippostasin prostate type (Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310015108 product:protease, serine, 20, full insert sequence) (Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310040F07
Product:protease, serine, 20, full insert sequence).
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MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
 5,
 Length 249;
 Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N., "CDNA cloning and tissue-specific splicing variants of mouse hippostasin/TLSP (PRSS20).";
 GO; GO: 0005615; C: extracellular space; TAS.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001214; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001314; Pept Ser_Gys.
Pfam; PR00182; CHYMOTRYPSIN.
SWART; SM00020; TTYP SFC; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Protease; Serime protease.
SEQUENCE 249 AA; 27604 MM; F9FF9CB457D727D5 CRC64;
 95; Indels
 Yamaguchi N., Mitsui S.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
[3]
 DB 2;
 .4e-40;
 43.5%; Sco. No. 5...
47.0%; Pred. No. 5...
**** 33; Mismatches
 Biochim. Biophys. Acta 1494:206-210(2000)
 MEROPS; S01.257; -.
MGD; MGI:1929977; 2310015108Rik.
EMBL; AB016226; BAA88825.1;
 Matches 118; Conservative
 238 VDWIRMIMRNN 248
 239 FNWIHEVMRNN 249
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 Best Local Similarity
 Mus musculus (Mouse).
 P00760; 1EZX.
 SEQUENCE FROM N.A.
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 TISSUE=Prostate,
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 1 MGLSIFLLLCVIGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
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 Query Match 43.5%; Score 597.5; DB 2; Length 276; Best Local Similarity 47.0%; Pred. No. 6e-40; Matches 118; Conservative 33; Mismatches 95; Indels 5;
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PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 276 AA; 30753 MW; 90BDC03A8ABI78D6 CRC64;
 238 VDWIRMIMRNN 248
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266 FNWIHEVMRNN 276
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